POLLINATION PATTERNS IN SAFFLOWER

(*Carthamus tinctorius* L.)

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ABSTRACT

The influence of environmental conditions on safflower *(Carthamus tinctorius* L.*)* floret characters and insects were studied in relation to pollination in this species.

Insect activity was studied in a field experiment using part of the world germplasm collection of safflower. Honey bees were the most likely cross-pollinators. Activity of honey bees did not vary between genotypes studied. Correlations between insect and weather data were mainly non-significant.

A sample of 12 genotypes from the world collection were intensively studied in controlled environment rooms. Single plants were used as plots in a randomised complete block design, in each of four environments (day/night temperature treatments of 28/22°c and 24/18°c in combination with vapour pressure deficit treatments of -1.0 and -0.4 kPa). Environments reflected New Zealand summer conditions.

Coefficients of variation were acceptable for most characters. Considerable genotypic, environmental and genotype-environment interaction variances were observed for most characters. Standardised partial regression coefficients (path coefficients) and principal factors were utilized to determine the characters most important in self-pollination of safflower. These characters were: the length of the style-stigma; the rate of style-stigma growth; the rate of corolla tube growth and amounts of viable pollen present during floret expansion.

Pollen viabilities remained high for the longest time in higher humidity environments. Large amounts of pollen were produced at the lower humidity. Floral parts were largest in the cool dry environment, however rates of style-stigma and corolla expansion were greater at lower temperatures. It was concluded that synchronization of the rates of style-stigma and corolla tube growth were important in maintaining the stigma in close proximity to viable pollen, and thus promoting the possibility of self-pollination. Self-pollination was greatest at the lower temperature and lower humidity.

The basic self-pollination mechanism observed was in agreement with previous authors.

A number of improvements for future controlled environment experiments involving safflower were suggested.

The implications of pollination of safflower on germplasm collection and maintenance, artificial crossing and breeding plans were discussed.

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INTRODUCTION

Safflower *(Carthamus tinctorius* L.) is an errect annual thistle-like herb adapted to semi-arid areas. It has a deeply penetrating taproot (Henderson, 1962) and strong stem with many appressed or spreading branches (Leon and Knowles, 1964) each terminating in a capitulum. Lower leaves of most genotypes are entire and free of spines. Upper leaves vary from spineless to strongly spined (Rao, 1943; Claassen, 1952). A short rosette phase may exist (Zimmerman, 1973). Height at maturity ranges from 0.5m to 1.5m (Purseglove, 1968). Considerable genotypic variation in morphology exists (Ashri *et al.*,1976). Environmental changes also have considerable impact on morphology (Beech and Norman, 1966).

Safflower is known only in the cultivated form (Wiess, 1971), and is thought to have evolved in the area bounded by the Eastern Mediterranean and the Persian Gulf (Ashri and Knowles, 1960; Hanelt, 1963). Widespread domestication and dispersion have resulted in the plant having had many varied uses, e.g. as a dye, vegetable, cosmetic and medicinal herb (Wiess, 1971; Knowles, 1960a).

Current interest centres on safflower's hydrophobic oil which is light coloured and easily clarified. Non-yellowing properties have led to its widespread use in paints and varnishes. Meal made from seed is also utilised as a protein supplement in animal diets (Knowles, 1958). Cultivars exist today with improved oil quality and quantity, disease and insect resistance (Wiess, 1971).

Interest in New Zealand centres on its use as a summer growing oilseed crop for North Island areas prone to drought. Such environments are also associated with high humidities, fogs and late summer rainfall, which lead to disease problems in the crop, and sprouting damage to the seed. Resistance of safflower to *Botrytis cinerea* (the most troublesome disease in N.Z.) and sprouting damage are thought to exist (Knowles, 1958; Kotecha and Zimmerman, 1978).

An effective breeding program is needed to produce cultivars suited to the New Zealand environment. A knowledge of population gene structure within the species is required if selection methods and breeding plans are to be utilized efficiently. To this end a study of pollination patterns in safflower was initiated as past and present pollination patterns influence population structure. The present study consisted of two parts:

A. A field study was conducted to observe insect activity on the crop. The objective was to acquire knowledge of the role played by insect pollinators. The opportunity was taken to study floral characters such as floret morphology, pollen presence and stigmatic extrusion which might be of interest in subsequent studies.

B. The second part consisted of a controlled environment study of plant and floral characters. The objectives were to observe genotypic and environmental differences in characters potentially related to self-pollination; and to determine characters most important in self-pollination. Examples of such characters include amounts and viabilities of pollen, stigma receptivity, corolla characteristics and lengths of flowering.

1 REVIEW OF LITERATURE

1.1 Taxonomic Back Ground of Safflower.

The genus *Carthamus* (first described by Linnaeus in 1735) belongs to the family Asteraceae (Bentham and Hooker) subfamily Tubiliflorae and tribe Cynarae (Harvey and Knowles, 1965). Ashri and Knowles (1960) believe the genus contains approximately 25 valid taxonomic species of which only *C.tinctorius* is of economic importance. The genus is distributed naturally in the Mediterranean and Irano-Turanic floristic region. Its centre of variability is situated in the Western part of the Near East in the Southern Aegeis. A second smaller centre lies in the South Western part of the Mediterranean (Hanelt, 1963).

Classification of the genus is in flux with frequent revision as more information from interspecific crossing experiments is obtained (Estilai and Knowles, 1978). Basic chromosome numbers in *Carthamus* L. are X=10, 11 and 12 (Gregory, 1935; Patel and Narayana, 1935; Estilai and Knowles, 1976). Polyploid species are also present in the genus (Khidir and Knowles 1970 a and b).

Cultivated safflower has twelve pairs of chromosomes. Gregory (1935) reported Coimbatore types with n=10. *C.tinctorius* is closely related to *C.flavescens*, *C.oxyacantha*, and *C.palaestinus*, all of which can be intercrossed to form fully fertile F_2 (Deshpande, 1952; Imrie and Knowles, 1970; Ashri and Knowles, 1960; Ashri and Efron, 1964). These taxa are called species here realising that they can be considered races of one biological species (Claussen *et al.*,1939).

Imrie and Knowles (1970) postulated that *C.tinctorius* evolved concurrently with its wild relatives *C.oxyacantha* and *C.flavescens* which are weeds occupying disturbed habitats associated with man. Ashri and Efron (1964) considered *C.oxyacantha* to be a divergent type, where as *C.tinctorius* had closer affinities to *C.flavescens* and *C.palaestinus*. As *C.palaestinus* grows in habitats not associated with man it was considered to be an old species, and perhaps the progenitor of the others (Ashri and Knowles, 1960; Ashri and Efron, 1964). Evidence of a close genetic relationship between *C.flavescens* and *C.tinctorius* was given weight by the fact that many of the characters by which they differed were under monogenic control (Imrie and Knowles, 1970).

Such close association of the species permits easy transfer of economically important characters such as preharvest seed dormancy (Zimmerman, 1972a), cold tolerance (Zimmerman and Buch, 1977), rust resistance (Zimmer and Urie, 1968), vigour and insect resistance from wild to domesticated species (Knowles, 1977).

Morphological variability in domestic safflower was reviewed by Howard *et al.*(1915)and Sabnis and Phatak (1936).

1.2 Overview of Pollination.

1.2.1 Introduction

Pollination constitutes transference of pollen to the stigma. Factors influencing this process include sexual differentiation, microsporogenesis, macrosporogenesis, structural modifications of flowers and pollen dispersal and ecology.

Pollination mechanisms have decisive bearing upon rational plant breeding procedures in sexually reproducing species, because of the implied fertilisation which follows. Assemblage of new cultivars depends to a large degree on the extent of natural recombination of traits, on genetic uniformity within a population, and on degrees of homozygosity. All are subject to past and present pollination systems. Self-pollinating species tend to be more homogeneous within lines, when compared to cross-pollinating species which are heterogeneneous (Mayo, 1980; Allard, 1960).

A knowledge of pollination mechanisms is necessary in the development of crossing techniques for breeding both open pollinated and hybrid varieties. Cultivar maintenance programs will also be significantly influenced by pollination mechanisms.

Pollination mechanisms are a function of plant, pollinator and environment. All factors interact, making studies difficult.

1.2.2 Plant Factors to be Considered in Pollination Studies

Breeding new cultivars, cultivar maintenance and proper pollination of crops, depend upon synchronization of male and female functions. Chronological adjustment of anther dehiscence and pollen supply to pollen vector activity and stigma receptivity are requisites for successful pollination.

Duration of anther dehiscence differs between species (Percival, 1955). Temperature and relative humidity may regulate it (Meinders and Jones, 1950). It is necessary for pollen to survive under natural conditions from maturation through release and dispersal to germination on a receptive stigma. Separation of male and female functions by time or space as described by Frankel and Galun (1977), must be bridged by an appropriate period of pollen longevity. Over this period, pollen may be exposed to quite severe environmental conditions, but normally this phase is only a matter of minutes or hours. Investigations of pollen physiology, revealed that longevity depends on conditions such as atmospheric humidity, temperature, gas composition of the air and pressure; as well as on pollen vigour. The latter may be modified by plant nutrition, viruses and other pathogens (Frankel and Galun, 1977). Similarly, persistence of stigma receptivity differs between species. Emasculated flowers of self-pollinated species generally show brief persistence of receptivity although optimal environmental conditions may extend receptivity somewhat (Frankel and Galun, 1977).

Much of this information is not available for safflower. It is therefore necessary to glean information from other species of the Asteraceae phylogenetically related to safflower.

1.2.2.1 Pollen

Pollen falls into two cytological types termed binucleate and trinucleate. Within the intine of binucleate pollen is the generative cell and vegetative nucleus. Trinucleate pollen grains have undergone the haploid mitosis of the generative nucleus before dehiscence, to incorporate twin generative nuclei and a single vegetative nucleus. This represents an advanced type, where the pollen grain completes maturation protected by the male sporophyte (Brewbaker, 1959). Such pollen has fully developed mitochondria at dehiscence allowing rapid germination (Hoekstra, 1979). Hoekstra and Bruinsma (1979) concluded that rapid tube initiation and growth was invariably associated with completed or rapidly proceeding protein synthesis. The attainment of the fully developed metabolic state was thought to be more essential than the trinucleate nature, in speed of tube initiation and rapid fertilization (Hoekstra and Bruinsma, 1978).

Several links between self-incompatibility systems and pollen types have been suggested. A summary of these is provided in Table 1.1. Explanations of these phenomena are generally based on metabolic requirements for mitosis of the generative cell prior to shedding in trinucleate pollen.

Phylogenetic trends have been observed for pollen type. Primitive families tend to have binucleate pollen (Brewbaker, 1959). Only in rare instances have both types of pollen been observed in the same species. Brewbaker (1967) commented that 'the uniformity of cytology and morphology of Composite pollen is noteworthy.' All species of the **Asteraceae** investigated by Brewbaker (1957, 1967) had trinucleate pollen.

Table 1.1 Relations of incompatibility type with pollen and pistil characteristics and sites of pollen inhibition.

	Incompatibility System	
	Gametophytic	Sporophytic
Pollen	Binucleate	Trinucleate
	Lesser developed mitochondria at dehiscence	Fully developed mitochondria at dehiscence
	Low respiratory rate	High repsiratory rate
	High protein synthesis in lag phase before germination	Low protein synthesis at germination
	Long lived	Short lived
	Ready germination in artificial media	Germination in artificial media difficult controlled hydration required
	Exine has little protein storage	Exine with abundant tapetal protein storage
Stigma	Surface with fluid secretion in the receptive phase	Without fluid secretion; papillae with extracultticular receptor layer
Site of incompatibility inhibition	Tissues of trnasmitting tract or stylar canal	Stigma surface.

(J. Heslop-Harrison, 1978; Hoekstra and Bruinsma, 1979; Hoekstra, 1979)

1.2.2.1.2 Pollen Viability Assay

1.2.2.1.2.1 Germination Assays

In Vivo Methods

Pollen is placed on receptive stigmas and counts are made of pollen tubes which penetrate them. It is assumed no inhibition of pollen growth by the stigma occurs. Stain techniques differentiating between pollen tubes and stylar tissues have been developed (Nebel, 1931; Nair and Narashan, 1963; Pandey and Henry, 1959; Shellhorn *et al.*, 1964).

In Vitro Methods

Growth of pollen on artificial media assumes optimum conditions have been established. Many chemical and physical factors are known to influence optimum pollen germination *in vitro* e.g. boron (Schmucker, 1932 as in Stanley and Linskens, 1974), calcium (Kwack, 1965), magnesium and potassium (Brewbaker and Kwack, 1963) and water (Bar Shalom and Mattson, 1977). Sugar concentration and pH of the media are also critical (Kwack, 1965; Bar Shalom and Mattson, 1977). Much of this information has been gleaned from studies of stigmatic exudates. Style and stigma slices have been incorporated in media (Stanley and Linskens, 1974 report many authors).

Plating techniques are summarized by Stanley and LInskens (1974). Special plating techniques allowing controlled hydration have been outlined by Narasimhan (1963) and Bar Shalom and Mattson (1977).

Such techniques are normally used with species having binucleate pollen types, as trinucleate pollen is generally difficult to germinate on artificial media (Heslop-Harrison, 1978).

1.2.2.1.2.2 Non-germination Assays.

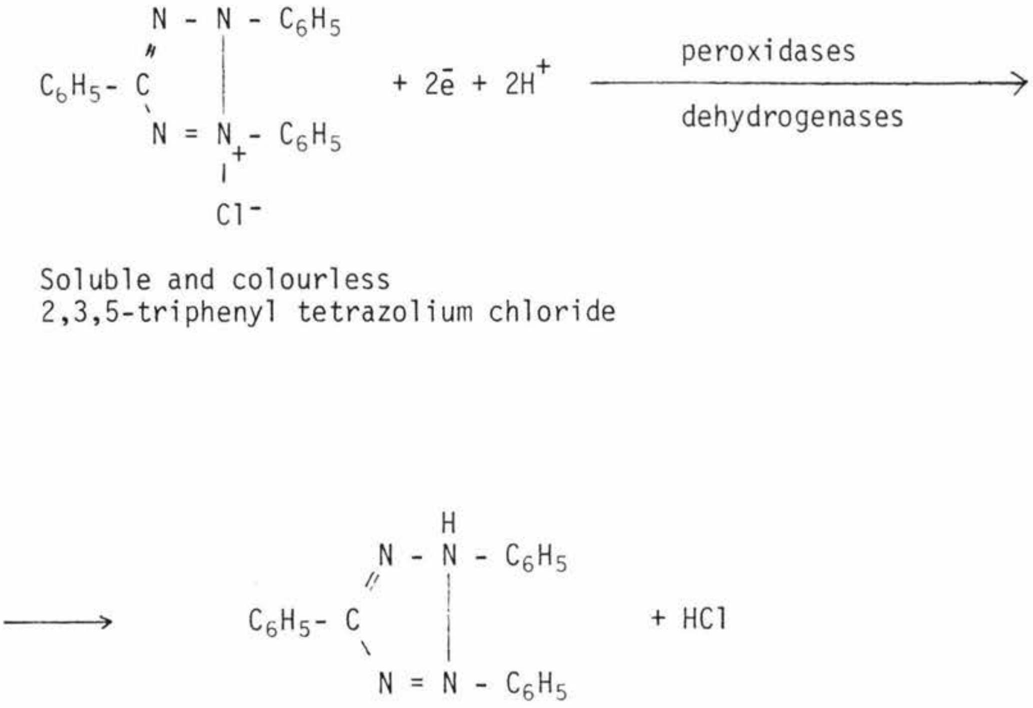
Specific stains such as aniline blue in lactophenol, potassium iodide, and inorganic acids have been used in ascertaining pollen viability. These are now largely outmoded by the redox dyes (Stanley and Linskens, 1974). Such techniques are of use in evaluating viabilities in trinucleate species.

Redox dyes.

Viable pollen contains functioning enzymes. Changes from colourless to coloured state by redox dyes indicate functional enzymes. Tetrazolium salts forming formazan compounds on reduction have been evaluated (Aslam *et al.*,1964; Smith, 1951). The chemical 2,3,5-triphenyl tetrazolium chloride has been widely used (Hamdi and Soliman, 1977; Sarvella, 1964). Other uses include seed testing and tissue culture assay (Towill and Mazur, 1975). The reaction is presented in Figure 1.1. Maximal colour (formazan) production occurs at pH=7.5 (Towill and Mazur, 1975). Kovacik *et al.* (1977) found the tetrazolium technique to give higher viability estimates than *in vitro* germination.

Fluorescent reaction.

Heslop-Harrison and Heslop-Harrison (1970) used fluorescein diacetate hydrolysis by esterase in the pollen grain as a pollen viability index. The reaction was reliant on the functional plasmalemma of the vegetative nuclei.



Soluble and colourless
2,3,5-triphenyl tetrazolium chloride

insoluble red coloured

triphenyl formazan

(Smith, 1951)

Figure 1.1 Reaction of a tetrazolium salt to form a formazan compound

1.2.2.2 The Stigmatic Surface.

Heslop-Harrison and Shivanna (1977) found that members of the Asteraceae have dry stigmas. Receptive cells were concentrated in zones, with unicellular surface papillae. Papillae had a loose extracellular protein coating covering the entire cuticle, called the pellicle. Cracks and fissures readily form in this, on older stigmas (Mattson *et al.*,1974). Radially orientated cutinized rodlets, separated by pectocellulosic wall material, form breaks of the cuticle at papillae tips. These control hydration of the pellicle (Heslop-Harrison *et al.*,1975). Eisikowitch and Woodell (1975) suggest that humidity and water uptake are of utmost importance for pollen germination.

Receptive surfaces of all stigma types almost invariably show cytochemically detectable esterase activity (Matteson *et al.*,1974). Pollen capturing sites can be identified by such activity in complex styles (Heslop-Harrison and Shivanna, 1977). Intense non-specific esterase activity in the pellicle, concentrated toward papillae tips of Asteraceae has been noted (Heslop-Harrison *et al.*,1975). Esterase activity continues from papilla to papilla forming a receptive external sheath.

1.2.2.2.1 Sporophytic Incompatibility Response Mechanism.

de Nettancourt (1977) provides an extensive review of incompatibility systems.

In homomorphic sporophytic incompatibility systems which characterise Asteraceae, behaviour of the pollen is determined by the pollen parent genotype (Heslop-Harrison *et al.*,1975; Heslop-Harrison and Shivanna 1977; Brewbaker, 1959).

The pellicle is the attachment surface for pollen of the Asteraceae. Suitably orientated grains rapidly extract water from the papillae with which they are in contact (Heslop-Harrison *et al.*,1974). Pollen wall materials are released onto the stigma surface. These include exine held proteins and glycoproteins derived from the anther tapetum (and so are of sporophytic origin), and corresponding intine fractions (of gametophytic origin). Sporophytic fractions transfer first (Heslop-Harrison *et al.*,1974). Such emitted proteins bind to the pellicle, being the likely site of primary recognition (Mattson *et al.*,1974). Enzyme activation follows. Activation of callose synthetase in stigma papillae adjacent to incompatible grains leads to callose deposition (Dickinson and Lewis, 1973 a and b), which prevents pollen tube entry. Cutinase activity, eroding the papilla cuticle in anticipation of pollen tube entry results from compatible pollination (Mattson *et al.*,1974).

1.3 Factors Influencing Pollination in Safflower.

1.3.1 Morphology of the Capitulum.

Tubular florets of the disc type are borne in capitula. Capitula are enclosed by a series of involucral bracts. The number, shape and spininess of bracts vary considerably. Numbers of capitula per plant range up to 150, each with diameters of 1.25 to 4 cm. Close spacing and salinity directly affect the number of capitula (Williams, 1962; Francois and Bernstein, 1964; Claassen, 1950).

The number of florets contained in a capitulum normally ranges from 20 to 100, differing with genotype and environment (Claassen, 1950). The receptable of the capitulum is flat or slightly convex, and is covered with abundant bristles (Weiss, 1971).

1.3.2 Floral Differentiation.

Differentiation of floral parts occurs in the succession:- petals, stamens, sepals and carpels (Banerji, 1940). Sepals do not become fully developed but remain as minute angular projections. The gynoecium consists of two free carpels in the early stages. They soon cohere to form a single ovary and style, but remain free at the apex. The resultant floret is syncarpous (Banerji, 1940).

1.3.3 Floret Morphology.

Hermaphrodite florets of the disc type are tube like with a five point expanded tip to the corolla tube (Knowles, 1955). Individual florets are provided with sepals which remain as minute angular projections (Banerji, 1940). The five fused anthers lie inside the corolla, and are attached by very short filaments to the neck of the corolla tube (Claassen, 1950). Scattered multicellular hairs occur at the junction of the filament and anther. At maturity the anther column rises above the spreading corolla segments as a bright yellow cylindrical structure. Introrse anther dehiscence commences at the tip of the tube (Claassen, 1950). Before flowering the bifid brushlike stigma is enclosed by the anther column. The stigma is coated with many appressed short hairs on its outer surface, which progressively become shorter towards the apex. These hairs are single-celled papillae, having a bulbous base (Weiss, 1971). A collar of outward flexing hairs approximately four times longer than the rest is situated at the base of the stigma (Ebert and Knowles, 1966). Howard *et al.*(1915) considered the collar of outward flexing hairs to be part of the style, and not part of the stigma as recent workers suggest.

The nectary occurs in the form of a ring at the base of the corolla tube surrounding the style (Banerji, 1940). Nectar accumulates filling the tube (Leppik, 1977). It is gathered by pollinators from the filaments at the base of the anther column (Boch, 1961; McGregor, 1976). Extrafloral nectaries may exist in the area between the florets and bracts (Langridge and Goodman, 1980).

1.3.4. Flowering.

Flowering commences on the primary stem first. As soon as secondary branches have completed their growth and carried capitula into the flowering region, flowers begin to open. Other secondary and tertiary branches continue the process in regular fashion (Howard *et al.*,1915); the upper branches first and lower ones last (Claassen, 1950).

Florets at the margin of the head open first and flowering proceeds centripetally (Howard *et al.*,1915), 3-6 days being required for its completion (Banerji, 1940; Claassen, 1950). Considering all capitula on the plant, flowering may extend over a period of 10 to 40 days (Knowles, 1955).

High temperatures, salinity and application of artificial growth promoting substances accelerate the onset of flowering (Weiss, 1971; Francois and Bernstein, 1964; Yermanos and Knowles, 1960).

1.3.5 Safflower Microspore Development.

Young microspores at first lie enclosed in a mucilaginous material, which gradually disorganizes leaving them free in the anther. At first they appear shrunken, but soon they become rounded, and the exine thickens slightly and develops many spine-like projections. Three germpores exist on the exine. Tapetal cell growth ends in the formation of a plasmodium, filling the anther cavity. As the plasmodium disintegrates some is incorporated on the exine (Banerji, 1940).

Detailed information regarding the structure of the exine is provided by Skvarla *et al.*(1977) and Dittrich (1977).

Pollen cytology is discussed in Section 1.3.7.

1.3.6 Pollination Mechanism.

Three patterns of floret opening have so far been outlined in the literature.

1. Howard *et al.*(1915) observed that florets usually began to open in the early morning, the process continuing to midday. A few however opened in the afternoon. While still in the bud stage, the style elongated, and the upper portion of the stigma usually emerged from the anther column before pollen was liberated. Stylar elongation was due to cell division and/or cell elongation (Banerji, 1940). Soon after extrusion of the stigma commenced, the corolla opened and anther dehiscence took place, while the base of the stigma was still within the tube. Continued style elongation enabled the numerous hairs to sweep pollen from the anther tube. Examination of the upper portion of the stigmas showed most to be free of pollen. In only a few cases did dehiscence occur before commencement of extrusion.

2. Claassen (1950) found dehiscence prior to extrusion to be the normal pattern. Florets that were to open on a given day had begun elongation by sunrise. Anthesis occurred soon after sunrise, as the stigma emerged from the anther tube. By the time style elongation was complete, a coating of the florets own pollen entirely

covered the stigma.

3. Ebert and Knowles (1966) found anthesis occurred sometime before the floret emerged from within the involucral bracts. Some stigmas extended beyond anthers at dehiscence. Emergence of florets commenced early in the evening and continued into the early morning. As florets were exposed the corolla tube opened and styles began a brief period of rapid elongation, during which pollen adhered to the hairs at the base of the stigma. Stigma size increased by a half over this period.

The small variations in the pollinating mechanisms reported may be due in part to environmental effects on anther dehiscence timing.

Florets remain open for 1 to 2 days (Howard *et al.*,1915). The stigma may also remain receptive for this period. Despite intimate contact between the stigma and the florets own pollen, there is still every chance of cross-pollination by insects (Wiess, 1971), and consequent cross-fertilization with or without self-incompatibility mechanisms operating.

To date most authors have concluded that cultivated safflower is self-pollinated, with a potential for natural crossing (Howard *et al.*, 1910; Howard *et al.*,1915; Claassen, 1950; Kadam and Patankar, 1958). Some authors have stated that it is cross-pollinated (Karve *et al.*,1976).

1.3.7 Safflower Pollen and Pollen Tube Cytology and Endosperm Development.

A comprehensive examination of microsporogenesis in safflower has been provided by Banerji (1940). Pollen was found to be binucleate, but showed prophasic changes in the nuclei. Imrie and Knowles (1971) reported the genus *Carthamus* to have sporophytic incompatibility. Brewbaker (1957) had reported the trend in Asteraceae to be towards sporophytic incompatibility and trinucleate pollen. Banerji (1940) noted that earlier authors had observed trinucleate pollen in the closely related genera *Carduus* and *Centaurea*.

Before fertilization, the vegetative nucleus degenerated, then the pollen tube entered the embryo sac via the micropyle. The embryo sac corresponds to the normal type, being monosporic and 8-nucleate (Banerji, 1940; Maheshwari, 1950). Two small nuclei were observed in the swollen tip of the pollen tube; these were generative nuclei. Thus pollen may be released in the binucleate condition, with mitosis of the generative nuclei occurring during pollen tube growth.

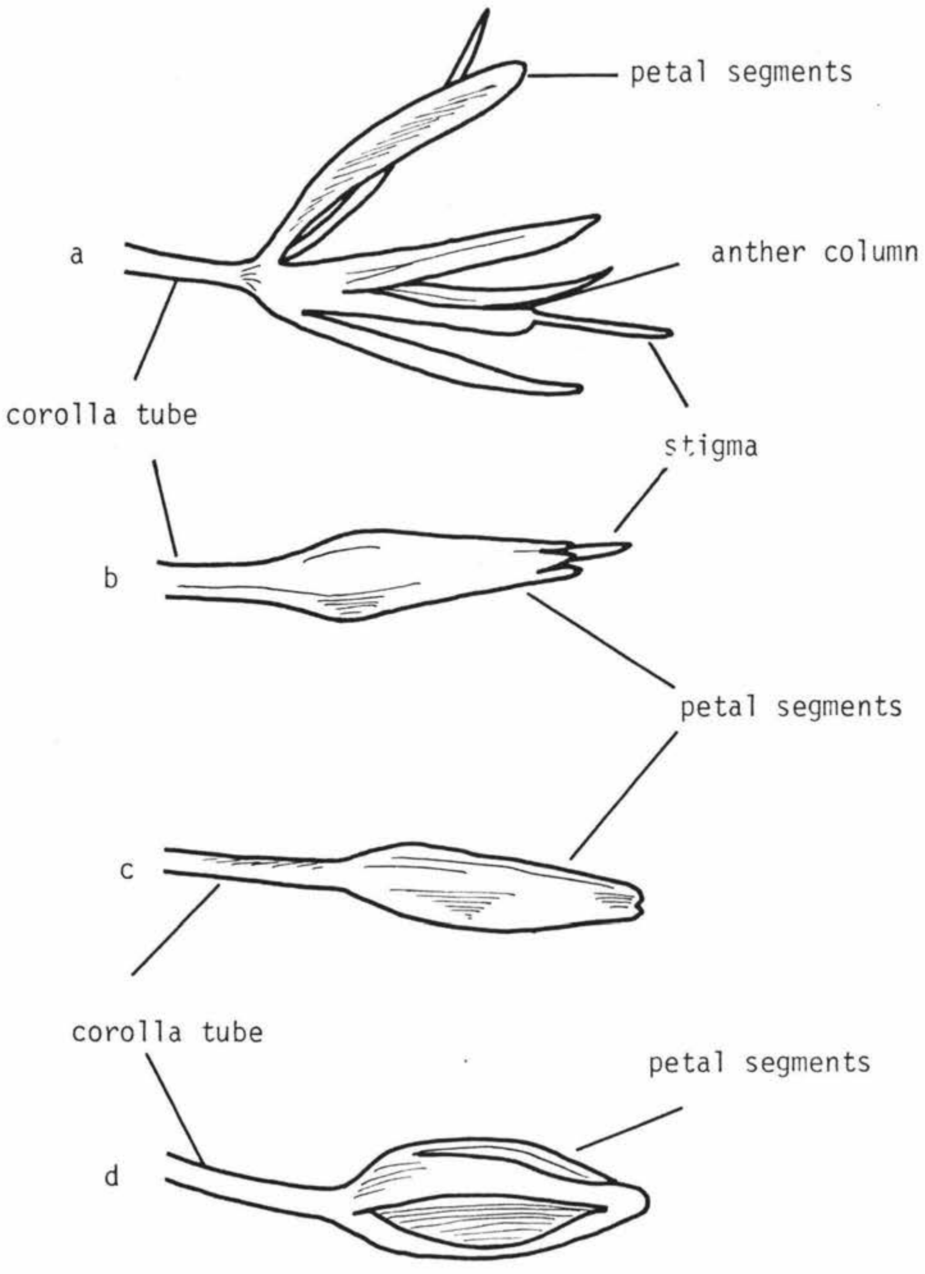
Achene endosperm of the nuclear type grew by mitotic division. Endosperm chromosome number was greater than 2n (Banerji, 1940). It is from the endosperm that oil is derived.

1.3.8 Pollination Controls

1.3.8.1. Closed Flower Condition

Three closed flower types have been identified in *C. tinctorius* (Dillé and Knowles,1975). The term closed flower, designates flowers which do not open, but may or may not be strictly autogamous (details follow).

The closed flower phenomenon results from corolla fusion, caused by recessive alleles. In the arrowhead type, insects were able to modify the phenotype by loosening one or more corolla segments during pollination. High winds had a similar effect. Bar and cage types completely precluded crossing by insects. (Refer to Figure 1.2).



a Normal safflower floret
b Arrow head closed flower
c Bar closed flower
d Caged closed flower (corolla segments slightly separated)

(adapted from Dillé and Knowles, 1975)

Figure 1.2 Types of closed flower in safflower

The closed flower phenotype may have some value in forcing self-pollination. Genetic nurseries could be handled without the need for bagging.

1.3.8.2 Thin-hull Gene

A recessive mutant called the thin-hull gene was discovered by Rubis (1962) (cited by Rubis *et al.*, 1966). It reduces hull percentage and affects several other plant characters including anther dehiscence. In homozygous plants anther dehiscence is delayed several hours and the stigma protrudes from the anther column free of pollen. Delayed anther dehiscence results in a functionally male sterile plant (Ebert and Knowles, 1968). Most thin-hull lines are low in selfed seed set and high in crossability (Urie and Zimmer 1970b); however with several cycles of recurrent selection, lines with high selfed seed set and low crossability have been developed (Rubis *et al.*, 1966).

Bees have been used to cross normal and thin-hull lines to produce F_1 hybrids (Rubis 1970b). Some limited self-fertility (required for maintenance of the female line), results in some selfing and sibbing in the hybrid seed field, leading to seedlots frequently containing more than 30% female selfs. High percentages of such plants decrease potential yield (Urie and Zimmer, 1970a).

1.3.8.3 Male Sterility

Two safflower lines segregating for genetic male sterility have been isolated (Heaton and Knowles, 1980). Control is via a single nuclear recessive gene (Heaton *et al.*, 1979). The ratio of normal to male sterile plants is 3:1 in the F_2 and 1:1 in backcross generations. The lines are maintained as a source of male sterility genes for the production of hybrid seed, by crossing heterozygous parental lines with the homozygous male sterile line. Pollen viability of the heterozygote is normal. Expression of male sterility is complete, with arrested pollen development, manifested by visible anther collapse. Female fertility is nearly normal in the male sterile plants. Insect pollinated male sterile plants averaged 93% of achene yield of adjacent isogenic male fertile plants. Linkage with other characters has not been found. Male sterile plants are indistinguishable from male fertile plants up to flowering (Heaton *et al.*, 1979).

Cytoplasmic male sterility has also been found in *C. alexandrinus*. Estilai (1977) found that this species was not a good candidate for transferring desirable genes to cultivated safflower.

1.3.8.4 Complete Sterility

Sterility in some instances has complicated breeding programs by showing up in segregating populations (Carapentian and Knowles, 1976). Both male and female gametophytes are affected.

The most common form, reported by Claassen (1952), resulted from a single recessive gene. Flowers appeared normal at flowering but had few or no seeds. Seed set was not increased by artificial pollination. Carapentian and Knowles (1976) proposed a three gene hypothesis. Sterility occurred when a homozygous recessive allel at the A locus, combined with a homozygous recessive allele at the B or C loci. Earlier work supporting monogenic control could be explained in terms of the three gene hypothesis. Carapentian and Rupert (1977) postulated that such sterility was caused by interference with some component essential for normal mieosis.

Other types have been reported. Deshpande (1940) and Claassen

(1952) found a sterile type having a single terminal head without florets; this was determined by a single recessive gene. Roa (1943) studied a rosette type with close set radial leaves, developing into tall late plants, with inheritance via a simple recessive gene. Sterility due to lack of normal development was observed by Richaria (1941) as reported by Ebert and Knowles (1966). Ebert and Knowles (1966) reported a further type where plants developed young flowering buds, but only a few florets formed. They reported that data of Ebert (1964) suggested monogenic inheritance.

1.3.8.5 Bagging Treatments

Howard *et al.* (1915) observed little seed set under parchment paper bags, compared with free flowering capitula. When muslin or mosquito net were used this difference largely disappeared. Further experimentation using lamp chimneys to increase humidity, revealed an inhibiting effect on seed set. Genotype differences in seed set under parchment paper bags were observed.

Differences in seed set, resulting from bagging with different materials was noted by Patil and Chavan (1958) (cited by Wiess, 1971). Percentages of seed set for three types of bag were: butter paper 90, muslin cloth 85.3 and newspaper 71.9, compared to a control with no bag.

Zimmerman (1972b) found seed yield depression to be most pronounced when capitula were subjected to high temperatures and humidities during pre-anthesis and anthesis. Bagging materials may increase temperatures and humidities within the bag. Cultivar differences in tolerance to high temperature and humidity during flowering were observed (Zimmerman 1972b, 1978). This may in part explain the genotype differences in seed set under bags.

Pruning off of side branches improved seed set under newspaper bags to a level comparable to unbagged heads. The common practice of trimming bracts off to allow use of smaller bags, and to make handling easier, had no effect on seed set (Karve *et al.*,1976).

1.3.8.6 Artificial Crossing

Several methods of emasculating safflower exist. Wiess (1971) summarizes the methods of Claassen (1950); Knowles (1958) and Chavan (1961). All the techniques involve removal of anthers the afternoon prior to the morning of floret elongation and stigma emergence. Bracts are first removed from heads which are expected to open the following day. Only the outer whorl of florets was emasculated. Claassen (1950) split and removed the petal segments, before removing the anthers. Knowles (1958) squeezed the floret just below the attachment of the anthers with sharp tweezers, then gently slipped the corolla segments and anther tube off the style. This technique minimized the amount of escaped pollen. Chavan (1961) (after Wiess, 1971) removed the entire corolla tube complete with anthers. A rinse in 57% ethanol was used if pollen escaped during emasculation.

Controlled pollination was conducted when stigmas had elongated. As noted in Section 1.3.8.5, bags used to prevent further crossing by natural means, may have a detrimental effect on seed set.

Claassen (1950) reported on the relative efficiency of artificially crossing safflower. Emasculations conducted on 298 capitula resulted in 228 setting 1 or more seeds after crossing. The average number of seeds per capitulum which set seed was only 6.2.

1.3.8.7 Isolation of Breeding Fields

Isolation of breeding fields is required because of natural crossing. In India where insects are not considered to be such active pollinating agents 30 metres with a grain crop between was considered adequate to isolate improved genotypes (Kadam and Patankar, 1942). In South Africa a minimum of 200 m has been recommended while in the U.S.A. 200 to 250 m is suggested (Weiss, 1971).

Co-evolution with pollinating insects may have occurred in India. Active cross-pollination by such species would have been expected. Isolation distances do not reflect this. It is therefore probable that a large degree of self-pollination occurs.

1.3.8.8 Pollination/Fertilization Control: Self-incompatibility

Self-incompatibility systems are means of eliminating homozygosity, (Pandey, 1974) and are regarded as outcrossing mechanisms (de Nettancourt, 1977). The genus *Carthamus* L. has a homomorphic sporophytic self-incompatibility system. The genetics of such a system have been studied in the wild relatives of *C. tinctorius*. *C. flavescens* has a six allele, single locus system (Imrie and Knowles, 1971). The S_f allele of self-compatibility in *C. tinctorius* is dominant to two of the self-incompatibility alleles of *C. flavescens*. There was evidence that the dominance relationship was temperature sensitive. de Nettancourt (1977) has summarized mechanisms of incompatability breakdown. Ramanamurthy (1963), as reported by Imrie and Knowles (1971), found *C. oxyacantha* to have a single locus system with eight alleles of which one was for self-compatibility. This S_f allele was recessive to all others in this species.

Imrie *et al.* (1972) studied genetic mechanisms of maintaining such incompatiblity systems by computer simulation. Maintenance was enhanced by increased population size, and particularly by migration, where alleles lost from one local population could be re-introduced from adjacent populations.

Self-compatibility in *C. tinctorius* has most likely resulted from selection by man, during the domestication of this species. Changes in the mating system could be explored with a view to improving crop yield, as successful weedy relatives of *C. tinctorius* are cross-pollinated. (Knowles, 1977).

All artificially produced polyploids have been self-incompatible (Khidir, 1969; Harvey and Knowles, 1965). Self-incompatible species have increased numbers of heads compared with self-compatible ones. (Schank and Knowles, 1964; Khidir, 1966 after Khidir, 1969).

1.4 The Influence of Pollen Vectors on Safflower

1.4.1 Natural Crossing in Safflower

In the U.S.A. Claassen (1950) demonstrated genotypic differences in natural crossing ranging from 0 to 100%. Most plants were outcrossed from 5 to 40%. Within line variation in natural crossing rate was also large. Plants having a high degree of natural crossing tended to have low self seed yield, and their progenies showed heterosis in outcrosses. Such lines could be utilised in the production of synthetic or hybrid varieties. Under screened glasshouse conditions where insects were eliminated, no natural crossing occurred. Claassen (1950) suggested that plants with low natural crossing were fertilized earlier in the day, before insects were active; or they had faster pollen tube growth.

Such genotypic differences in natural crossing among lines of safflower may reflect indirect genetic effects acting on pollinators (e.g. flower colour, nectar secretion, odours) and/or internal polygenic sterility mechanisms acting on the plant.

In India, natural crossing ranged from 11.5 to 27%, with an average of 16.5% (Howard *et al.*, 1915). Kadam and Patankar (1958) recorded a range of 1.85 to 28.24% with an average of 10% for their most crossable line, and a range of 1.48 to 2.28% for their remaining lines which had similar crossing percentage; for six white flowered lines grown approximately 14 m from an orange flowered tester. De and Dalal (1976) recorded 1.9% natural crossing in cultivar Nagpur-7.

1.4.2 Pollen Vectors of Safflower

The majority of research reports on safflower pollen vectors, have come from areas outside the natural range of the species. As a result the plant is exposed to new vectors which have not necessarily evolved with it. These vectors may or may not work pollination mechanisms correctly. (Faegri and Van der Pijl, 1966).

1.4.2.1 Abiotic Vectors: - Wind.

Slides covered with a thin film of vaseline were placed at different heights, angles and directions in a *Carthamus* L. species nursery by Ashri (1957) (as reported by Wiess, 1971). Examination of the slides showed wind to be a negligible pollinating agent. Claassen (1950) conducted similar trials, but did not collect any pollen when slides were placed at 75 and 130 cm above the ground. Groups of four or five pollen grains which became attached to slides at 45 cm above the ground were considered to have dropped from florets directly above. With low wind velocity aggregations of pollen were often visible on the outer involucral bracts.

Langridge and Goodman (1980) using a rotorod sampler observed means of 17.2 grains m^{-3} of air in uncaged plots and 8.4 grains m^{-3} in caged plots, at 30 cm above the crop. The range over caging treatments was 0 to 45.5 grains m^{-3}. Differences were not significant. They suggested that wind may play a small part in the pollination of the cultivar Gila.

Although pollen transfer by wind appears to involve the same proportions of binulceate and trinucleate pollen types, Brewbaker (1959) predicted that trinucleate grains would fare less well in long distance wind dispersal, based on the correlates listed in Table 1.1. The adequacy of short isolation distances with trinucleate pollen species like maize, sugarbeet and raddish appears to confirm this.

1.4.2.2 Biotic Vectors: - Insects

Large numbers of insects are attracted to safflower during flowering, due to the abundant supply of nectar and pollen (Rubis *et al.*, 1966).

Many potential pollinators have been reported on safflower but, in most cases, the domestic honey bee *Apis mellifera* is the most frequent visitor (Claassen, 1950; Boch, 1961; Eckert, 1962; Levin and Butler, 1966; Langridge and Goodman, 1980). Claassen (1950) reported several other species on safflower capitula in Nebraska of which *Halictus pictus, Agapostemon radiatus* (bees) and *Chauliognath basalis* (beetle) were most common after honey bees. In India Howard *et al.* (1915) noted the presence of bees on safflower. Forty species of North American native Hymenoptera were reported by Butler *et al.* (1966) to visit safflower in Arizona. Twenty-five percent of these species were represented by a single specimen. Levin and Butler (1966) indicated that *Melissodes* spp and *Agapostemon* spp were the most frequent native bees. Boch (1961) found 95% of native bees to be bumble bees. Solitary bees constituted the remaining 5%. Barbier and Nadir (1976) noted numerous Hymenoptera on safflower in France. Australian native bees of *Lasioglossum* spp. (Halictidae) were observed by Langridge and Goodman (1980).

Eckert (1962) noted solitary butterflies, wasps and other insects visiting safflower. Boch (1961) observed Syrphid flies; which were noted along with other Diptera by Langridge and Goodman (1980). *Lygus* species have also been involved with pollination in safflower (Scott, 1978).

1.4.3 Response of Safflower Yield to Insects

The importance of the relationship between pollinator and genotype can be directly related to the degree of self-pollination. In commercial cultivars a high degree of self-fertility exists in order to achieve stable yields over environments where pollinator activity may vary (Rubis 1970a). Examples of such cultivars include Gila and Rio with high self-fertility at 85 to 95%, and Dart and Rio with self-fertility at 75 to 80%. Low yields associated with low self-fertility in other cultivars could be overcome by using beehives in the fields. Appropriate management techniques to ensure a hive deficit of pollen, would increase the number of bees seeking pollen, and thereby improve cross-pollination (Roberts pers. comm.) Knowles and Miller (1965) (reported by McGregor, 1976) suggested that because safflower was not wind pollinated abundant pollinators would increase yields in pollen deficient cultivars. Introduction of insects and a pollen source caused yield increases in thin-hull lines. (Rubis *et al.*,1966).

Claassen (1950) found no difference in the degree of natural crossing at two sites in Nebraska; implying that pollinator activity did not differ between the sites. Langridge and Goodman (1980) found insects to have no influence on cultivar Gila yield in Australia. Barbier and Nadir (1976) in France, recorded improved yield in the presence of insects for the same cultivar. Denis and Rubis (1966) (as reported by McGregor 1976); Rubis (1962) (after Rubis *et al.*,1966) obtained similar results in the U.S.A. The variation of response in cultivar Gila may be due to two factors, genotype-environment interaction, or hive management. The existence of genotype - environment interaction for self-fertility could explain recorded differences in yield improvement by insect pollination. Alternatively hive requirements, and climatic conditions may have influenced pollinator foraging.

Boch (1961) demonstrated a 47% increase in yield of cultivar "Selection Ottawa-8", when insects were unrestricted. Similar results were obtained by Eckert (1962) when cultivar N-8 with low self-fertility and N-6 with high self-fertility were exposed to insects in open plots and excluded from insects in caged plots. Substantial increases in the number of seeds per head in open plots of N-8 occurred, but no difference in N-6.

1.4.4 Relative Efficiency of Insect Pollinators.

Levin *et al.* (1967) confined various insect species in sleeve cages on safflower and observed the percentage crossing, using recessive flower colour as a guide. Table 1.2 shows the results. Sleeve cage size and age of pollinators influence behaviour and may bias results. Such results should not be extrapolated to the open field. Young bees removed from the hive before their first flight would react better to confined environments, than older bees that had already foraged. (Roberts pers. comm.)

The crossing observed by Levin *et al.* (1967) in the control was thought to be due to manipulation of the heads for bagging. Table 1.2 indicates that Hymenopterous species (*Apis mellifera, Polistes exclamans* and Halictidae) achieved the most cross-pollination.

It remains unknown whether honey bees collecting nectar only are less effective pollinators than pollen gatherers (Boch, 1961).

After observing the behaviour of Syrphid flies and other Diptera, Langridge and Goodman (1980) concluded that these insects were not significant pollinators in this crop.

Table 1.2 Pollination of caged safflower by confined insects (Levin *et al*., 1967)

Insect species	Insects/ cage	No of cages	Total No of plants	Percentage crossing
Hippodamia convergens	4	11	96	10
Lygus hesperus	6	11	117	28
Notoxus calcaratus	4	10	92	2
Apis mellifera	3	13	314	56
Halictidae	2	4	94	35
Polistes exclamans	2	6	132	53
Control	0	14	143	10

The female parent genotype was a thin-hull line with orange flower. The male parent a yellow flowered normal type.

1.4.5 Insect Activity Patterns

1.4.5.1 Activity of the Domestic Honey Bee *(Apis mellifera)*

Table 1.3 gives a summary of the peak honey bee activity times. Generally activity occurs during early or mid morning. Boch (1961) observed that peak honey bee activity coincided with peak nectar sugar concentrations (as shown in Table 1.4).

Individual honey bees seek either nectar or pollen at any one time. If pollen is inadvertently collected by nectar foragers it is packed and returned to the hive. Pollen foragers seek only pollen. Bumble bees collect both simultaneously. (Faegri and Van der Pijl, 1966). Levin and Butler(1966) observed more nectar foragers than pollen foragers on safflower. Langridge and Goodman (1980) found 92.2% of bees present to be nectar foragers. Eckert (1962) found most bees had pollen loads. Such variations are likely to reflect hive requirements at the time of observation.

It is generally conceded that variation in honey bee activity is caused by changes in relative attractiveness of the plant to the foraging bee. If this is true, the attractiveness of safflower relative to other crops blooming at the same time must have been greatest in the morning and decreased as the day progressed (Boch, 1961). Rubis (1970b) predicted that preferences between plant species would affect the population size of bees available for pollination, especially at the beginning of the flowering season. Variation in attractiveness may have been caused by changes in safflower's own pollen and nectar yields. Subjective estimates of pollen and nectar available indicated to Boch (1961) that during peak visitation the volume of accumulated nectar and pollen rapidly declined. By noon most had been collected, and thereafter only currently maturing pollen and nectar just secreted

Table 1.3 Times of peak honey bee activity on safflower, reported by various authors.

Country	Time of peak activity	Bees seeking	Source reference
Victoria, Australia	9.00-11.00	Nectar in the main	Langridge and Goodman (1980)
Ottawa	9.00-11.00	-	Boch (1961)
Arizona, U.S.A.	8.00-10.00	Nectar	Levin and Butler (1966)
	8.00-10.00	Pollen	
Arizona, U.S.A.	9.00- 2.00	Nectar	Rubis *et al.* (1966)
	8.00-10.00	Pollen	

Table 1.4 Number of honey bee visitors observed on five 4-square-yard plots related to nectar sugar concentration, as measured in the stomach using a portable refractometer.

Time	Numbers	Average nectar sugar concentration
6-7 a.m.	1	12.7%
7-8	63	16.8%
8-9	254	26.1%
9-10	425	29.5%
10-11	432	28.6%
11-12	255	25.9%
12-1 p.m.	99	23.8%
1-2	39	23.8%
2-3	7	24.0%
3-4	6	24.7%
4-5	6	
5-6	5	

Boch (1961)

% = percent total solids of nectar in the honey stomachs.

could be collected. Rates of nectar secretion were not determined (Boch, 1961).

Individual bees visited many plants in the course of their foraging activities. The overall average time spent by a bee on one plant was 12.2 seconds. In 88.3% of cases bees visited only one capitulum per plant, 10.9% visited two per plant and 0.3% visited three capitula on the same plant. An average of 9.4 florets per capitulum were visited per bee (Langridge and Goodman, 1980). Thus 'cross-pollination' between florets within the same head is likely to occur. i.e. geitonogamy.

Pollinator activity tends to be much higher at the field perimeter than in the middle (Levin and Butler, 1966). Because of this hives should be spread evenly throughout the field.

Levin and Butler (1966) recorded a range in the number of flowers available per bee of 485 down to 22. These figures represented variations in activity at different locations.

Todd and Reed (1969) found insecticide application early in the morning to reduce pollen gathering and presumably nectar foraging. Pollen yields collected on traps at the hives were reduced from approximately 1kg per day to 0.3 kg/day. The number of pollen foragers was reduced by a half. Butler *et al*.(1966) suggested insecticides for the control of pests should be applied late in the day during diminished pollinator activity, if minimum mortality is sought.

1.4.5.2 Activity of Other Pollinators

North American native bee activity generally coincided with that of honey bees, except that of *Agapostemon* spp which were more active from 7.00 to 8.00 a.m. Prior to 10.30 a.m. native bees were relatively common, however later their percentage was low (Levin and Butler, 1966). Butler *et al*.(1966) found native bees represented 10 to 15% of the pollinators in experimental fields, but in commercial fields constituted 8 to 13% of pollinators, at field edges; and were completely absent from the centre. Honey bees accounted for the remainder. Similar results were obtained by Levin and Butler (1966) with native bees constituting 10.9% of pollinators at field edges and 5.7% in the middle. Overall native bees reached a maximum of 13.3% of pollinators. In Australia, Langridge and Goodman (1980) observed that native bees of Halictidae constituted 21% of visiting insects.

Boch (1961) observed that bumble bees commenced foraging earlier than honey bees; simultaneously gathering nectar and pollen.

Syrphid flies foraged late into the afternoon when attractiveness was not sufficient to maintain honey bee activity (Boch, 1961).

1.5 Plant Factors Influencing Pollinator Activity

Potential pollinators visit plant flowers because of some attraction. Visual and olfactory mechanisms play an initial role in the long distance 'attraction' of insects to plants. Once near or on the plant, localised visual cues play an important role in guiding the insect to its destination; be it food sources such as nectar, pollen and other tissues or protection, or shelter for brood (Faegri and Van der Pijl, 1966). The many factors influencing insect visits to plants are discussed by Percival (1965) and Van der Pijl (1966); only a few will be discussed here.

The major reason for bee visits to flowers appears to be the abundance and sugar concentration of the nectar and chemical attractants in the pollen (Martin and McGregor, 1973).

1.5.1 Visual Cues

1.5.1.1 Visual Cues to the Crop from a Distance

Faegri and Van der Pijl (1966) reported Kugler (1943) as showing the size of flowers to be important in the attraction of bumble bees at distance. Knoll (1921) was reported by Faegri and Van der Pijl (1966) as finding upper and lower size limits for attraction. In the capitulum of many members of the Asteraceae the peripheral ray florets have assumed an attraction function, while central florets have sexual function. The aggregation of florets into capitula has the effect of increasing the "flower" size (Leppik, 1977). Leppik (1977) summarizing previous work, found there was a tendency for insects from the Hymenoptera, Diptera, Lepidoptera and Coleoptera to visit the haplomorphic capitula of the tribe Cynareae (which includes safflower). The shape of the flowers is thought to be important in attracting bumble bees to plants (Percival, 1965).

1.5.1.2 Visual Cues on Safflower Petals

Ultraviolet reflectance and absorbance properties of flowers are usually invisible to man but readily discernable to certain species of insects. Patterns produced by ultraviolet reflectance and absorbance often indicate nectaries. Most knowledge of insect vision is based on the domestic honey bee (*Apis mellifera*) which has visual capacity to see wavelengths from 300-650nm, compared to man with a range from 400-800nm (Von Frisch, 1950).

Freshly opened safflower florets are often yellow, but they soon assume a slight orange tinge, and ultimately become red (depending on genotype) (Shimokoriyama and Hattori, 1955). This reaction involves oxidation of carthamine (a yellow soluble glycoside with λ max = 370nm) to carthamone (a red sparingly soluble quinone with λ max = 445nm) (Seshadri and Thakur, 1960). Polyphenol-oxidase and peroxidase enzymes are involved with optimal pH = 6 (Shimokoriyama and Hattori, 1955).

A further water soluble pigment known as "safflower yellow" is present in florets (Wada, 1953) and must influence flower colour. It is not a precursor of carthamone (Wada, 1953; Shimokoriyama and Hattori, 1955).

Murti *et al.*(1962) isolated to kaempferol glycosides in ivory-white flowers. The major one had two λ max's, one at 267nm and the other one at 345nm. The other kaempferol was not isolated. Carthamine is also present in very small amounts, but large amounts of neo-carthamine (a colourless flavone glycoside) were detected (Seshadri, 1956; Seshadri and Thakur, 1960).

Flavonoid compounds not unlike these have acted as ultraviolet guides on the capitula of Asteraceae (Scogin and Zakar, 1976; Harborne and Smith, 1978). Floret surface microcharacteristics, impart textural qualities to the surface, and may create perceptions of saturated colour zones (Baagoe, 1977). King and Krantz (1975) in a photographic report on the Asteraceae showed most members of the tribe Cynareae to be completely ultraviolet absorbing. In two species of this tribe marginal disc florets were ultraviolet reflective and the inner disc florets ultraviolet abosrbing. Insects after alighting on flowers turn in the search for food to places of more saturated colour (Boagoe, 1977).

Bees visiting white safflower flowers do not move indiscriminately to other colours, but selectively forage white flowers (Rubis, 1970b). There is no apparent selection difference between yellow and orange flowers (Rubis 1970b).

Many categories of flower colour have been recorded in safflower ranging from white to red (Howard *et al.*, 1915; Sabnis and Phatak, 1935; Claassen, 1950). Several authors have investigated inheritance of flower colour in safflower (Roa, 1943; Claassen, 1952; Imrie and Knowles, 1970; Kotecha, 1980). A general consensus is that yellow is dominant to orange which is dominant to white.

1.5.2 Nectar

Sugar concentration in nectar influences flower visitors. Table 1.5 gives examples of preferences displayed by various pollinators. With increasing sugar concentration, nectar becomes more viscous and hence sampling more difficult (Corbett, 1978). Betts (1930) showed honey bee sucking rates to decline when concentrations reached 50-60%. Simpson

Table 1.5 Sugar concentration in the nectar of flowers pollinated by various agents.

Type of pollinator	% sugar concentration	Number of plant species
Moths	8-18	2
Bats	14-16	2
Birds	13-40	7
Butterflies	21-48	2
Honey and bumble bees	10-74	24
Short tongue bees	Higher (*sic*)	
Long tongue flies	Higher still (*sic*)	

From Corbett (1978) who adapted it from Percival (1965).

(1964) found honey bees diluted concentrated solutions with watery saliva, whilst taking it up. Short tongued flies, take nectar at high concentrations and may feed directly on sugar crystals.

Boch (1961) recorded changes in sugar concentration throughout the day on safflower (Table 1.4). Corbett (1978) postulated that flowers dispensed nectar at the right concentration and time in such a way as to interact with local climate; so the concentration was right for specific pollinators. Walker *et al.* (1974) found temperatures to affect quantity of nectars, total sugars, and ratio of constituent sugars in lucerne. Time of day did not affect any nectar characteristic.

During peak honey bee activity on safflower, Boch (1961) recorded a sugar concentration of 29.5% with cultivar 'Selection Ottawa-8". Rubis *et al.* (1966) recorded 19% and 20% for cultivar Gila and a thin - hull line. Both authors used hand held refactometers to determine the sugar concentration from honey bee stomachs. Concentrations of 41% and 45% were obtained in samples directly from the flowers (Rubis *et al.*,1966).

Nectar seeking bees utilize nectar which they collect as an energy source while foraging. Pollen foragers consume honey before leaving the hive. (Roberts, pers. comm.) The differences in nectar concentration between the flower and honey bee stomach, shown by Rubis *et al.* (1966), may indicate dilution of the original nectar by the bee or sugar uptake in the stomach. Nectar is collected from the base of the anther filaments from outside the anther tube, rather than through the tube (McGregor, 1976).

Proportions of various sugars in nectar are characteristic of species (Wykes 1952a). Bees do display preferences for solutions of single sugars or specific combinations (Wykes 1952b).

Volumes and sugar concentrations in nectars may reflect energetic demands of pollinators (Cruden, 1976). Barnes and Furgala (1978) after observing variation in a lucerne germplasm, postulated that it should be possible to select for increased nectar production.

Fluorescence of nectar has been observed (Thorp *et al.*,1975). Scogin (1979) found flavonoid compounds to cause fluorescence in *Fremontia* spp nectar. Fluorescent nectar and nectary guides on petals (Thompson *et al.*,1972), serve as visual cues to nectar.

Nectars containing high levels of amino acids have been associated with flies and butterflies. (Baker and Baker 1973; 1975). These levels may indicate the usual microhabitat of the insects, and therefore serve as attractants.

1.5.3 Pollen

Honey bees collect pollen, which provides a large part of their dietary protein, for brood rearing. Other insects, such as beetles, feed directly on pollen (Faegri and Van der Pijl,1966). Like nectar it is presented during certain times of day. Boch (1961) found most safflower pollen to be released in the morning. Presentation of pollen is of course dependent on the flower being open. Odours may be associated with pollen. Plants which have pollen as the sole attractant for insects frequently produce large amounts, and may develop special anthers, which produce specialized pollen for consumption and for fertilization as in *Lagerstroemia indica* (Faegri and Van der Pijl, 1966).

Stanley and Linskens (1974) discuss many constituents of pollen. The most interesting being the presence of flavonoid and cartenoid colouring pigments. These may serve as visual cues to pollen presence.

Rubis *et al.* (1966) observed the lack of pollen collecting bees on thin-hull lines. Pollen foragers worked only normal lines, whereas nectar collectors worked both lines equally. This indicated that nectar collectors would be wholely responsible for practically all seed set in thin-hull lines with little or no self-fertility.

Variation in pollen colour between species in the genus is known to exist (Khidir, 1970; Ashri and Knowles, 1960).

1.6 Scales of Measurement

Measurement involves assigning numbers to observations in such a way as to be amenable to analysis. Different analyses require different assumptions about underlying distributions. Analysis may yield new information about objects being measured. There are four basic levels of measurement each with specific statistical tests associated with them (Siegel, 1956).

1.6.1 Nominal or Classificatory Scale

Numbers or symbols are used to identify discrete groups in which objects are placed. The scale is divided into a set of mutually exclusive subclasses. Members within any subclass are equivalent in the property being scaled. Subclasses can not be ordered relative to each other (Siegel, 1956). Such scales of measurement apply to dicnotomous and discrete variables (Anderberg, 1973).

1.6.2 Ordinal or Ranking Scale

"Objects in one category of a scale are not just different from the objects in other categories of that scale, but they stand in some kind of relation to them" (Siegel, 1956). The ordinal scale includes not only equivalence within classes, but also a directional relationship amongst classes (Anderberg, 1973).

The assumption is often made that such discrete categories are drawn from some underlying continuous distribution. Observations may fall into discrete categories, but there is an underlying continuum of possible results (Steel and Torrie, 1960; Clifford and Stephenson, 1975).

If the scale is to be regarded as continuous, rather than discrete, the number of categories must be sufficiently large to allow determination of the underlying distribution. If high precision is required class intervals should not be greater than a quarter of the standard deviation (Steel and Torrie, 1960).

1.6.3 Interval Scale

Scales satisfying the requirements of ordinal scales but having distances between categories of constant, known size, are interval scales. (Siegel, 1956). That is they are characterized by a common and constant unit of measurement (Anderberg, 1973). The zero point and unit of measurement are arbitrary (Siegel, 1956). Such scales are continuous.

1.6.4 Ratio Scale

Ratio scales have all the properties of interval scales, and in addition have a true zero point (Anderberg, 1973). The ratio of any two points on the scale is independent of the unit of measurement (Siegel, 1956).

1.7 Parametric and Non-parametric Statistics

Parametric statistical techniques are reliant on validity of their underlying assumptions, particularly those specifying the form of the distribution. Assumptions are normally assumed to hold, leading ultimately to the estimation of population parameters, and significance testing related to hypotheses. Measurement for parametric tests needs to be such that the underlying continuous distribution can be determined, so enabling valid significance testing (Siegel, 1956; Steele and Torrie, 1960).

In many situations the underlying distribution is not easily specified and distribution-free statistics are needed. Assumptions for such non-parametric tests are less rigorous than those for parametric tests, and thus the 'precision' of measurement need not be great. (Siegel, 1956; Steel and Torrie, 1960).

1.7.1 Crosstabulations

When data can be placed into discrete categories according to two or more variables, crosstabulations can be conducted. Measurement of these variables need only be in the nominal scale. No assumptions need be made about underlying distributions. Such tables can be analysed using non-parametric techniques to determine independence; these frequency tables can be summarized by a number of measures of association, which describe the degree to which values of one variable predict or vary with those of another (Steel and Torrie, 1960; Seigel, 1956). Appropriate measures of association are dependent on the scale of measurement (Nie *et al.*, 1975). Several measures of association for nominal scale variables are discussed in the following.

1.7.1.1 Chi-square Test (χ^2)

Chi-square in this instance is used to test the hypothesis of independence between two variables.

The test criterion is given by:

$$\chi^2 = \frac{\Sigma\,(\text{observed-expected})^2}{\text{observed}}, \ (r-1)\ (c-1)\text{df}$$

r = number of rows

c = number of columns.

Expected values are estimated under the assumption that the null hypothesis is true (i.e. independence of variables) for each cell on the table.

A large Chi-square indicates lack of independence of variables but gives little information about the degree of dependence (Steel and Torrie, 1960).

1.7.1.2 Cramer's V (V)

Cramer's V is a measure of association, which adjusts the value of Chi-square for the number of columns and rows in the table, depending on which is the smaller. This gives χ^2 a "degree of association" meaning which was absent before.

$$V = \left(\frac{\chi^2/N}{\min(r-1),(c-1)}\right)^{\frac{1}{2}}$$

Where N is the number of cases,

c is the number of columns,

r is the number of rows.

It ranges from 0 to +1:high values signifying a high degree of association (Nie *et al.*,1975).

1.7.1.3 Contingency Coefficient (C).

When nominal scale variables are used the contingency coefficient is a useful measure of association. Its formula is

$$C = \left(\frac{\chi^2}{\chi^2 + N} \right)^{\frac{1}{2}}$$

where N is the number of cases.

The minimum value attainable is zero indicating independence. Maximal values are a function of the number of categories. For square tables i.e. $k = r$ this value is

$\sqrt{\frac{(k-1)}{k}}$ where k = number of columns

r = number of rows.

The upper limits for rectangular tables i.e. $k \neq r$ are unknown. Therefore comparisons should only be made between tables of the same dimension. (McNemar, 1949).

An observed value for C is significant if the χ^2 for the data is significant (Siegel, 1956).

1.7.1.4 Lambda (λ)

This statistic is a measure of association for contingency tables based on nominal scale variables.

Asymmetric λ measures the percentage of improvement in ability to predict the value of the dependent variable when the value of the independent variable is known. It is assumed the best strategy for prediction is to select the modal category, since this will minimise the number of wrong guesses. Unlike other measures of association, λ is not based on Chi-square.

The maximum value is zero when prediction is made without error.

The symmetric λ is a bi-directional average of asymmetric lambdas. It makes no assumption about which variable is dependent, and measures the overall improvement when prediction is done in both directions (Goodman and Kruskal, 1954).

These statistics are calculated as shown:

$$\text{Asymmetric} \quad \lambda_V = \frac{\sum_k \text{max. } fjk - \text{max.} f.k}{N - \text{max.} f.k.}$$

$$\text{Symmetric} \quad \lambda = \frac{\sum_k \text{max. } fjk + \sum_j \text{max. } fjk - \text{max.} f.k - \text{max.} fj.}{2N - \text{max.} f.k - \text{max.} fj.}$$

where V is the dependent variable,

$\sum_k$ max.fjk is the sum of the maximum values of the cell frequencies in each column.

$\sum_j$ max.fjk is the sum of the maximum values of the cell frequencies in each row.

max.f.k is the maximum value of the row totals

max. fj. is the maximum value of the column totals

N is the number of cases.

(Nie *et al.*,1975).

1.7.1.5 Uncertainty Coefficient (U)

This statistic is designed for contingency tables, of nominal level variables.

The asymmetric coefficient is the proportion by which uncertainty in the dependent variable is reduced by knowledge of the independent variable. This approach considers the entire distribution and not just the mode (as does Lambda).

The maximal value is 1.0, indicating complete elimination of uncertainty. When no improvement occurs the uncertainty coefficients take on a value of zero.

The symmetric version of the coefficient measures the proportional reduction in uncertainty which is gained by knowing the joint distribution of cases. (Nie *et al.*, 1975).

These statistics are calculated as shown below.

$$\text{Asymmetric uncertainty coefficient} = \frac{U(Y) - U(Y/X)}{U(Y)}$$

$$\text{Symmetric uncertainty coefficient} = \frac{U(Y) + U(X) - U(Y,X)}{U(Y) + U(X)}$$

where $U(Y) = - \sum_j p\ (Y_j) \log p\ (Y_j)$

$p\ (Y_j)$ stands for the probability of a particular category in Y or proportion of Y_j.

and $U(Y/X) = - \sum_{k}\sum_{j} p\,(Y_j, X_k) \log p\,(Y_j/X_k)$

and $U(Y,X) = - \sum_{j}\sum_{k} p\,(Y_j,X_k) \log p\,(Y_j X_k)$

(Nie *et al.*, 1975)

1.7.2 Spearman and Kendall Rank Correlations

These statistics require that variables be measured at least on an ordinal scale. Both are subject to tests of significance. The Kendall rank correlation coefficient can be extended to a partial correlation coefficient.

The Spearman and Kendall rank correlations have different underlying scales, and numerically they are not directly comparable to each other. Sampling distributions of Spearman and Kendall forms are such that with a given data set, both will reject the null hypothesis (that variables are unrelated in the population) at the same level of significance.

Rank correlation coefficients are measures of agreement between ranks assigned to observed values of the two variables involved. Values of the statistics range from -1 to +1 (Siegel 1956).

These statistics are estimated as shown: Spearman rank correlation coefficient

$$r_s = 1 - \frac{6\sum_i d_i^2}{(n-1)n(n+1)}$$

(Seigel, 1956)

where n is the number of d's

and $d_i = X_i - Y_i$ and X_i and Y_i are corresponding ranks of the variables being correlated.

Kendall rank correlation coefficient

$$\tau = \frac{S}{\frac{1}{2}N(N-1)} \qquad \text{(Siegel, 1956).}$$

Where N is the number of cases, and S is a displacement index. (refer Section 2.3.2.1 for more details).

1.7.3 Techniques of Missing Data Estimation

Yates (1933) developed a procedure for estimating missing data. Where a single value is missing in a randomised complete block design the missing value (X) is calculated as

$$X = \frac{r\,B + tT - G}{(r-1)\,(t-1)}$$

where r and t are the number of blocks and treatments respectively and B and T are totals of the observed observations in the block and treatment containing the missing unit.
G is the grand total of the observed values (Steel and Torrie, 1960).

Where several values are missing iteration is necessary to obtain the best estimate.

These procedures result in estimates where the error sum of squares in the analysis of variance is a minimum, but treatment sum of squares are biased upward.

Bartlett (1937) proposed a covariance technique. This procedure, leads directly to unbiased estimates of treatment and error sums of squares. The technique uses regression with dummy variables (Draper and Smith 1966; Edwards, 1979) to obtain direct estimates of missing values. When two plots are missing from a set of data the model is :

$$Y_i = \beta_o X_o + \beta_1 X_1 + \beta_2 X_2 + \varepsilon_i$$

Where i = 1.......n, n = total number of observations. The β's are the slope of the regression lines fitted by means of the least squares technique.

X_o is a dummy variable for the intercept with the value unity. The term $\beta_0 X_o$ (ie β_0) estimates the population mean.

X_1 and X_2 are dummy variables specifying the missing observations, when they take a value of 1 instead of 0.

ε_i is the residual (error).

The signs of the β_1 or β_2 are changed to give the estimates of missing values. Such estimates when substituted for missing data lead to minimum error sum of squares and unbiased treatment sum of squares. Error degrees of freedom should be reduced by one for every estimated missing value, as the estimate does not include random error (ε_i).

1.7.4 Multiple Regression

When the functional relationship between one variable and several others is required, multiple regression will estimate the relationship. The proposed regression model is:

$$Y_i = \mu + \beta_1 X_{1_i} + \ldots\ldots \beta_k X_{ki} + \varepsilon_i$$

where i = 1......n observations and Y_i is the ith observation of the dependent variable.

μ is the mean Y for the population of Y's for the set of X's; $X_i \ldots\ldots X_k$.

X_k is the independent variable. The subscripts i....k identify each of these independent variables.

β_k is the regression slope of Y on each independent variable (X_k).

ε_i is the i^{th} observation individual residual ("error").

Error effects are considered random and independent with mean zero and variance $\sigma^2_{y.x}$, the latter being the variance about regression (Draper and Smith, 1966; Edwards, 1979).

1.7.4.1 Dummy Variables in Regression

Dummy variables are commonly used to insert a nominal scale variable into a regression equation. Sets of dummy variables are created by treating each category of a nominal scale variable as a separate variable and assigning arbitrary scores for all cases depending on the presence or absence in each category. (Draper and Smith, 1966; Edwards, 1979; Kleinbaum, 1978).

For any set of data there will be (k-1) dummy variables, where k is the number of categories required. The category not represented by a dummy variable becomes a reference point (estimated as β_0), by which the effects of other dummies are interpreted (Nie *et al.*,1975). This technique also forms the basis of estimating missing values through regression. (Section 1.7.3).

Dummy variables can be utilised to remove intrinsic differences in the data which may have deterministic effects on the dependent variable (Y), other than effects taken out by the independent variables (X_K's) (Draper and Smith, 1966; Kleinbaum, 1978; Edwards, 1979).

1.7.4.2 R^2: coefficient of multiple determination.

R^2 is a measure of the regression equations explanation of variation in the Y data. Its definition is given by

$$R^2 = \frac{SSy - SSresidual}{SSy} = \frac{SS\ regression}{SSy}$$

$$= \frac{\text{Variation in Y explained by combined linear influence of independent variables}}{\text{Total variation of Y}}$$

The larger R^2 the better the fitted regression equation explains variation in Y (Draper and Smith, 1966).

This statistic must be used with caution, as R^2 can be made equal to 1 by using properly selected coefficients and a small number of Y observations. An increase in R^2 associated with the addition of another independent variable to the regression equation should be checked for real significance by comparing residual sums of squares before and after addition. The reduction in the residual sums of squares may be accompanied by an increase in the mean square, as one degree of freedom is removed for each variable entered (Draper and Smith, 1966).

Changes in R^2 give some indication of the relative deterministic importance of an X variable with respect to Y (Draper and Smith, 1966).

1.7.4.3 Standardised Partial Regression Coefficients (β')

Standardised partial regression coefficients are used to determine relative importance of each X variable in determining Y from a functional point of view. The standardised regression equation is

$$Y'_i = \beta'_1 X'_{1i} + \beta'_2 X'_{2i} + \ldots\ldots \beta'_k X'_{ki} + \varepsilon'_i$$

where there are 1 to k independent variables, i = 1.....n observations,

$$\beta_1' = \beta_1 \frac{\sigma_{x_k}}{\sigma_y} \quad ,$$

and $$X_{ki}' = \frac{(X_{ki} - \overline{X}_k)}{\sigma_{x_k}} \quad ;$$

where:

Y_i'	is the ith standardised observation of Y;
β_k'	is the kth independent variable standardised regression coefficient;
β_k	is the kth independent variable regression coefficient;
X_{ki}'	is the ith standardised observation for the kth independent variable;
X_{ki}	is the ith observation for the kth independent variable;
$\overline{X}_k$	is the mean of the kth independent variable;
σ_{x_k}	is the standard deviation of the kth independent variable;
σ_y	is the standard deviation of the dependent variable;
ε_i'	is the ith observations standardised residual ("error").

β_k' expresses partial functional relationships between the kth standardised independent variable and the standardised dependent variable. Since each β_k' is free of the original scale of measurement comparisons of the realtive importance of the independent variables in determining the dependent variable can be made. Thus if β_1' is twice the size of β_2' then X_1 is approximately twice as important as X_2 in estimating Y (Steel and Torrie, 1960). All standardised data have mean zero and variance equalling unity. Such standardised regression statistics are also the basis of path analysis (Li, 1975).

1.7.5 Principal Factor Analysis

Principal factor analysis examines underlying relationships in the data and summarizes these as a set of factors (Cooley and Lohnes, 1971). Such factors are often used as a means of data reduction. Factors are estimated as

$$\phi_i = \sum_{j=i}^{n} \alpha_j \zeta_j$$

where $j = 1......n$ observed variables.

$i = 1 ......m$ factors.

and $\alpha_1 .....\alpha_j$ are coefficients chosen to maximise the variance of the ζ_j's

$\zeta_1 ......\zeta_j$ are observed variables in the standardised form.

ϕ_i is the i^{th} factor.

Often the number of factors is less than the number of observed variables. (Harman, 1976).

The first factor is the best linear combination of the variables, which explains the greatest portion of variation in the data. The second factor is the best linear combination of the variables that account for the most variation in the residual after the effects of the first factor have been removed, and is orthogonal to the first factor. Subsequent factors are added in a similar manner until all the variance has been explained. (Harman, 1976).

These factors are a "score" measuring what the variables have in common. They maximise the variance among individuals thereby increasing discrimination (Cooley and Lohnes, 1971). The complete set of factors explains all the variation in the data base.

The first few factors normally explain most of the variation. The first factor often is a "general magnitude" one, whose coefficients α_{j1} $(j = 1,2.....,n)$ are all positive when the solution is based upon a table of positive correlations. Often approximately half of the coefficients for each of the other factors (ϕ_2, $\phi_3 \ldots \phi_n$) are negative, making the factors bipolar. However, the meaning of the factors can be improved with respect to the input variables by rotation of the reference axes, if required (Cooley and Lohnes, 1971; Harman, 1976).

1.7.6 Analysis of Variance Procedure

Various linear models, assuming fixed and/or random effects, have been utilised to describe data in plant breeding. These include models for data from: single environments (Osborne and Paterson, 1952; Gordon *et al.*, 1972), a series of environments, sites and/or years in annual species (Hanson, 1964; Gordon *et al.*,1972); serial observations on perennial species (split-plot in time) (Steel and Torrie, 1960; Le Clerg *et al.*, 1962; Gordon, 1979).

Total variance is partioned into variance components by equating the observed mean squares to expectations of mean squares based on the model. Validity of significance testing of the observed mean squares is dependent on the assumptions underlying the analysis of variance. Discussion of the assumptions and consequential errors when they are invalid are given by Eisenhart (1947); Cochran (1947); and Bartlett (1947).

Extracted variance components may be utilised to obtain heritability estimates of the general form. $h^2 = \sigma^2_G/\sigma^2_P$

where σ^2_G is an appropriate genetic variance.

σ^2_P is a model related phenotypic variance (Sprague and Federer, 1951). This gives an idea of the relationship between σ^2_G and σ^2_P; however it gives no indication of the amounts of additive genetic variance (σ^2_A) in σ^2_G (Allard, 1960). Estimators of standard errors of some heritability-estimating models are outlined by Gordon *et al.* (1972)

and Gordon (1979).

1.7.6.1 Homogeneity of Error Variances

One of the assumptions underlying analysis of variance is that variances of subsets of data are homogeneous. Heterogeneous error variances can arise from mishaps; the use of variable material, or less carefully controlled conditions.

Several methods of testing homogeneity of variances are available (Bartlett, 1937; Bishop and Nair, 1939; Stevens, 1936). When data is homogeneous, subsets may be considered as random samples from a population with common variance. Heterogeneous error variances result in the probability of F values being different from those assumed, consequently significant differences are obtained more frequently than should be the case (i.e. Type I error rate is increased). Also, t-tests among means of subsets having heterogeneous errors, but based on a pooled error variance may give serious distortion of significant differences. Similarly standard errors derived from pooled error variance may be biased (Cochran, 1947).

Principal methods for dealing with heterogeneity of error variance are:

1. Subdivision of the error variance by grouping homogeneous subsets, or omitting parts of the data (Cochran, 1947).
2. Weighting each observation in proportion to the inverse of its error variance or standard deviation. (Prerequisite knowledge of error variances of the subsets is required) (Cochran, 1947).
3. Other transformations (Hinz and Eagles, 1976; Cochran, 1947; Bartlett, 1947).

1.7.7 Adaptation Analysis

Organisms adapt to environments by evolving genetic systems which produce stable phenotypes, or by developing phenotypes adjusted to the environment (Langridge, 1963). Ability to resist environmental variations where the phenotype remains constant is termed individual buffering. It is conspicuously a property of heterozygotes. Where co-existing genotypes in the same population are each adapted to separate ranges of environment, population buffering exists e.g. mixtures of pure lines (Allard and Bradshaw, 1964).

Presence of significant genotype-environment interaction variance implies that the relative behaviour of the genotypes in the trial depends upon the particular environment in which they are grown (Hill, 1975).

Finlay and Wilkinson (1963) and Eberhart and Russell (1966) developed regression techniques to study adaptability, as suggested initially by Yates and Cochran (1938). Environments were quantified on the basis of their means across all genotypes. Then genotype means within each environment were regressed against the environment means. Such techniques have now been widely used in plant breeding.

Problems have been noted with such techniques. Freeman and Perkins (1971) commented on the selection of measures of environment. It would be desirable to measure environment effects independent of the plant, or as a separate experiment. This would overcome any dependence between genotype and environment means. Byth *et al.* (1976) commented on the lack of linearity of response to improving environments. They suggested the use of multivariate techniques such as principal components analysis and cluster analysis as an alternative to regression.

2. FIELD EXPERIMENTS

2.1 Introduction

Over the summer of 1978/79 227 lines of the world germplasm collection of safflower were examined in a randomised complete block design with three blocks. Each plot consisted of a three metre single row. Rows were spaced at 90 cm intervals. Beehives where situated approximately 500 m away.

The field of safflower germplasm was used to study the activity of pollinators. The study was divided into three parts.

1. The time of effective cross-pollination.
2. Time of insect activity and influences of weather.
3. Effects of safflower genotype on insect activity.

2.2 Time of Effective Cross-Pollination

A bagging experiment was designed to examine the effects of time on wind and insect pollination.

2.2.1 Experimental Design

A randomised complete block design was utilised consisting of 4 blocks each with 7 plots of 10 heads. The experiment was conducted on border rows of the previously mentioned experiment, that is on cultivar 022. Because of time constraints, blocks were run at different times; blocks 1 and 2 ran from 19/2/79 to 26/2/79 and blocks 3 and 4 from 28/2/79 to 7/3/79.

2.2.1.1 Treatments

Muslin and glassine bags were used to cage individual heads to prevent insects reaching them.

The treatments were

1. Open pollinated - no bagging treatment.
2. Covered with a muslin bag 24 hours per day.
3. Covered with a muslin bag during daylight hours i.e. head exposed to nocturnal insects.
4. Covered with a muslin bag overnight i.e. head exposed to day active insects .
5. Covered with a glassine bag 24 hours per day.
6. Covered with a glassine bag during daylight hours i.e. head exposed to nocturnal insects.
7. Covered with a glassine bag overnight i.e. head exposed to day active insects.

It was hoped muslin bags would allow wind pollination to occur.

Where appropriate, bags were put on or removed before 8.00 a.m. and after 7.30 p.m. standard time.

Heads at a suitable growth stage and size were randomly allocated to treatments in such a way that the ten heads for any one treatment were spread throughout the block. Colour coded labels attached to the heads, enabled speedier bag changeovers.

2.2.1.2 Measurements and Analysis.

Seed was allowed to mature on the plant before individual heads were hand harvested, and air dried in the glasshouse. Seed counts were then made on each of the ten heads per experimental unit. Means on an experimental unit basis entered analysis of variance on the computer program PHANIE (Gordon unpubl.).

2.2.2 Results and Associated Discussion

Estimates of variance components, standard errors and significances are given in Table 2.1. Both block and treatment effects were significant at the 5% level.

Table 2.2 ranks the means and places them in significance groups. Heads unbagged during the day were in the same significance group as the control. Those uncaged during the night, but bagged during the day gave moderate seed counts while those continually bagged gave the lower yields.

Daytime active pollinators appear to be most important in safflower, as maximal seed counts were obtained from treatments where heads were exposed during daylight. Capitula exposed during the night were in the same significance group as those bagged in muslin for 24 hours. This suggests insect vectors active at night had no effect, and/or equivalent effect to wind pollination (pollination at night may be due to wind).

Treatments where flowers were never exposed to day pollination gave lower seed yields. Glassine bagging for 24 hours had the lowest yield, but some seed was set. This indicates that cultivar 022 has some degree of self-fertility, with the possibility of a small degree of self-incompatibility. Cross-pollination may thus enhance yield. The higher yields achieved with muslin bags for 24 hours might indicate some wind pollination; however when glassine and muslin bagging treatments are compared within bagging times no significant differences exist. Such differences would have been expected if wind was a significant pollen vector.

Table 2.1 Analysis of variance table for time of effective cross-pollination experiment, based on seed counts.

Source	Variance component	Standard error	Significance
Blocks	22.7943	16.6663	***
Treatments	77.6483	41.9307	****
Error	24.4944	7.7458	

coefficient of variation = 0.1684

*** $0.005 \geq P \geq 0.001$, **** $P \leq 0.001$

Table 2.2 Table of ranked means for time of effective cross-pollination experiment, based on seed counts.

$LSD_{0.05}$ = 7.3527

Treatment number	Treatment summary	Mean	Significance groups based on $LSD_{0.05}$
7	glassine night	37.9750	a
4	muslin night	37.8000	a
1	open 24 hours	37.1750	a
3	muslin day	29.7000	b
6	glassine day	26.3000	b
2	muslin 24 hours	23.1750	b
5	glassine 24 hours	13.6000	c

The low seed yields with glassine bagging might result from higher temperatures and humidities inside the bag. Such factors are known to have detrimental effects on seed set in safflower (Zimmerman, 1972b). Lowered light intensity might also be a factor. Glassine bags have been used widely in many crops to ensure selfing (Poehlman, 1979). Differences between glassine and muslin 24 hour bagging treatments could also have resulted from insect pollination of stigmas which penetrated the muslin. Such stigmas without petals as background are unlikely to attract insects: no insects were noted on such stigmas.

It was assumed that the coarse muslin bags used in this experiment would have allowed wind borne pollen to pass through to the enclosed stigmas. If this assumption did not hold wind pollination may not have occurred (although "wind" pollination within the bag may have occurred),and differences in the 24 hour bagging treatments must have resulted from bag environment effects (created by different bagging materials) on reproductive physiology.

2.3 Timing of Insect Activity and Influence of Weather

2.3.1 Introduction

Determination of insect species most likely to cross-pollinate safflower requires a knowledge of frequency distributions of potentially active species. The previous experiment showed daytime pollinators to be most important, and this experiment concentrated on them.

2.3.2 Methods

At half hour intervals, commencing at 7.30 a.m. (standard time) counts were made of insects present on floral parts of flowering safflower heads. Counts were obtained by walking through the germplasm nursery twice (a total of approximately 135 m row length). A different path was used each time so as to minimise genotype and paddock-position effects.

Insects were divided into main categories as listed.

1. Nectar collecting bees: no pollen load; foraging for nectar only. (Hymenoptera:*Apis mellifera*).
2. Pollen collecting bees: pollen load present, and obvious (Hymenoptera: *Apis mellifera*).
3. Dung flies (Diptera: family Anthomyidae greater than 3 mm in length).
4. Small flies (Diptera: All dipterous insects less than 3 mm in length).
5. Hover flies (Diptera: family Syrphidae, greater than 5 mm in length; mainly *Eristalis tenax* the drone fly).
6. Bumble bees (Hymenoptera: *Bombus* spp).
7. Butterflies (Lepidoptera: mainly *Picis rapae* the white butterfly).
8. Moths (Lepidoptera: family Crambidae, the grass moths).

Counts were conducted, when weather permitted, over the peak flowering period of the germplasm nursery.

The time of pollen presence was recorded. It was defined as being the time when approximately 30% of florets opening on a given day had pollen exuding from the anther column tip.

Brief notes were also made on insect foraging behaviour.

A summary of weather data was also obtained, from a weather station approximately 400 m away.

2.3.2.1 Statistical Analysis

Crosstabulations of data were conducted using the computer program SPSS/CROSSTABS (Nie *et al.*,1975). Crosstabulations of insect type by time of day, for each day, and of day by time of day for each insect type, were obtained. Methods used for estimating crosstabulation summary statistics applicable to nominal scale variables used in this study are outlined below. Their interpretations are discussed in Section 1.6.2.

Chi-square test (χ^2)

Chi-square was calculated as

$$\chi^2 = \frac{\Sigma\,(\text{observed-expected})^2}{\text{observed}} \quad , \ (r-1)(c-1) \text{ df}$$

where r = number of rows

c = number of columns.

Expected values are estimated under the assumption that the null hypothesis is true, (i.e. independence of variables) for each cell on the table.

(Steel and Torrie, 1960).

Contingency Coefficient(C)

$$C = \left(\frac{\chi^2}{\chi^2 + N}\right)^{\frac{1}{2}}$$

where N is the number of cases,

is the chi-square statistic (Nie *et al.*, 1975).

Cramer's V (V)

$$V = \left(\frac{\chi^2/N}{\min(r-1),(c-1)}\right)^{\frac{1}{2}}$$

where χ^2 is the chi-square statistic.

N is the number of cases and the denominator is the number of rows or columns minus 1; whichever is the smaller (Nie *et al.*, 1975).

Lambda (λ)

Asymmetric $$\lambda_v = \frac{\sum_k \max.f_{jk} - \max.f.k}{N - \max.f.k.}$$

where $\sum_k$ max.fjk represents the sum of the maximum values of the cell frequencies in each column

max.f.k is the maximum value of the row totals.

N is the number of cases.

The asymmetric λ is computed for each of the variables (v).

Symmetric λ $$= \frac{\sum_K \max.fjk + \sum_j \max.fjk - \max.f.k - \max.fj.}{2N - \max.f.k. - \max.fj.}$$

where $\sum_k$ max.fjk is the sum of the maximum values of the cell frequencies in each column.

$\sum_j$ max.fjk is the sum of the maximum values of the cell frequencies in each row.

max.f.k is the maximum value of the row totals.

max.fj. is the maximum value of the column totals

This is computed for each pair of variables (Nie *et al.*, 1975).

Uncertainty Coefficient (U)

Asymmetric $U_Y = \frac{U(Y) - U(Y/X)}{U(Y)}$

where U(Y) is the average uncertainty in the marginal distribution of Y calculated by

$$U(Y) = - \sum_j p\,(Y_j) \log p\,(Y_j)$$

where

$p(Y_j)$ stands for the probability of a particular category in Y or proportion of Y_j.

U (Y/X) stands for the conditional uncertainty of Y given X and is calculated by

$$U(Y/X) = - \sum_k \sum_j p\,(Y_j, X_k) \log p\,(Y_j/X_k)$$

In the definition of asymmetric uncertainty coefficient above Y is the dependent variable.

Asymmetric $U(U_X) = \frac{U(X) - U(X/Y)}{U(X)}$

Asymmetric uncertainties are calculated for both variables. The symmetric uncertainty coefficient is defined as

$$\text{symmetric } U\ (U) = \frac{U(Y) + U(X) - U(Y,X)}{U(Y) + U(X)}$$

where U(Y) and U(X) are defined as above, and

$U(Y,X) = - \sum_j \sum_k p(Y_j, X_k) \log p\,(Y_j X_k)$ is the joint uncertainty (Nie *et al.*, 1975).

Kendall rank correlation coefficient (τ)

Rank correlation coefficients were estimated between weather information and total insect activity on each day for each insect type.

Observations of both variables were ranked from 1 to N (the number of cases). Ranks of the X variable were then arranged in their natural order, that is 1,2,3 to N. The corresponding ranks of Y are then used to determine a value of S. S is determined by starting with the Y rank associated with the lowest rank of X, and counting the number of ranks larger than this. The number of ranks which are smaller than the Y rank are then subtracted from this. This is done for every rank of X, and the sum of these values result in S.

The Kendal rank correlation coefficient (τ) is then calculated as

$$\tau = \frac{S}{\frac{1}{2}N(N-1)} \qquad \text{(Seigel, 1956).}$$

The computer program SPSS/NONPAR CORR was used (Nie *et al.*,1975). The SPSS package computes actual probabilities of obtaining the observed correlation statistic. Therefore statistical significance at the 5% level is indicated by a probability value equal to or less than 0.050.

2.3.3 Results and Associated Discussion

Weather permitted insect counts to be obtained on nine days (Table 2.3). Table 2.4 summarises the weather data obtained from a nearby meteorological station.

The time of pollen presence varied from day to day, ranging from 10.00 a.m. to 11.30 a.m. standard time. Times are listed in Table 2.3.

Table 2.3 Timing of pollen presence (std time) in the field

Day	Date	Time of pollen presence
1	14/2/79	10.30 a.m.
2	15/2/79	11.30 a.m.
3	18/2/79	11.30 a.m.
4	19/2/79	11.00 a.m.
5	21/2/79	11.30 a.m.
6	24/2/79	10.00 a.m.
7	25/2/79	10.30 a.m.
8	26/2/79	10.00 a.m.
9	6/3/79	10.30 a.m.

Table 2.4 Summary of weather data for days (24 hour period) on which insect counts were made.

Day	Rain (mm)	Rel. Humidity % (9.00 am)	Temperature (^{o}C)				Bright sunshine (hours)	Anemometer (miles run)	Raised pan evaporation (mm)
			Max	Min	Ave	Grass min			
1	5.9	79	21.7	10.4	18.1	7.3	2.9	136	4.1
2	3.7	75	21.7	13.3	17.5	10.9	5.3	185	4.9
3	0.0	82	20.3	14.0	17.2	13.0	0.0	122	3.3
4	0.0	70	19.6	10.0	14.8	5.4	6.2	256	4.9
5	1.2	89	20.3	5.6	13.0	2.1	9.1	134	3.8
6	0.0	67	18.7	11.6	15.2	8.5	5.1	150	4.0
7	0.0	68	21.8	9.7	15.3	3.3	9.5	155	5.0
8	0.0	74	23.3	11.5	17.4	6.4	11.4	84	4.8
9	1.4	66	17.1	7.0	12.1	5.0	1.0	267	2.0

Figures 2.1 to 2.9 show the activity of the most frequent insect visitors through the day for each day sampled. Insects such as bumble bees, hoverflies, butterflies and moths were not included in the figures because of their relatively sporadic visitation. Numbers of these insects visiting safflower are given in Appendix 1. The vertical lines on figures indicate the time of pollen presence as defined in Section 2.3.2. Bees constitute the main insect visitors about late morning and midday when safflower pollen is present. Dipterous species, although active all day constitute the vast majority of insects present in the early morning and late afternoon to early evening. Other insect types were low in numbers and were scattered throughout the day (Appendix 1). Table 2.5 groups insect types into families, and presents the total numbers of individuals within each family calling on safflower each day. It is clear that Hymenoptera and Diptera are the most important families as indicated by the percentages (Table 2.5). Leppik (1977) reported that the families of insects most frequently observed on capitula of the same morphological class as safflower were Hymenoptera, Diptera, Lepidoptera and Coleoptera (in descending order of importance). Data collected in this study tend to support this.

Pollen foraging bees were present in substantial numbers for a relatively short period, while nectar foragers were present for extended periods. The activity of pollen foragers coincided with pollen release on most days. The period of their activity was most likely limited by the pollen resource available. This resource would have become exhausted sometime after stigma extrusion had ceased, when no fresh pollen would be entering the resource. Peak honey bee activity varied considerably but was generally reached in the mid to late morning. Boch (1961) recorded similar results. Such variation in numbers of insects probably results from climatic variations affecting availability of the resource attracting bees. Availability relative to availability in other species flowering at

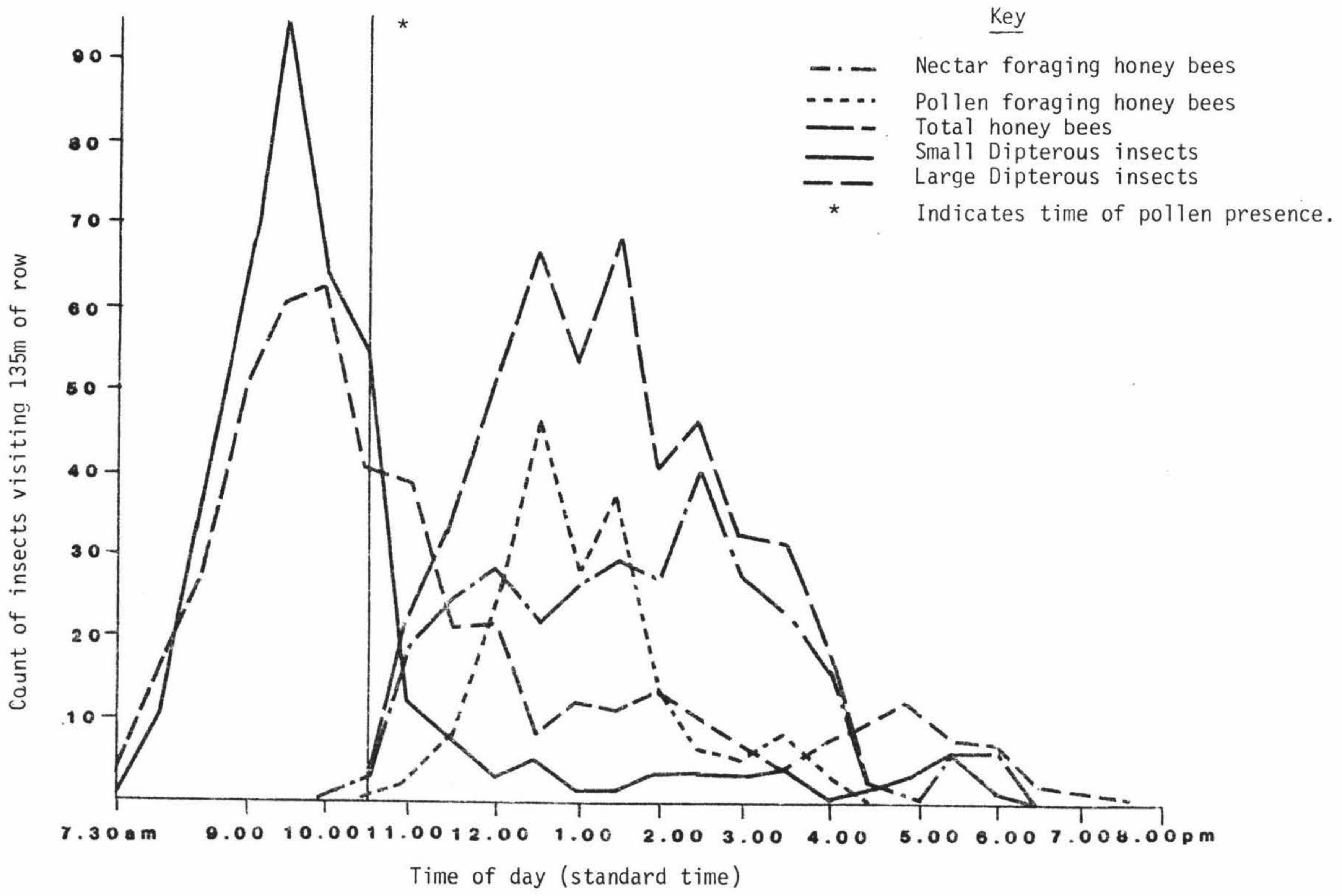


Figure 2.1 Number of insects visiting safflower capitula versus time of day (Day 1).

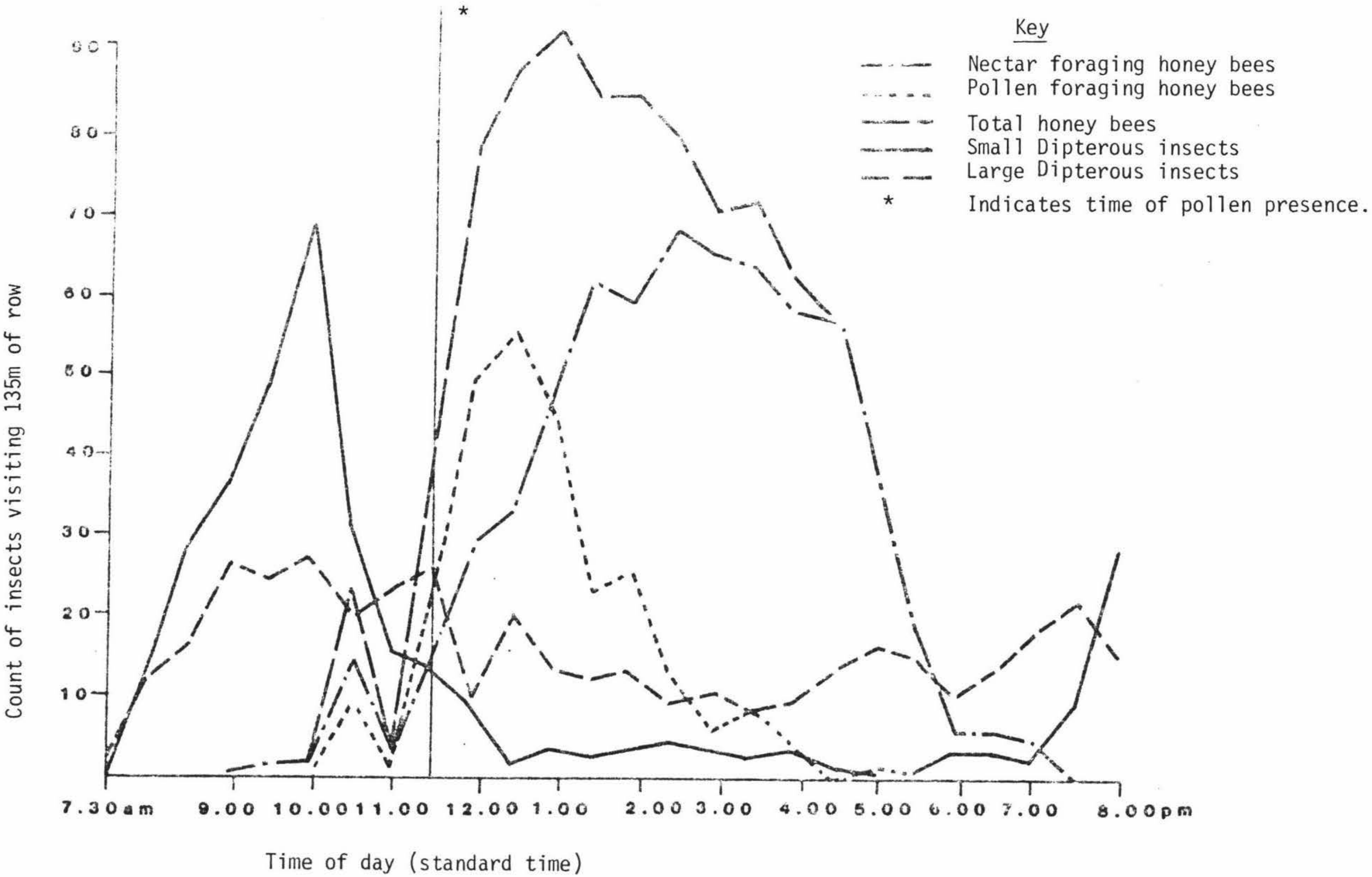


Figure 2.2 Number of insects visiting safflower capitula versus time of day (Day 2).

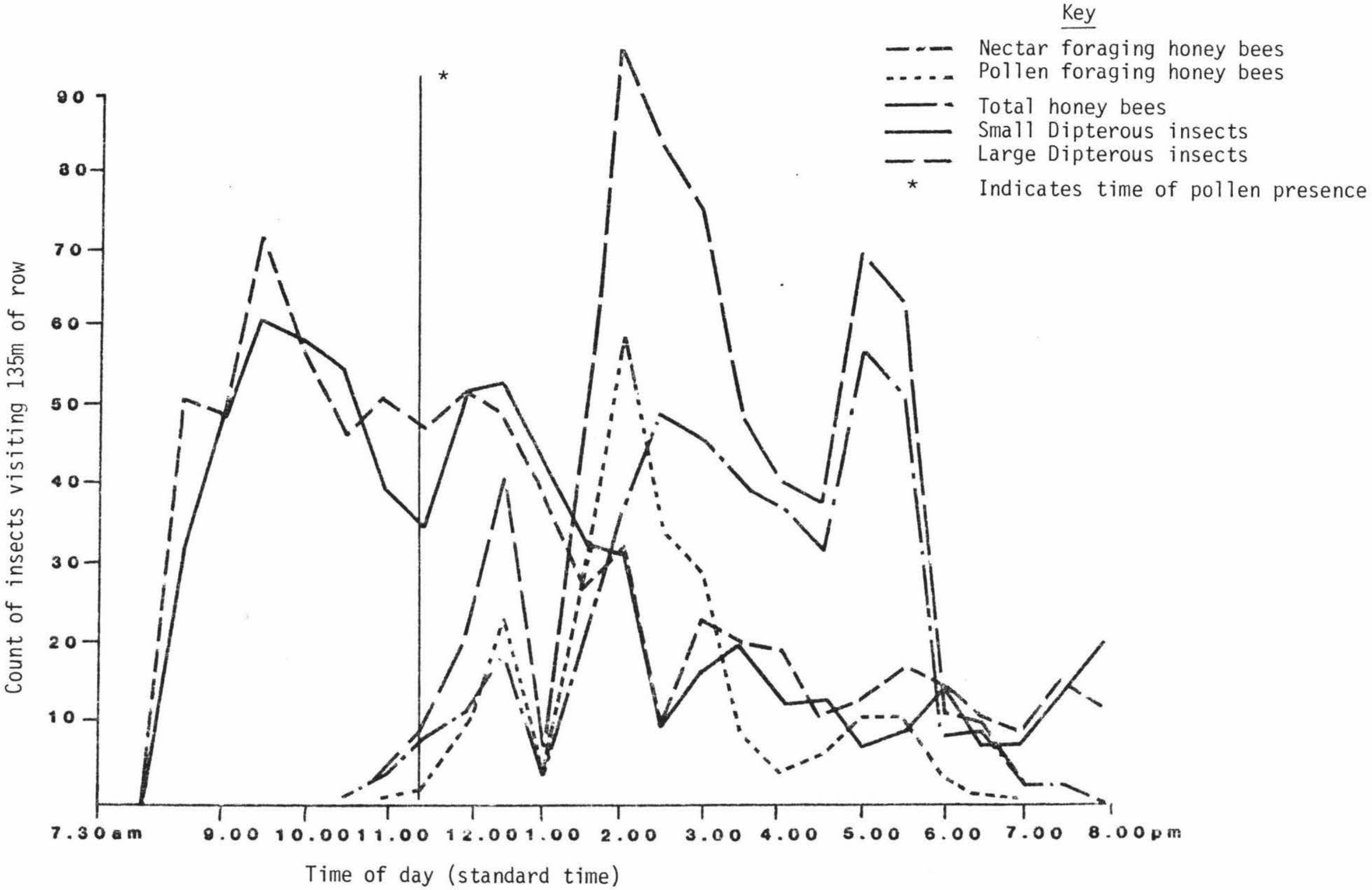


Figure 2.3 Number of insects visiting safflower capitula versus time of day (Day 3).

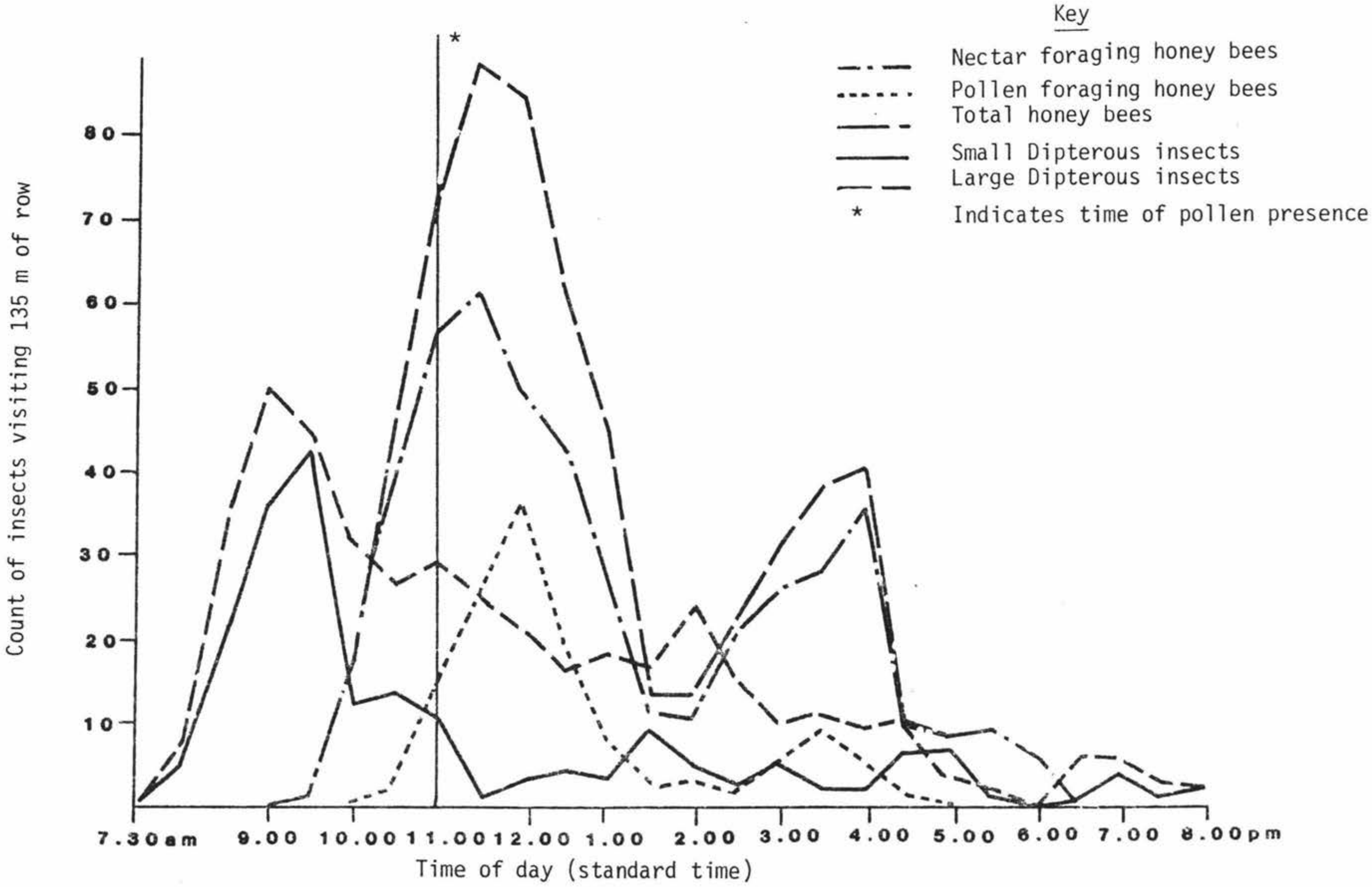


Figure 2.4. Number of insects visiting safflower capitula versus time of day (Day 4.)

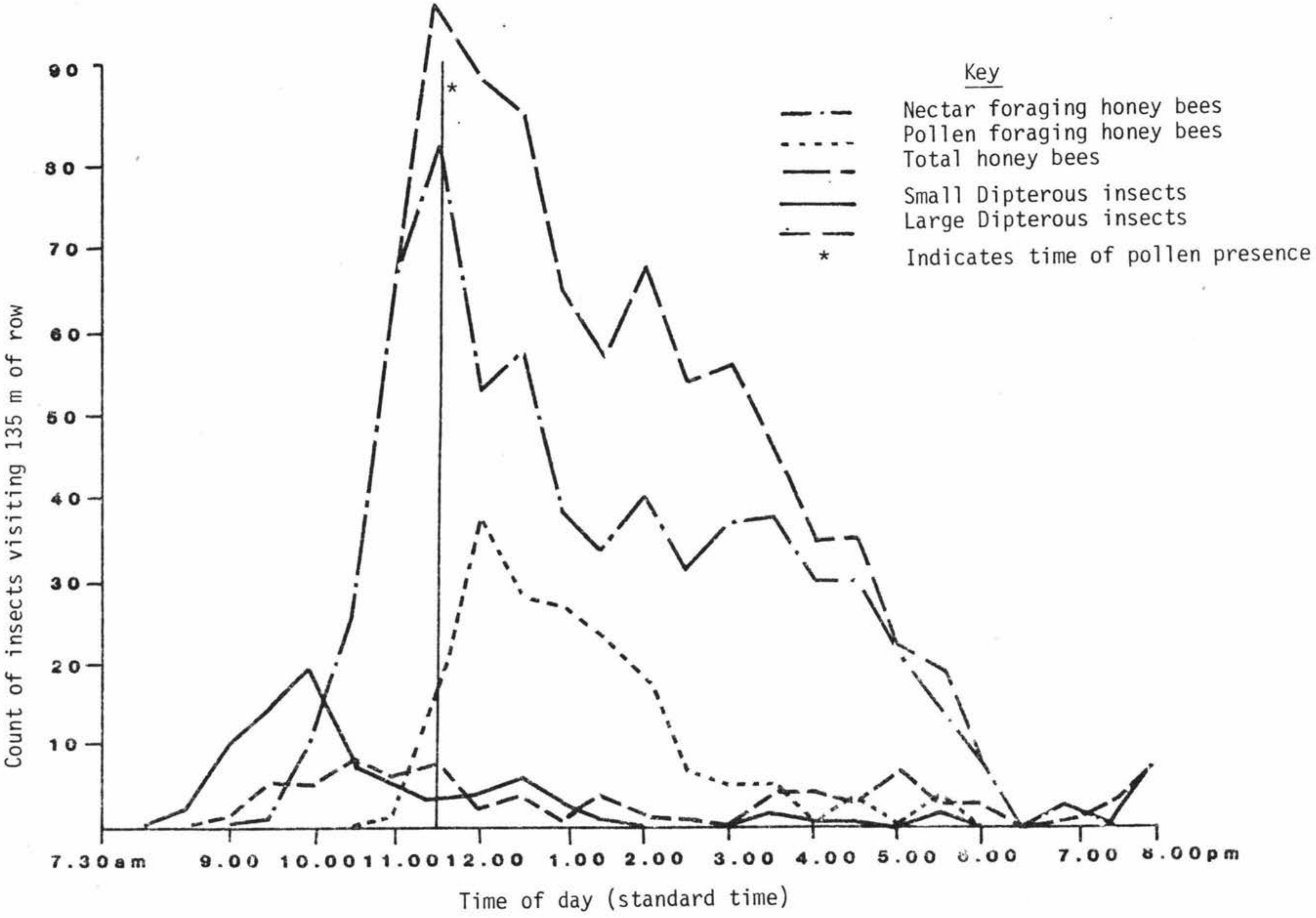


Figure 2.5 Number of insects visiting safflower capitula versus time of day (Day 5.)

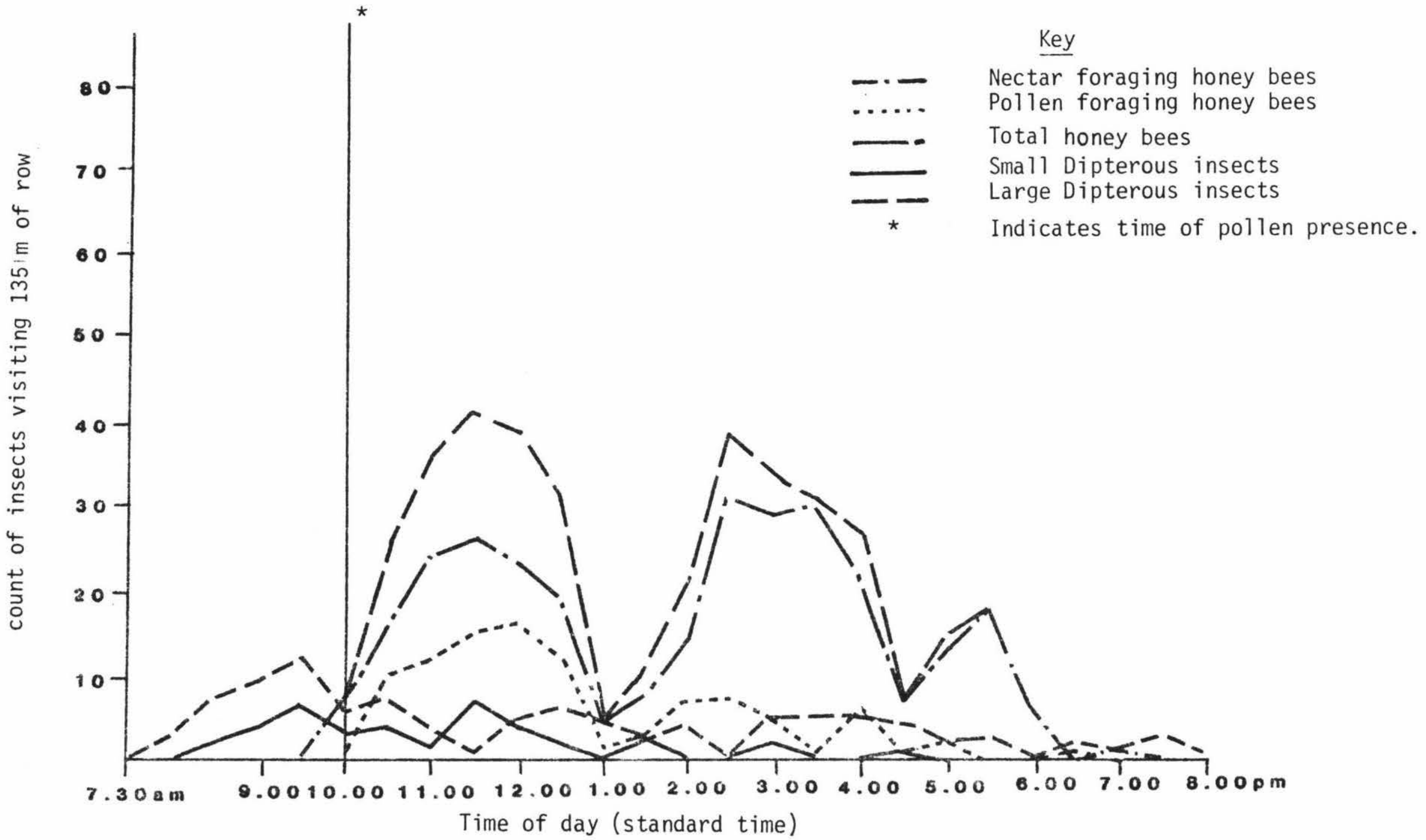


Figure 2.6: Number of insects visiting safflower capitula versus time of day (Day 6).

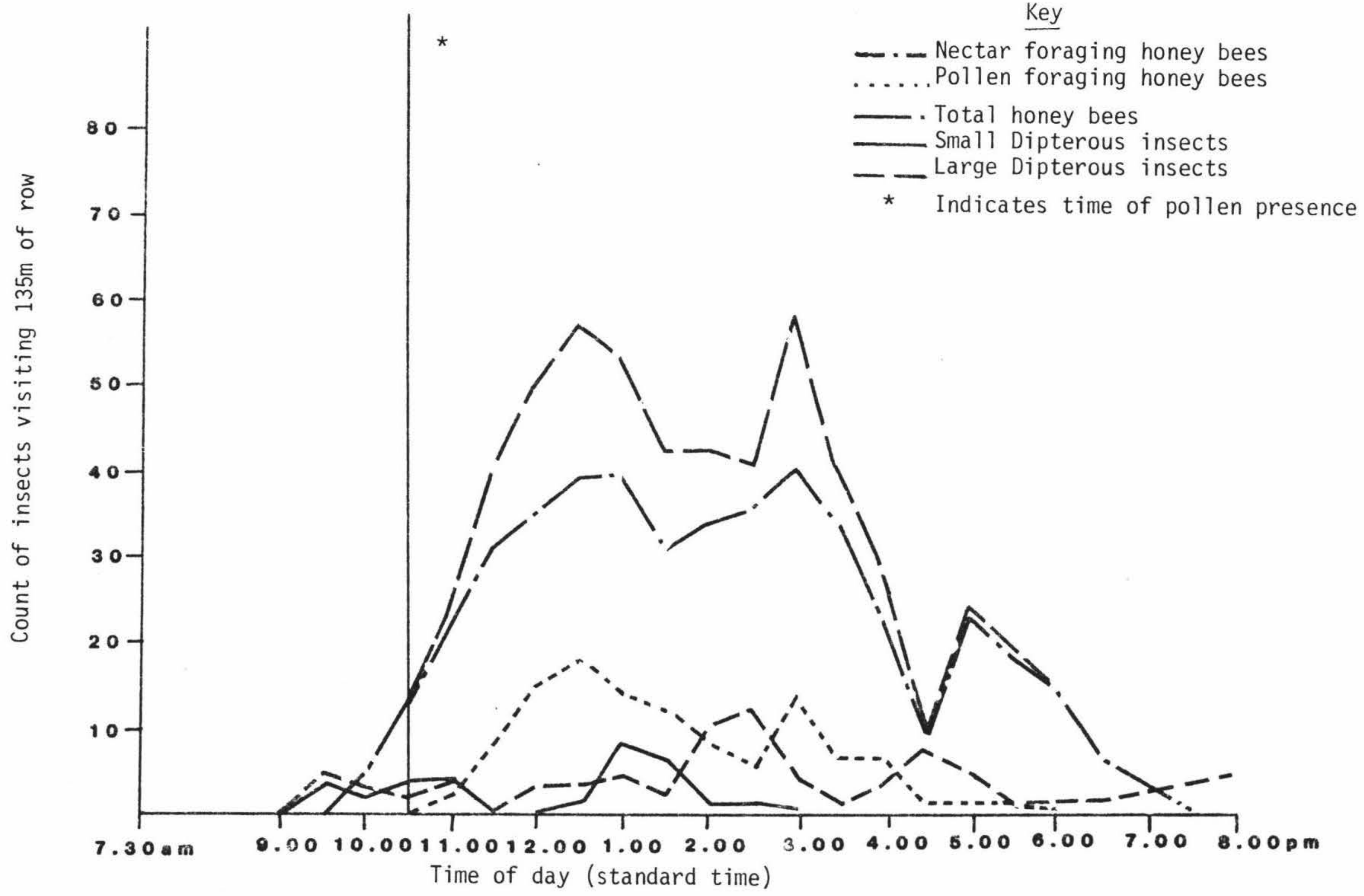


Figure 2.7: Number of insects visiting safflower capitula versus time of day (Day 7)

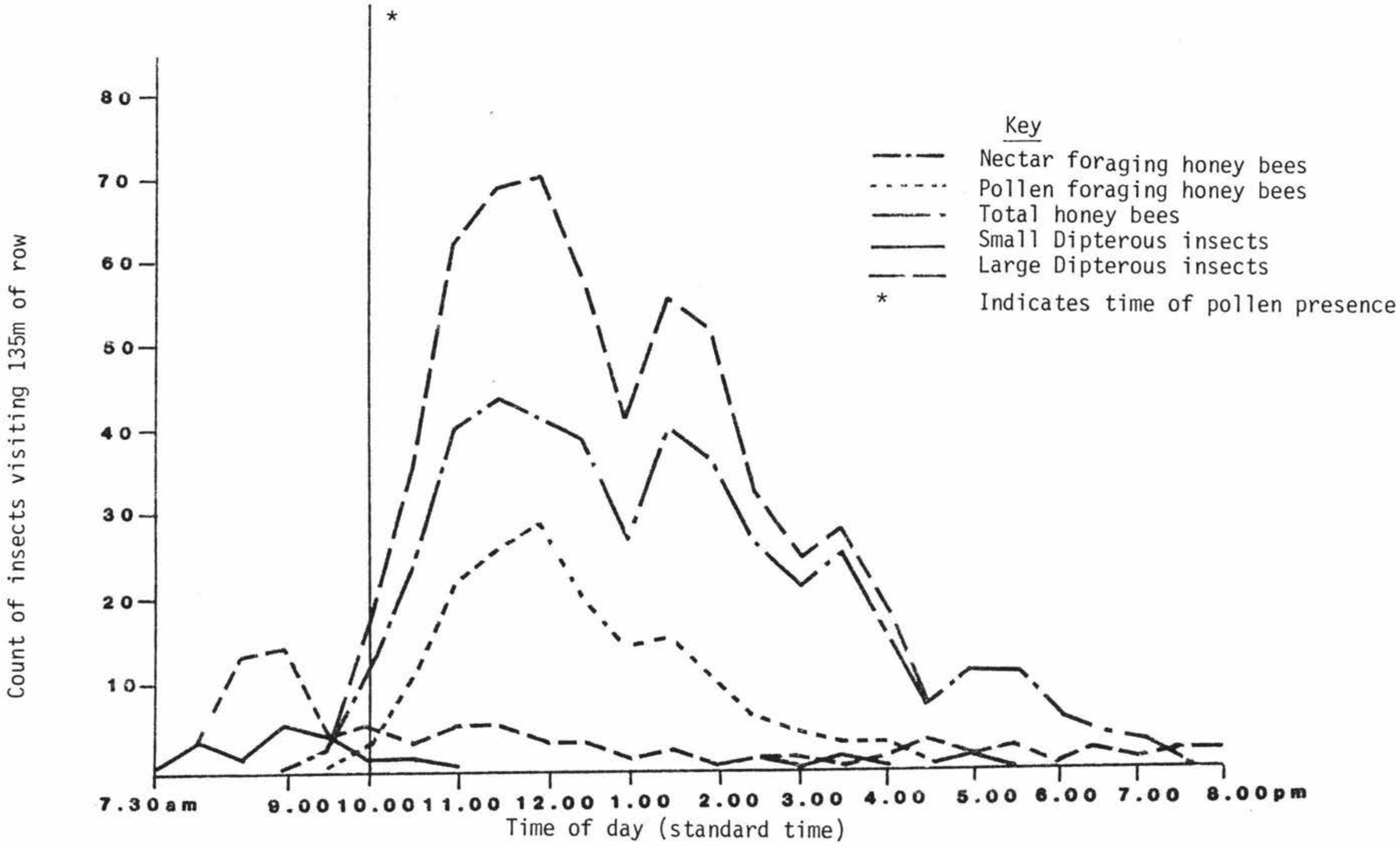


Figure 2.8: Number of insects visiting safflower capitula versus time of day (Day 8).

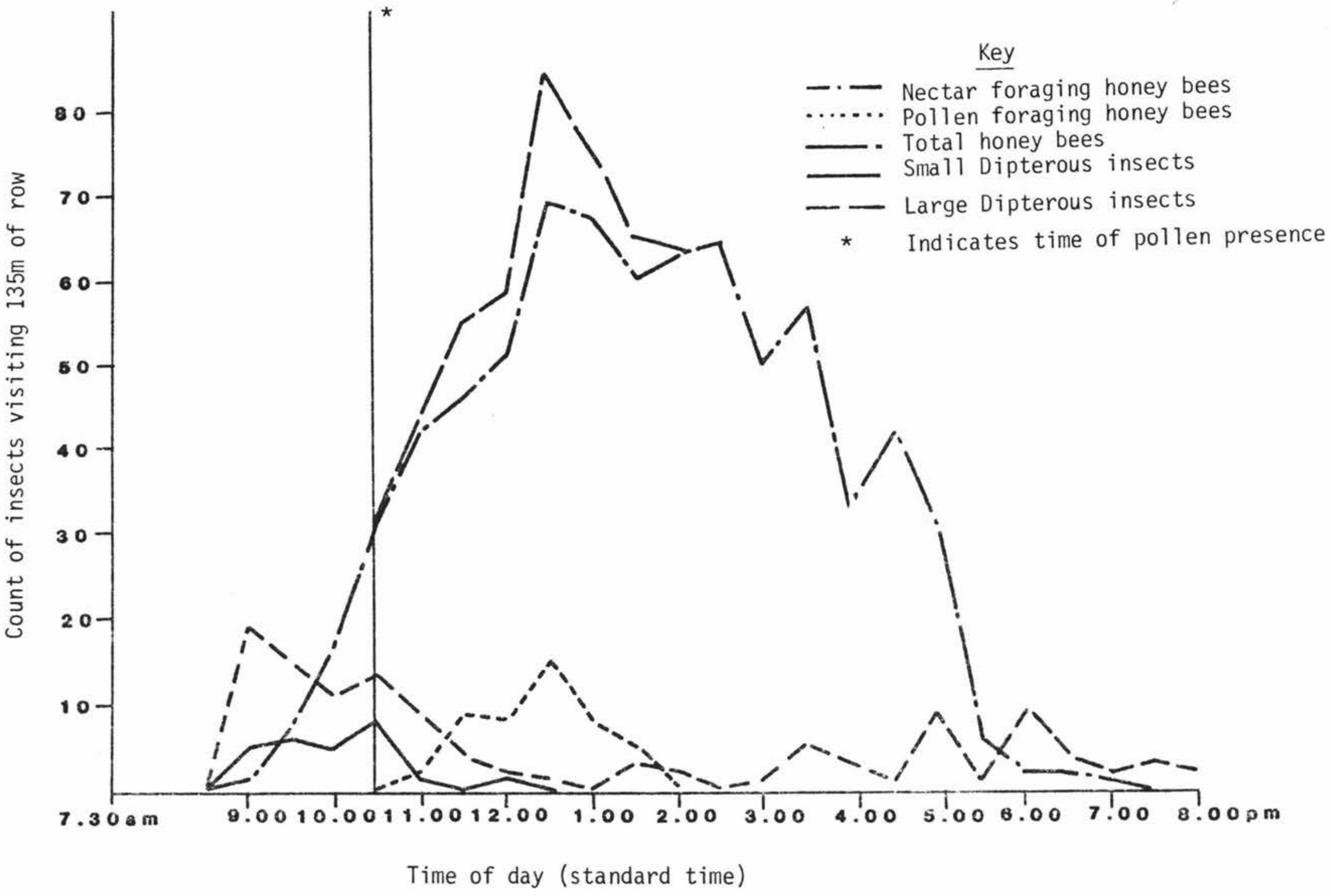


Figure 2.9: Number of insects visiting safflower capitula versus time of day (Day 9).

Table 2.5 Total numbers of insects visiting safflower over the course of the day for various insect families. Percentages of the total are in brackets.

Day	Hymenoptera	Diptera	Lepidoptera	Total
1	504 (35.2)	885 (61.9)	40 (2.8)	1429
2	953 (49.1)	900 (46.4)	86 (4.4)	1939
3	704 (29.4)	1668 (69.6)	24 (1.0)	2396
4	589 (46.8)	653 (51.9)	16 (1.3)	1258
5	806 (75.4)	238 (22.3)	25 (2.3)	1069
6	429 (70.9)	167 (27.6)	9 (1.4)	605
7	584 (73.0)	188 (23.5)	28 (3.5)	800
8	626 (78.5)	150 (18.8)	21 (2.6)	797
9	810 (81.5)	166 (16.7)	18 (1.8)	944

the same time may also be important. Small climatic fluctuations during the day may have caused some of the fluctuations in insect activity within days.

More Diptera than Hymenoptera visited flowers on days 1 and 3 (Table 2.5). This may have been due to weather conditions on the day. No significant correlations with weather data are noted in Section 2.3.3.1, for other than hover flies which constituted a small percentage of Diptera. An alternative possibility is that weather conditions prior to these days had resulted in large numbers of Dipterous larvae hatching out.

Table 2.6 provides a summary of the foraging behaviour of insects in the field. Largest pollen loads were noted on individuals of Hymenopterous species mainly *Apis mellifera*. These insects also moved actively within and among capitula. This suggests that they may play the greatest role in cross-pollination of safflower.

Summary statistics for crosstabulations of day by time of day for each insect type are presented in Table 2.7. Significant chi-square values at the 5% significance level for insects, except bumble bees indicate that day and time of day are not independent of each other. Climatic conditions which may influence the timing of pollen release and stigmatic extrusion are specific to any single day, and thus may be associated with insect visitation patterns during the day. Climatic conditions may also directly influence insects, rather than acting indirectly via the plant. The lack of a significant chi-square for bumble bees suggests that these insects are less influenced by the day, and may thus forage under conditions more unfavourable to other pollinators.

Table 2.6 Summary of Insect Foraging Behaviour .

Insect Type	Alights on	Visiting florets	Foraging for	Sampling within heads	Intensity between heads	Pollen load
Nectar bee	Fresh florets	Turgid florets	Nectar	High	High	Moderate
Pollen bee	Fresh florets	Turgid florets	Pollen	Very high	High	Very High
Dung fly	Bracts or any florets	Fresh or wilted florets	Nectar?	Moderate	Moderate	Very low
Small fly	Anything	Any florets	Nectar?	Very low	Low	Very low
Hover fly	Fresh florets	Fresh florets	Nectar	Moderate	Low	Very low
Bumble bee	Fresh florets	Turgid florets	Nectar and pollen	High	High	Moderate to very high
Butterfly	Fresh florets	Fresh florets	Nectar	Moderate	Low	Very low
Moths	Fresh florets	Fresh florets	Nectar	Low	Low	Low

Table 2.7 Summary statistics for crosstabulations of day by time of day for each insect type.

Insect	Table size RxC	χ^2	C	V	λ_{time}	λ_{day}	λ	U_{time}	U_{day}	U
Nectar bee	22 x 9	982.3 S(0.000)	0.43	0.17	0.319	0.067	0.048	0.043	0.055	0.048
Pollen bee	18 x 9	712.7 S(0.000)	0.57	0.25	0.063	0.133	0.097	0.100	0.116	0.107
Dung fly	26 x 9	608.5 S(0.000)	0.44	0.18	0.016	0.032	0.023	0.041	0.067	0.051
Small flies	25 x 9	726.6 S(0.000)	0.54	0.22	0.022	0.076	0.045	0.073	0.122	0.091
Hover fly	23 x 9	239.4 S(0.000)	0.58	0.25	0.067	0.097	0.081	0.089	0.128	0.105
Bumble bee	24 x 9	216.0 S(0.051)	0.67	0.32	0.058	0.145	0.100	0.140	0.195	0.163
Butterfly	19 x 9	256.1 S(0.000)	0.75	0.40	0.138	0.140	0.139	0.210	0.299	0.247
Moths	25 x 8	209.5 S(0.015)	0.87	0.67	0.148	0.478	0.290	0.361	0.630	0.459

Significance at the 5% level for χ^2 occurs when the value inside the brackets is less than 0.050.

The high contingency coefficient for bumble bees tends to suggest that there was some association with days even though the chi-square was not significant. (Weather correlations are discussed in Section 2.3.3.1).

Measures of association given by Cramer's V tended to be low with the exception of moths.

Values of Lambda were low for most insect types, indicating that ability to predict was good when the day and time of day were known. Asymmetric Lambdas for nectar foraging bees indicated that knowledge of the day was more important than the time of day, in predicting visitation levels of this insect. Symmetric Lambdas showed that knowledge of both day and time of day led to good prediction of honey bee and Dipterous insect visitation.

Uncertainty coefficients indicated that a considerable degree of uncertainty of prediction remained.

Summary statistics for crosstabulations of insect type with time of day for each day are presented in Table 2.8. Significant chi-square values were obtained in all cases indicating that insect type and frequency of visitation at any time of day were not independent. Contingency coefficients were significant, and moderately high. Cramer's V values also indicated association, but not to such a strong degree. Asymmetric Lambdas indicated that knowledge of time of day aided prediction of visitation more than insect type. High degrees of uncertainty remained as shown by the uncertainty coefficients.

Table 2.8 Summary statistics of crosstabulations for insect by time of day tables for each day.

Day	Table size		C	V	λ time	λ insect	λ	U time	U insect	U
1	24 x 8	1295.6 S(0.000)	0.69	0.36	0.084	0.259	0.160	0.159	0.284	0.204
2	26 x 8	1657.8 S(0.000)	0.68	0.35	0.076	0.291	0.164	0.144	0.264	0.187
3	24 x 8	116.0 S(0.000)	0.58	0.28	0.049	0.179	0.103	0.093	0.193	0.125
4	25 x 8	695.8 S(0.000)	0.59	0.28	0.076	0.227	0.139	0.100	0.198	0.133
5	24 x 8	898.1 S(0.000)	0.67	0.34	0.050	0.095	0.065	0.101	0.217	0.138
6	25 x 8	405.9 S(0.000)	0.63	0.30	0.043	0.123	0.072	0.104	0.207	0.139
7	22 x 8	373.4 S(0.000)	0.56	0.26	0.073	0.149	0.098	0.073	0.149	0.098
8	25 x 8	642.2 S(0.000)	0.67	0.37	0.029	0.099	0.053	0.977	0.208	0.133
9	23 x 8	660.3 S(0.000)	0.63	0.31	0.039	0.160	0.065	0.941	0.282	0.141

Significance at the 5% level for χ^2 occurs when the value inside the brackets is less than 0.050.

Results of crosstabulations suggested insect types have separate and distinct distributions, which are specific to environments existing on a given day. Environmental conditions existing on any day affected both plant and insect. The way these factors simultaneously interact is very much an open question.

2.3.3.1 Weather Correlations

Kendall rank correlations between weather information and insect counts and percentages are presented in Tables 2.9 and 2.10, respectively.

Significant positive rank correlations at the 5% significance level were observed between nectar collecting bee numbers and evaporation; pollen collecting bees % and average temperature, and hover fly % and wind. A significant negative rank correlation between butterfly % and wind was noted.

The positive correlation between numbers of nectar collecting bees and evaporation probably results from higher sugar concentrations occurring as water in nectar evaporates. Higher temperatures tend to increase activity of most insects and the activity of pollen collectors may be no different. In this instance the increased percentage of pollen collectors present not only reflects greater physiological activity, but also greater incentive to collect pollen because the plant is providing more pollen. Higher temperatures may have resulted in greater rates of extrusion, leading to a large supply of pollen over a shorter period, thus attracting greater numbers of pollen collectors. Alternatively more pollen may have been released. High winds may have caused more hover flies to settle on flowers, rather than to actively forage. High winds would be damaging to butterflies, which probably resulted in the negative correlation.

Table 2.9 Kendall rank correlations of daily total insect counts with daily weather

Insect	Rain (mm)	Relative humidity %	Temperature				Bright sunshine (hours)	Anemometer (miles run)	Raised pan evaporation (mm)
			Max	Min	Ave	Grass			
Nectar bee	0.057 S(0.833)	0.319 S(0.244)	-0.141 S(0.600)	-0.254 S(0.345)	-0.366 S(0.173)	0.085 S(0.753)	-0.141 S(0.600)	-0.310 S(0.249)	0.571 S(0.035)
Pollen bee	-0.028 S(0.917)	0.400 S(0.140)	0.000 S(xxxx)	0.056 S(0.835)	-0.056 S(0.835)	0.167 S(0.532)	-0.056 S(0.835)	0.056 S(0.835)	-0.310 S(0.835)
Dung fly	0.085 S(0.753)	0.400 S(0.140)	-0.222 S(0.404)	-0.056 S(0.835)	-0.388 S(0.144)	0.056 S(0.835)	-0.278 S(0.297)	-0.167 S(0.532)	-0.141 S(0.600)
Small fly	0.141 S(0.600)	0.343 S(0.206)	0.056 S(0.835)	0.111 S(0.677)	-0.222 S(0.404)	0.000 S(xxxx)	-0.111 S(0.677)	0.000 S(xxxx)	-0.310 S(0.249)
Hover fly	0.479 S(0.075)	-0.229 S(0.399)	0.278 S(0.297)	0.000 S(xxxx)	0.444 S(0.095)	-0.111 S(0.677)	-0.222 S(0.404)	0.333 S(0.211)	-0.028 S(0.917)
Bumble bee	-0.197 S(0.463)	0,114 S(0.573)	0.111 S(0.677)	0.389 S(0.144)	-0.056 S(0.835)	0.278 S(0.297)	0.278 S(0.297)	0.056 S(0.835)	-0.366 S(0.173)
Butterfly	0.235 S(0.392)	0.269 S(0.333)	0.203 S(0.456)	0.203 S(0.456)	0.261 S(0.338)	0.145 S(0.595)	0.145 S(0.595)	0.319 S(0.242)	0.206 S(0.454)
Moths	0.229 S(0.399)	0.377 S(0.168)	0.141 S(0.600)	0.366 S(0.173)	-0.028 S(0.917)	0.028 S(0.917)	-0.085 S(0.753)	0.141 S(0.500)	-0.057 S(0.833)

Significance at the 5% level occurs when the value inside the brackets is less than 0.050 (xxxx indicate very large values). Nine cases were used to estimate each correlation statistic.

Table 2.10 Kendall rank correlations of daily percentage of insect type with daily weather .

Insect	Rain (mm)	Relative humidity %	Temperature				Bright sunshine (hours)	Anemometer (miles run)	Raised pan evaporation (mm)
			Max	Min	Ave	Grass			
Nectar bees %	0.085 S(0.753)	-0.229 S(0.399)	0.167 S(0.532)	-0.222 S(0.404)	0.222 S(0.404)	-0.222 S(0.404)	-0.111 S(0.677)	-0.111 S(0.677)	0.423 S(0.116)
Pollen bees %	-0.085 S(0.753)	-0.229 S(0.399)	0.222 S(0.404)	0.167 S(0.532)	0.611 S(0.022)	-0.056 S(0.835)	0.278 S(0.297)	0.157 S(0.532)	-0.310 S(0.249)
Dung flies %	-0.028 S(0.917)	0.172 S(0.527)	-0.333 S(0.211)	0.056 S(0.835)	-0.389 S(0.144)	0.278 S(0.297)	-0.056 S(0.835)	-0.056 S(0.835)	-0.028 S(0.917)
Small flies %	0.141 S(0.600)	0.343 S(0.206)	0.056 S(0.835)	0.111 S(0.677)	-0.222 S(0.404)	0.000 S(xxxx)	-0.111 S(0.677)	0.000 S(xxxx)	-0.310 S(0.249)
Hover flies %	-0.085 S(0.753)	-0.172 S(0.527)	0.222 S(0.404)	0.389 S(0.144)	0.500 S(0.061)	0.056 S(0.835)	0.389 S(0.144)	0.611 S(0.022)	0.141 S(0.600)
Bumble bees %	-0.251 S(0.379)	-0.287 S(0.320)	0.217 S(0.444)	0.340 S(0.229)	0.464 S(0.101)	0.031 S(0.913)	0.464 S(0.101)	0.340 S(0.229)	-0.063 S(0.826)
Butterfly %	0.028 S(0.917)	-0.286 S(0.292)	-0.333 S(0.211)	-0.278 S(0.297)	-0.056 S(0.835)	-0.056 S(0.835)	-0.167 S(0.532)	-0.722 S(0.007)	-0.310 S(0.249)
Moths %	0.471 S(0.087)	-0.209 S(0.452)	-0.145 S(0.595)	-0.087 S(0.750)	0.087 S(0.750)	0.087 S(0.750)	-0.261 S(0.338)	-0.029 S(0.915)	0.177 S(0.521)

Significance at the 5% level occurs when the value inside the brackets is less than 0.050. (xxxx indicate very large values).

Nine cases were used to estimate each correlation statistic.

2.4 Effects of Safflower Genotype on Insect Activity

2.4.1 Introduction

Rubis *et al.* (1966) and Rubis (1970) found frequency of honey bee visitation to vary depending on genotype factors such as pollen presence and flower colour. Specificity expressed by pollinators for different genotypes may lead to unequal crossing rates among lines from divergent genetic backgrounds. These genotypic aspects were examined for daytime pollinators, as this study had shown them to be most important. All insect types were studied as it had not been established whether or not different insect types showed specificity to different genotypes of safflower.

2.4.2 Methods

Nineteen genotypes at peak flowering were randomly selected out of the germplasm nursery. These are listed in Table 2.11 with their code numbers. All plots were in the central part of the nursery field.

Five counts were made on single three metre rows, over the period of sampling. Therefore insects on the open heads of 15 metres of each genotype were counted. Sampling periods were at 9.00 a.m. to 11.00 a.m., 12.00 a.m. to 2.00 p.m. and 3.00 p.m. to 4.30 p.m. (referred to as T1, T2 and T3 respectively) on four days, 6/3/79, 7/3/79, 8/3/79 and 9/3/79 (referred to as D1, D2, D3 and D4 respectively). Insects in the eight categories outlined in Section 2.3.2, were counted.

Crosstabulations of safflower genotypes by insect types for each day and time of day combination were performed. Summary statistics outlined in Section 2.3.2.1 were obtained.

Table 2.11 Genotypes used in the study of safflower genotype influences on insect activity .

Code	Genotype	Origin
1	P.I.240409	Egypt ex Pullman, U.S.A.
2	P.I.306593	Egypt ex Pullman, U.S.A.
3	P.I.253759	Iraq ex Pullman, U.S.A.
4	P.I.257582	Ethiopia ex Pullman, U.S.A.
5	P.I.250708	Iran ex Pullman, U.S.A.
6	P.I.253515	Portugal ex Pullman, U.S.A.
7	P.I.237538	Turkey ex Pullman, U.S.A.
8	P.I.306684	Italy ex Pullman, U.S.A.
9	P.I.262428	U.S.S.R ex Pullman, U.S.A.
10	P.I.250720	Iran ex Pullman, U.S.A.
11	P.I.209283	U.S.S.R ex Pullman, U.S.A.
12	P.I.226546	Ethiopia ex Pullman, U.S.A.
13	P.I.193473	Ethiopia ex Pullman, U.S.A.
14	P.I.288983	Hungary ex Pullman, U.S.A.
15	P.I.195925	Ethiopia ex Pullman, U.S.A.
16	69044	Australia (Univ. of New England)
17	P.I.253763	Iraq ex Pullman, U.S.A.
18	P.I.250596	Pakistan ex Pullman, U.S.A.
19	P.I.250006	Iran ex Pullman, U.S.A.

2.4.3 Results

Summary statistics of the crosstabulations between genotypes and insects for each day and time of day combination are listed in Table 2.12. The majority of chi-square tests were not significant at the 5% level. This indicated that genotypes and insects were independent, implying that all insect types randomly visited safflower genotypes. Such a result implies that there were no differences observed in the specificity of nectar and pollen foraging honey bees with this set of safflower genotypes.

Levels of association measured by the contingency coefficient and Cramer's V were moderate. Lambda values indicated excellent prediction of insect visitation when either the genotype and/or insect type was known. Good prediction was associated with low uncertainty values. Such results suggest there was little variation between safflower genotypes with respect to the levels of visitation by various insects examined.

Table 2.12 Summary statistics of crosstabulations for genotype by insect tables for each day and time of day combination .

Day and time categories	Table size R X C	χ^2	C	V	λ Gen	λ insect	λ	U Genot	U insect	U
D1T1	19 x 7	171.2 S(0.0001)	0.68	0.37	0.056	0.080	0.061	0.084	0.292	0.130
D1T2	19 x 6	145.3 S(0.0001)	0.59	0.33	0.029	0.000	0.026	0.058	0.357	0.100
D1T3	19 x 6	82.0 S(0.7176)	0.57	0.31	0.068	0.000	0.052	0.078	0.255	0.119
D2T1	19 x 7	159.1 S(0.0007)	0.59	0.30	0.049	0.069	0.055	0.075	0.209	0.110
D2T2	19 x 6	107.7 S(0.0974)	0.49	0.25	0.023	0.000	0.020	0.050	0.244	0.083
D2T3	19 x 6	104.2 S(0.1443)	0.60	0.33	0.044	0.000	0.036	0.070	0.288	0.113
D3T1	19 x 8	138.7 S(0.2089)	0.54	0.24	0.040	0.000	0.032	0.064	0.197	0.096
D3T2	19 x 6	105.2 S(0.1303)	0.49	0.25	0.030	0.000	0.025	0.052	0.203	0.083
D3T3	17 x 4	60.6 S(0.1050)	0.62	0.46	0.029	0.059	0.035	0.097	0.367	0.154
D4T1	19 x 8	132.6 S(0.3285)	0.47	0.19	0.026	0.000	0.023	0.038	0.177	0.063
D4T2	19 x 6	99.0 S(0.2445)	0.45	0.23	0.023	0.000	0.021	0.039	0.249	0.067
D4T3	18 x 6	62.0 S(0.9688)	0.57	0.31	0.023	0.045	0.027	0.081	0.277	0.126

Significance at the 5% level for χ^2 occurs when the value inside the brackets is less than 0.050.

2.5 General Discussion of Field Experiments

2.5.1 Pollinators and Their Activity

Daytime pollinators were found to be most important in cross-pollination of safflower. Most authors to date, have concluded that the honey bee *Apis mellifera,* was the most important cross-pollinator of safflower (Eckert, 1962; Levin and Butler, 1966). Presence of nectar seeking honey bees in the crop for a large part of the day indicates a potential pollination role. It is known that nectar seeking bees pick up pollen on their bodies whilst foraging. Because of this they may play an important part in pollination. Numbers visiting safflower fields were substantial. Activity of pollen foraging bees coincided with pollen release. Active foraging by pollen collectors would lead to much cross-pollination. There are considerable differences between pollen and nectar forager's behaviour on flowers. Pollen foragers tend to scramble about on flowers, and move their legs about much more than nectar collectors which just feed on nectar. It is not known which is the better pollinator of safflower.

Results of this experiment showed nectar collectors to be more frequent than pollen collectors. Variation in climate conditions and hive requirements from day to day, makes interpretation difficult. Other species flowering at the same time may have responded differently to climatic conditions. As a result, the relative attractiveness of safflower as a pollen and nectar source could have changed.

The large numbers of Dipterous insects present on the crop most likely played an insignificant part in cross-pollination. This was suggested because pollen loads on such insects were light, and movements on capitula were relatively restricted. Other pollinators such as bumble bees, butterflies and moths were present in very low numbers, although there was activity throughout the day. The low numbers involved implied a minor role as pollinators. These insects must be considered as potential supplemental pollinators.

2.5.2 Potential for Commercial Use of Bees in Safflower

Eckert (1962) indicated that safflower was a good pollen and nectar producer. The large numbers of bees observed on the crop would tend to suggest that this also applies in New Zealand.

McGregor (1976) suggested that growers of safflower would profit more than the bee keepers by having high populations of honey bees visiting the crop. Honey produced from safflower in North America has been classed as amber (Eckert, 1962) and of low quality (McGregor, 1976).

Eckert (1959) (after McGregor, 1976) recommended two honey bee colonies per acre (5 hives/ha) of safflower, but few if any farmers took steps to secure this pollinator population. Rubis (1970a) indicated that commercial cultivars were from 75% to 95% self-fertile; indicating that production improvement could occur with ample pollinator population. Low selfed seed set for cultivar 022 obtained in this study suggests that commercial safflower crops in New Zealand may also benefit from an adequate pollinator population.

2.5.3 Effects of Plant Genotype on Pollinator Activity

McGregor (1976) reported that no differences had been observed in the attractiveness of different safflower cultivars to honey bees. All cultivars seemed to be attractive. Results obtained in this study confirmed this.

Rubis *et al.* (1966) had noted that pollen collectors did not visit pollen deficient thin-hull lines. Such an observation would have been expected as pollen foragers specifically seek pollen. Pollen collectors must have some mechanism of detecting presence or absence of pollen on plants from a distance; as they did not even visit the thin-hull lines of Rubis *et al.* (1966). Bumble bees seeking both nectar and pollen simultaneously could be important pollinators of thin-hull lines. Cross-pollination of thin-hulled and normal pollen lines resulted from foraging by nectar collectors (Rubis *et al.*,1966) indicating that these insects are effective pollinators in safflower. No thin-hull lines were used in this study.

Rubis (1970 b) had observed that bees foraging on white flowers were specific to white flowered genotypes. This suggested that crossing of white flowered types with white flowered types is more probable than crossing white with other flower colours. Estimates of self-fertility based on flower colours of progeny involving parents with recessive white flower colour are therefore likely to be biased. Results of such experiments are mentioned in Section 1.4.1. Howard *et al.* (1915) noted that all their white and pale yellow flowered types bred true; however orange flowered types did not. This may have reflected either specificity of the pollinator for white, as well as pale yellow, flower colour or genotype variation in pollination pattern among the lines used.

Howard *et al.* (1915) observed geographic differences in levels of homozygosity and heterozygosity.Samples taken from farmers in various regions of India, indicated that, within regions, crops of safflower tended to be either purelines or very mixed and heterozygous. This may have indicated variation in pollinator activity between the geographic regions, and specific adaptation to it. The possibility of interference by man must also be relevant. Selection for dyeing properties has resulted in orange flowered types increasing in frequency. Such genetic changes in flower colour might have influenced the native pollinators of India. Alternatively man may have selected for self-pollinating types within certain environmentally stable regions. The presence of such geographic differences in pollination pattern within the crops native habitat, requires further study. Elucidation of the reasons for this could provide plant breeders with valuable guidelines on the adaptive ability of the crop in differing environments; as it pertains to pollination pattern. Such information could be used to determine whether region were best suited to self or cross-pollinated cultivars.

2.5.4 Implications

Abundant supplies of nectar and pollen were observed on the crop. Active foraging by honey bees suggests the crop may be a valuable resource for bee keepers.

The field study suggested that cross-pollination of safflower can occur in the presence of insects. Exclusion of insects resulted in depressed seed sets. In plant breeding projects where purity of lines is required bagging may be necessary. Higher seed yields were achieved under muslin bags when compared to glassine, although the possibility of wind pollination could not be completely ruled out.

The timing of pollen collecting bees activity coincided with pollen extrusion from florets. In artificial crossing situations, it would probably be advantageous to pollinate at this time, "attempting to mimic nature". It may be possible to utilise bees as pollinating agents in controlled pollination e.g. under cages or in glasshouses. Such use of insects would be reliant on some method of being able to positively identify crossed progeny e.g. comparisons with parents; use of male sterility; use of self-incompatibility. Selective foraging noted by other authors (but not observed in this study) might also be a useful tool in controlled pollination.

3. MAIN STUDY MATERIALS AND METHODS

3.1 Plant Materials

Safflower genotypes used were selected from part of the world collection (212 lines) plus 16 lines from Australia and 7 lines already in New Zealand.

These genotypes were surveyed for general flowering behaviour during seed increase in glasshouses. Scores were recorded of:

1. the number of stigmas with pollen present on them;
2. the amount of pollen adhering to the stigma;
3. the degree of stigmatic extrusion;
4. days to first sign of bud formation;
5. days to first flower.

The most critical factor in using a line in the main study was that sufficient seed be present; namely 50 seeds. Stratified random sampling was conducted with the flowering behaviour scores forming the basis for the strata.

On these bases the twelve genotypes, listed in Table 3.1, were used in this study.

Table 3.1 Genotypes used in the main study .

Number	Genotype	Origin	Inclusion criteria
			(based on glasshouse criteria)
1	P. I. 209289	Africa ex Pullman, USA	Full extrusion, with little pollen extruded.
2	P. I. 209290*	Egypt ex Pullman, USA	Normal dehiscence, large amount of pollen extruded.
3	P. I. 253384	Israel ex Pullman, USA	Normal dehiscence, moderate amount of pollen and extrusion.
4	P. I. 253515	Portugal ex Pullman, USA	Delayed dehiscence, small degree of stigma extrusion.
5	P. I. 253535	Portugal ex Pullman, USA	Normal dehiscence, moderate amount of pollen, moderate extrusion.
6	P. I. 253761	Iraq ex Pullman, USA	Delayed dehiscence, small degree of stigmatic extrusion.
7	P. I. 253763	Iraq ex Pullman, USA	Full extrusion, early flowering .
8	P. I. 254976	Greece ex Pullman, USA	Normal dehiscence, early flowering .
9	P. I. 262437	Africa ex Pullman, USA	Delayed dehiscence, large degree of stigmatic extrusion .
10	P. I. 306684	Italy ex Pullman,USA	Normal dehiscence, full extrusion, small amount of pollen. Late flowering .
11	022	New Zealand cultivar	Normal dehiscence, full stigmatic extrusion, large amount of pollen .
12	RIO	U.S.A. cultivar	Delayed dehiscence, large degree of stigmatic extrusion.

* *Botrytis* resistant (Knowles, 1958), but known not to be so locally.

(Gordon, unpubl.)

3.2 Trial Design

Four controlled environment rooms in a controlled environment laboratory were used. Each environment contained a randomised complete block experiment, with each block on a single trolley. There were 6 blocks per experiment with 12 genotypes per block. Each plot contained a single plant giving a total of 72 plants per room.

3.3 Controlled Environment Room Conditions

3.3.1 Environmental Conditions

Environments were selected to reflect North Island, New Zealand summer conditions. Their main features are listed in Table 3.2.

The lighting system consisted of 4 x 1000 W Sylvania "Metalarc" high-pressure discharge lamps plus 4 x 1000 W Philips quartz halogen lamps. Light was directed down in the room through a thermal barrier of glass and flowing water.

Photoperiod was graded from 12½ hours at planting to 14 hours at 4 weeks. Photosynthetically active radiation was given for the whole of this period. Average light irradiances for each room over the course of the experiment are given in Table 3.2

Temperature and humidity day/night and night/day changeovers were of 2 hours duration, with an abrupt light-dark change mid-way through the temperature changeovers.

Airflow down through the plants was 0.3 to 0.5 ms^{-1} as measured at the canopy with an Alnor Instrument thermonanemometer.

The CO_2 level was left uncontrolled; remaining within 330-360 ppm (i.e ambient conditions) as measured with an infra-red gas analyser.

Table 3.2 Main features of environments.

Env. No.	Temp. (± 0.5°C)		Rel. Hum. (± 5%)		VPD (kPa)	PAR* (Wm⁻²)
	Max	Min	Day	Night		Mean
1	28	22	74	62	-1.0	150.5
2	28	22	89	85	-0.4	151.5
3	24	18	67	52	-1.0	168.5
4	24	18	87	81	-0.4	163.5

* PAR = photosynthetically active radiation (DSIR, 1975).

3.3.2 Cultural Conditions

At least 2 pregerminated seeds were sown into each one gallon pot. These were later thinned to one plant per pot. More pots than required were planted as a precautionary measure. Extras were discarded later. Pregermination consisted of soaking seeds in water for 12 hours, then incubating them at 18°C for 48 hours on wet filter paper. Only seeds with radicles present were planted. The growing medium used was a mixture of coarse sand/peat/vermiculite (70:15:15 v/v).

Workload over the flowering period was eased by staggering planting. Environments 1 and 3 were planted on 12/3/79 and environments 2 and 4 on 7/5/79. To further distribute work load, the time of the night/day changeovers was varied for any two concurrent rooms. "Dawn" in one room was at 9.00 a.m. and in the other at 1.00 p.m. "Dawn" was the time when the lights turned on.

Modified Hoagland's nutrient solution (listed in Appendix 2) was supplied through the automated microtube system. The frequency of application increased as plants grew, to 4 x 100 mls per day. Pots were washed through twice weekly by hand with Modified Hoagland's nutrient solution to leach any accumulated mineral salts and to ensure good moisture distribution in the pot.

Orthene, a root absorbed systemic insecticide, was applied to pots at the late flowering stage to lower the incidence of thrips. Upon removal from the controlled environment room at the termination of flowering, plants were given a foliar application of a systemic fungicide (Benlate) and insecticide (Thiodan). They were then placed in a glass-house for seed development and maturation. Seed was harvested when plants had senesced.

3.4 Plant Characters Examined

Characters studied were those concerned with flowering and putative influences on pollination.

3.4.1 Amount and Viability of Pollen

Pollen viability was estimated three times in the "early morning" during early flowering on the plant. Samples were taken at 1½ hour intervals commencing at "dawn". Five freshly opened or elongating florets were removed from a single capitulum and placed in 2 mls of 1% (w/v) 2,3,5-triphenyl tetrazolium chloride, in 0.005M sodium phosphate buffer pH = 7.5*. This was incubated in the dark at 24^{0}C for 1½ to 1 3/4 hours. Florets were then macerated to release pollen. Counts were conducted on an improved Neubauer haemocytometer. Ten chambers were counted noting viable (stained red) and non viable pollen. For "Time 1" deformed pollen grains were counted separately. However, these were included with non stained grains at later times. Calculation of pollen viabilities took this into account. Deformed pollen grains were only counted in one time period to provide an index of pollen deformity among genotypes and environments. Amounts of pollen were estimated on a per floret basis. Coefficients used in such estimates were obtained from Bradbury (1973).

3.4.2 Length of Floret Parts

Two samples of five florets each were taken at "dawn" and at full extrusion. Florets opening contemporaneously were removed from a single capitulum and fixed in formalin-propionic acid-alcohol (Bradbury, 1973).

Plate 3.1 shows florets on which reference points used in measurements

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* Initial trial runs with various concentrations and incubation periods, demonstrated this technique to be satisfactory.

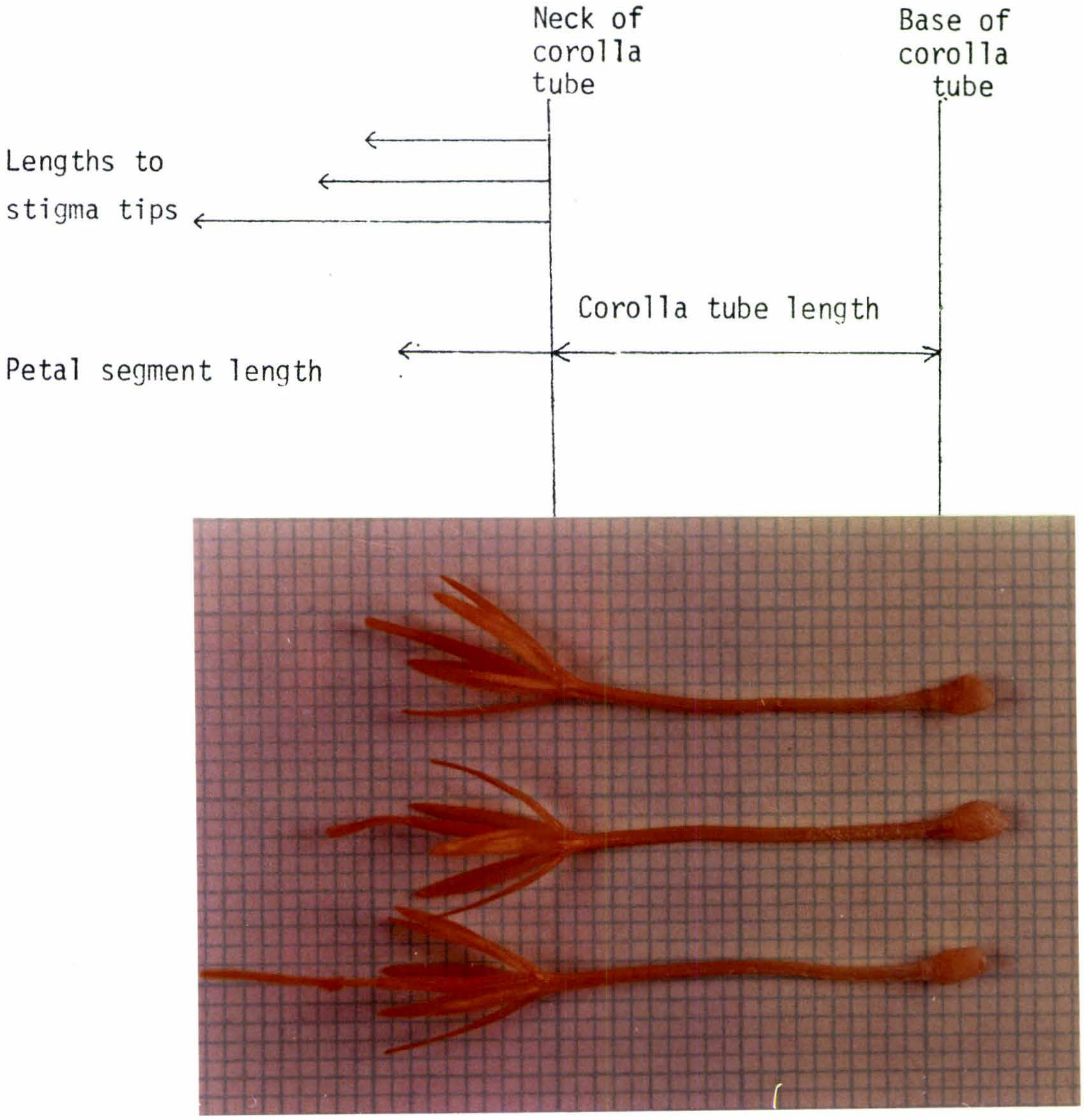


Plate 3.1 Florets at various stages of development, up to full stigmatic extrusion (1mm divisions on the grid)

are indicated.

Measurements listed below were made at a later time, for convenience, using the fixed material.

Corolla tube length: distance from the base to the neck of the corolla tube (mm).

Petal segment length: distance from the neck of the corolla tube to the anther column tip (mm). (This measurement was found in practice to approximate petal segment length, and to be easier to measure.)

Stigma tip distance: distance from the corolla tube neck to the stigma tip (mm).

Style gap: length of style exposed between the top of the anther tube and the ring of hairs at the stigma base (mm). (This measurement was used to estimate a frequency of complete stigmatic extrusion above the anther column).

Measurements were made without the use of a microscope, to the nearest 0.5 mm.

3.4.3 Number of Pollen Tubes Reaching the Stigma Base

Day old florets were collected from several capitula and fixed in formalin-acetic acid-alcohol (Bradbury, 1973). Sufficient were collected to ensure that ten would be available for observation (usually about 20). Staining was conducted at a later date, for convenience.

Styles with stigmas intact were removed carefully from the florets and washed in tap water. Tissue was then cleared by placing it in 2% (w/v) sodium hydroxide at 100°C for 10 minutes. Styles were then washed in distilled water and subsequently placed on slides in a drop of stain before being squashed and observed. The stain used was 0.1% aniline blue in

0.1N solution of potassium phosphate (Martin, 1959; Arasu, 1970).

Counts were made using an Olympus microscope with an ultra high pressure mercury illumination apparatus, in a darkened room. Illumination with ultraviolet light of a wavelength about 356 nm is necessary to cause fuorescence of the florescent pigments of the aniline blue stain, associated with the callose of pollen tubes (Martin, 1959). The excitation filters BG-12 and BG-3 were used to absorb ultraviolet wavelengths above 356 nm. The eye piece filter FY-3 (for eye protection) and the B-370 filter removed wavelengths above 470 nm (Olympus). Figure 3.1 shows the absorbance patterns of the filters used (adapted from Olympus).

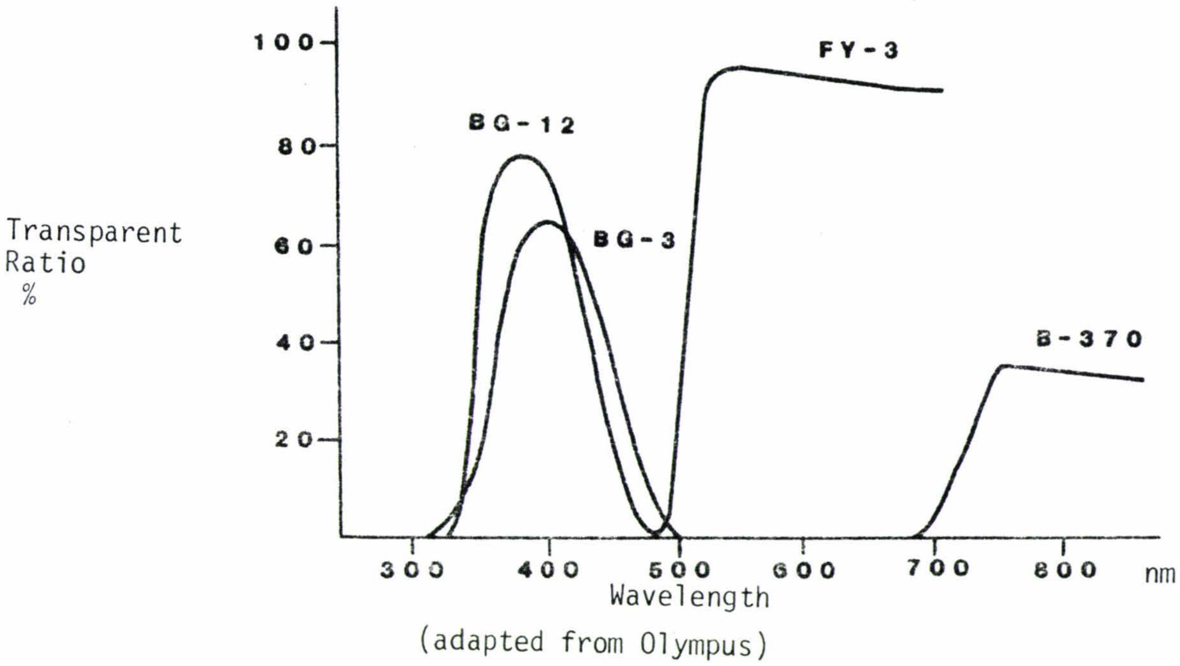
Numbers of pollen tubes were counted just below the ring of long hairs at the base of the stigma.

3.4.4 Stigma Receptivity

The use of artificial pollination as a means of assaying stigma receptivity was ruled out because of poor controlled cross seed yields (Claassen, 1950). The duration of stigma turgidity and associated esterase activity was used as a guide instead (Heslop-Harrison and Shivanna, 1977; Wiess, 1971).

Checks on stigma turgidity and esterase activity were conducted each morning, 1 to 2 hours after "dawn" on both emasculated and non-emasculated florets.

Initially freshly opened capitula were tagged. Emasculation was effected using the method of Claassen (1950), with two modifications:



(adapted from Olympus)

Figure 3.1: Absorbance of filters

1. Peripheral florets were removed, as they were found to be female sterile in all genotypes (refer to Plates 3.2 and 3.3).
2. Capitula were allowed to commence flowering before emasculation (refer to Plates 3.4 and 3.5).

Existing open florets were removed from non-emasculated heads to facilitate accurate identification of florets which had opened on a given day.

Duration of stigma turgidity was based on the number of days from floret opening, during which 50% of the florets remained unwilted.

The test for esterase activity was performed each day that stigmas were turgid. The method of Pearse (1972) was used with α-naphthyl acetate as a substrate in a coupling reaction with fast blue salt B. The test was speeded up by having stock solutions of the above in 0.005 M sodium phosphate buffer pH = 7.4 at concentrations of 0.1% (w/v) and 0.5% (w/v) respectively. Equal volumes of these solutions were mixed on five turgid stigmas. After staining for 15 minutes a score of intensity of blackness was assigned, averaged over all stigmas. The score ranged from 1 to 5 with halves:

1: no staining; 5: intense black.

3.4.5 Timing of Plant Development

The number of days from planting to:

1. the end of the rosette phase, when the first visible sign of stem elongation occurred;
2. first flower - opening of the first flower on a plant;
3. flowering median - when approximately half the number of capitula on a plant had opened. On all genotypes except genotype 10 (P.I.306684) this was about the time of opening of the last secondary head. This

Plate 3.2 A freshly opened head showing variation in the size of ovaries in the outer ring of florets. The long ones were found to be sterile. Shorter broad ones were fertile.

Plate 3.3 A head with developing seeds clearly showing the outer female sterile florets.

Plate 3.4 Safflower head at a suitable stage of growth for emasculation

Plate 3.5 Emasculated safflower head prior to elongation of stigmas.

measurement enabled the spread of flowering to be determined.

3.4.6 Flower Colour and Nectar Guide Colour

Flower colour and nectar guide colour were scored at about the flowering median. All open capitula on the plant at the time of scoring were considered. Scores from 1(cream) to 6 (red) with halves were used. (Refer to Plate 3.6).

It should be remembered that insects may see a completely different picture (Appendix 3).

3.4.7 Dead Flower Colour

Flies have been observed on safflower (Levin *et al.*,1967). It was thought dead flower colour may influence their activity. Attraction to wilting florets might inadvertently or otherwise influence pollination.

Several capitula were considered in assigning a score of wilted floret colour, at the flowering median. Scores ranged from 1 (grey) to 7 (red) with halves (refer to Plate 3.7).

3.4.8 Width of Open Capitula

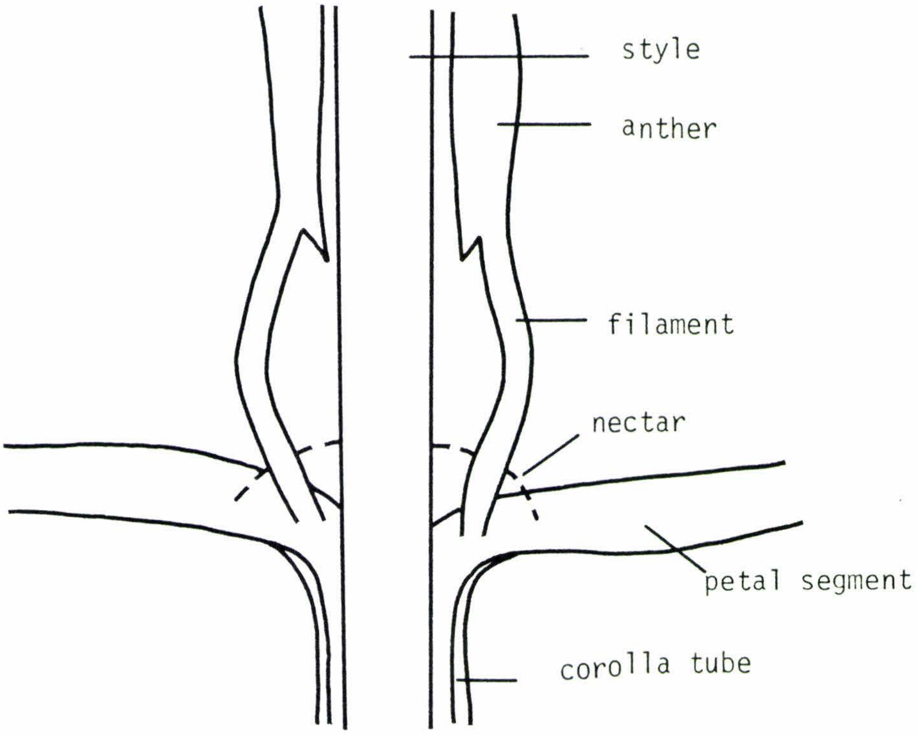
While in full flower, at about the flowering median, the diameter of three open capitula per plant were measured. Measurement was made from the extreme petal segment tips on either side of the capitulum, in mm.

3.4.9 Amount of Nectar in a Single Floret

Five classes were used to represent the amount of nectar secreted by individual florets at the flowering median; 1: no nectar present, 5: maximal nectar present. Figure 3.2 gives a schematic representation of a safflower floret with maximal nectar presence. Numerical classes

Plate 3.6 Flower colour scores for safflower heads: 1 = cream; 6 = red (lower right)

Plate 3.7 Scores of dead (wilted) flower colour: 1 = grey; 7 = red (lower right).



(from McGregor, 1976)

Figure 3.2: Longitudinal section of a safflower floret. The nectar droplet represents a score of 5.5.

were modified by +½ if the curvature of the nectar droplet was convex (as in Figure 3.2), and -½ if curvature was concave. These modifications were aimed at improving the accuracy of the score. In environments causing high evaporative losses, concave curvature might be more frequent. Where plants are still producing nectar, or where there are little or no evaporative losses, convex curvature might be more frequent. Only florets with nectar present were scored for the amount of nectar. Numbers of nectar producing florets were not recorded.

More accurate techniques of assessing nectar volume were used by Barnes and Furgala (1978). Time constraints prevented the use of such techniques in this study.

3.4.10 Floret Density

Open capitula in the second day of flowering were evaluated and given a score from 1 to 5 (with halves) based on increasing density of florets; 1: florets tightly packed; 5: florets loosely packed. (Refer to Plate 3.8).

3.4.11 Uniformity of Floret Emergence

Florets opening on a given day were either uniform or variable in their development. Scores from 1 to 5 (with halves) were assigned, indicating increasing heterogeneity of floret development. When capitula were split open in the early morning, florets formed basic patterns, indicating whether or not development was to be homo- or hetero-geneous. Such development could also be observed visually from above the capitula. (Refer to Plate 3.9).

Plate 3.8 Scores of floret density: 1 = tightly packed (lower right); 5 = loosely packed (upper left).

Plate 3.9 Scores of uniformity of floret emergence: 1 = uniform (upper left); 5 = highly variable (lower right).

3.4.12 Amount of Pollen Extruded

The amount of pollen extruded on stigmas was scored at full stigmatic extrusion. Scores increasing from 1 to 6 (with halves) indicated increasing thickness of the pollen coating on the stigma (refer to Plate 3.10).

3.4.13 Positioning of Pollen Adhesion

The positioning of pollen on the stigma at full extrusion indicates the relative position of the stigma at anther dehiscence. A full coating of pollen indicated that the stigma was still inside the anther column at dehiscence, and was assigned a value of 5. One indicated the complete lack of pollen at the base of the stigma. Intermediary scores indicated pollen presence further down the stigma from its tip. (Refer to Figure 3.3).

3.4.14 Number of Stigmas with Pollen Present

Deciles of stigmas with pollen present were indicated by scores from 1 to 10. Scoring was conducted about the time of the flowering median. All heads with full stigmatic extrusion at that time were considered.

3.4.15 Degree of Stigmatic Extrusion

Exposure of the stigma above the anther column was scored on a 1 to 5 (with havles) basis. A value of 1 signified complete lack of stigmatic extrusion above the anther column; 5 indicated complete extrusion with 2-3 mm of style showing above the anther column. Plate 3.11 shows the range of stigmatic extrusion.

3.4.16 Timing of Stigma Presence and Full Stigmatic Extrusion

The time of stigma presence and full stigmatic extrusion were recorded at about the flowering median. All capitula which had opened on previous days were considered.

Plate 3.10 Scores of amount of pollen extruded: 1 = no pollen (left); 6 = much pollen (right).

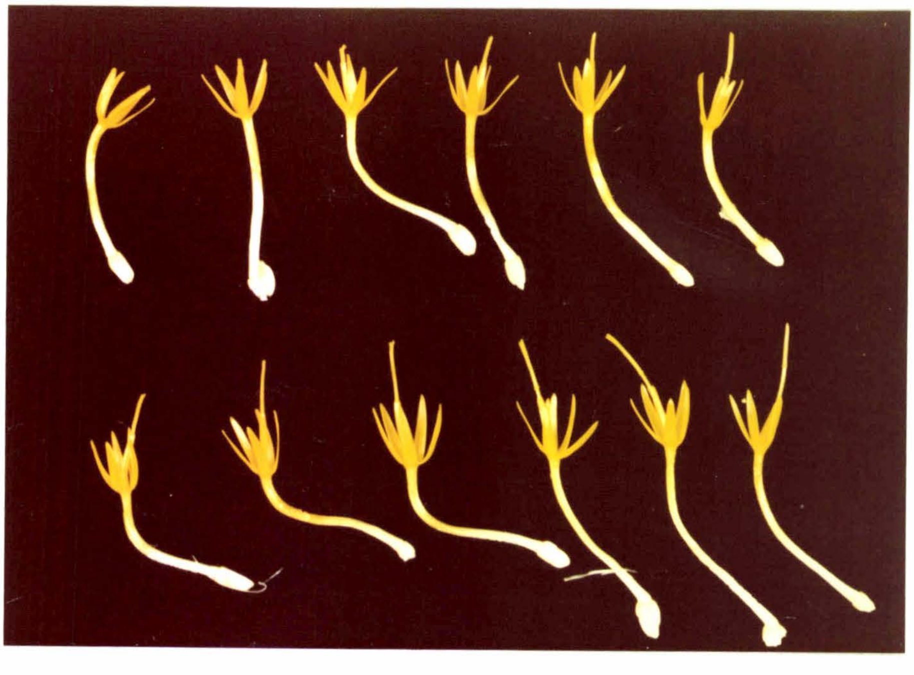


Plate 3.11 The range of stigma extrusion shown was represented by a score of 1 to 5: 1 = no extrusion; 5 = full

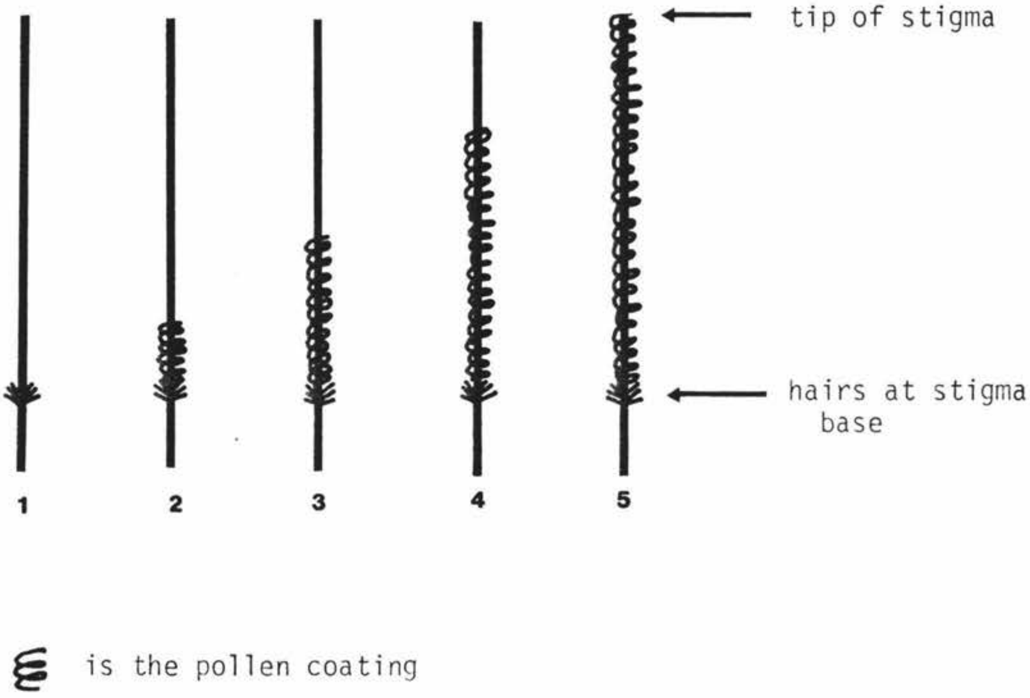


Figure 3.3: Diagrammatic representation of positioning of pollen adhesion.

Stigmatic presence was defined as being when 50% of opening florets had the stigma visible above the anther column. Similarly full extrusion was when 50% of the opening florets had reached equivalent stigmatic extrusion to older florets on the same capitulum.

The capitula were observed at hourly intervals from "dawn". If stigmas were present at dawn a value of 0 hours was given. In such cases no idea of the actual time of stigma presence could be estimated. Normally stigma presence was accompanied by pollen extrusion from the anther column. The time (in hours) taken for full extrusion to occur was also recorded.

These times were utilised with floral part length measurements, to estimate rates of development.

3.4.17 Number of Capitula

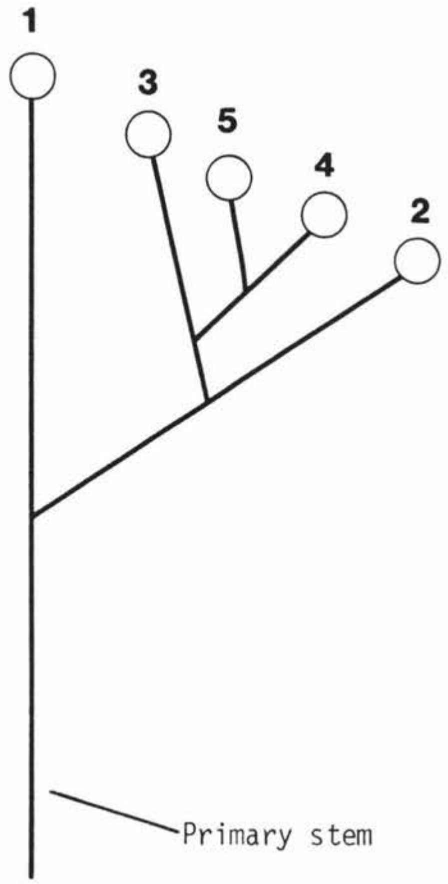
Counts were made at harvest of the number of heads falling into secondary, tertiary, quarternary and quinternary categories. Figure 3.4 defines these categories, and relates them to the branching pattern.

3.4.18 Plant Height

The distance (in cm) from the soil surface to the highest point on the plant was recorded at harvest. Only a single value could be obtained per plot.

3.4.19 Seed Set

Six to nine heads were labelled, with two to three being randomly assigned to each of three treatments. The treatments consisted of:



Capitula categories

1 = primary capitula
2 = secondary capitula
3 = tertiary capitula
4 = quarternary capitula
5 = quinternary capitula

Figure 3.4 : Diagrammatic representation of the branching pattern of safflower, and consequential categories of capitula.

1. Crossed seed set

Capitula were crossed to mimic insect pollination. Pollinations were accomplished by picking a single capitulum off any genotype and gently rubbing it on all other capitula to be crossed. Such pollinations were conducted in the "early morning". As the capitula used for crossing moved across all genotypes, and picked up pollen; pollen used was from a mixed source, and should have been viable, at this time. Such a pollen source should have overcome any pollen related genetic pollination and fertilization controls.

Tags on these capitula recorded the number of days duration, of flowering within a head.

2. Selfed seed set (bagged)

Glassine bags were used to prevent any cross pollination occurring. Bags were placed over capitula before the commencement of flowering, and removed after florets had wilted.

3. Selfed seed set (ordinary)

Capitula were left untouched, allowing complete expression of plant pollination influences within the controlled environment room.

Seed counts were made at harvest, on a per capitulum basis.

3.4.20 Character Abbreviations

A full list of abbreviations used as character labels is given in Table 3.3. These abbreviations are used widely in the text and tables.

Table 3.3 Abbreviations used for character names

1.	VP%1	Percent viable pollen at time 1.
2.	DP%	Percent abnormal pollen at time 1.
3.	VP%2	Percent viable pollen at time 2.
4.	VP%3	Percent viable pollen at time 3.
5.	AP1	Amount of pollen at time 1 (x 10^{-3})
6.	AP2	Amount of pollen at time 2 (x 10^{-3})
7.	AP3	Amount of pollen at time 3 (x10^{-3})
8.	AVP1	Amount of viable pollen at time 1 (x 10^{-3})
9.	AVP2	Amount of viable pollen at time 2 (x 10^{-3})
10.	AVP3	Amount of viable pollen at time 3 (x 10^{-3})
11.	TAVP	Total amount of viable pollen summed over time (x 10^{-3})
12.	LCT1	Length of the corolla tube at dawn (mm)
13.	LP1	Length of the petal segments at dawn (mm)
14.	LS1	Length from the corolla tube neck to the stigma tip at dawn (mm)
15.	LCT2	Length of the corolla tube at full extrusion (mm)
16.	LP2	Length of the petal segments at full extrusion (mm)
17.	FREQST	Frequency of style exposure above the anther tube.
18.	LS2	Length from the corolla tube neck to the stigma tip at full extrusion (mm)
19.	RSEXPA	Rate of style expansion (mm hr^{-1})
20.	RCTEXPA	Rate of corrolla tube expansion (mm hr^{-1})
21.	RPEXPA	Rate of petal expansion (mm hr^{-1})
22.	PPTEXT	Duration of stigmatic expansion (hr)
23.	RSEXPO	Rate of stigmatic exposure (mm hr^{-1})
24.	PT	Number of pollen tube reaching the base of the stigma
25.	ROSETTE	Duration of the rosette phase (days)
26.	FLOW	Days from planting to first flower (days)
27.	FLMED	Days from planting to the flowering median (days)

Table 3.3 continued

28.	FL	Duration of flowering within a head
29.	HEIGHT	Plant height at maturity (cm)
30.	TNH	Total number of capitula on the plants
31.	FCOL	Score of flower colour
32.	NCOL	Score of nectary guide colour
33.	DFCOL	Score of dead flower colour
34.	AC	Surface area of capitula (cm)
35.	NEC	Score of the amount of nectar present
36.	FDENS	Score of floret density within the head
37.	FE	Score of the uniformity of floret emergence
38.	AMTPOL	Score of the amount of pollen adhering to extruded stigmas
39.	ARPOLAD	Positioning of pollen adhesion to the stigma
40.	NSTIG	Score of the number of extruded stigmas with pollen present
41.	DEXT	Score of the degree of stigmatic extrusion
42.	PP	Timing of pollen presence from dawn (hr)
43.	TEXT	Timing of full stigmatic extrusion from dawn (hr)
44.	ESTA	Difference in esterase activity between emasculated and non-emasculated florets
	CROSS	Number of seeds obtained from crossed heads
	SELF1	Number of seeds obtained from bagged heads
	SELF2	Number of seeds obtained from untouched heads
	SELF1%	Percent self pollination under bags
	FS	Index of the spread of flowering (FLMED-FLOW)
	FLWID	Width of open capitula (mm)
	SEC	Number of secondary heads
	TERT	Number of tertiary heads
	QUART	Number of quarternary heads
	QUIN	Number of quinternary heads

3.5 Data Handling

Characters measured using scores ranging from 1 up to 7 had their values doubled so as to treat halves as units on the new scale. Such scales were quasi-continuous (Anderberg, 1973). All discussion of results relates to this scale. Data did not require centring.

Plot means were obtained for all characters where multiple observations had been made, on a single plot. Missing values were then estimated as outlined in Section 3.5.1.

3.5.1 Missing data

The regression technique using dummy variables, (as outlined in Section 1.6.4) was used to estimate missing values. Data utilised in the estimates came only from the genotype (within the environment) in question. Regressions were conducted using the computer program SPSS/ REGRESSION (Nie *et al.*,1975).

Degrees of freedom for error in this experiment were large at 55 for a single environment and 220 in the pool. F values associated with these were 1.97 and ≈ 1.83 respectively, for significance testing of genotypic variance (i.e. numerator degrees of freedom = 11). In the worst single environment there were 12 missing plots, and in the pool (across all single environments) there were 25, for the worst character. Missing plots were random across all genotypes. F values for reduced error degrees of freedom of 43 and 195 were ≈ 2.02 and ≈ 1.83 respectively. Such differences in F values were relatively minor. Therefore reduction of error degrees of freedom for each missing plot was not considered necessary, it having only trivial effect on any significance testing in this experiment. In addition, only genotype means in the pooled environment were examined, not those within single environments. Therefore only error degrees of freedom in the pooled environment would have needed consideration.

3.5.2 Statistical Analyses

3.5.2.1 Populations of Inference

As random effects models are to be used in the statistical analyses it is necessary to state the populations of inference, to which statistical parameters estimated by these experiments apply. The genotype population of inference is the locally held safflower germplasm collection from which the genotypes utilised in this study were drawn. The environment population of inference is more restricted, and is defined as controlled environment conditions reflecting North Island, New Zealand summer conditions.

3.5.2.2 Multiple Regression Analysis

Multiple regression analysis was used to assess relative importance of independent variables in determining self-pollination percent, under bags. The computer program SPSS/REGRESSION was used (Nie *et al.*, 1975).

Prior to regression, plots were made of Y (dependent variable) against each X (independent variable), using the computer program SPSS/SCATTERGRAM (Nie *et al.*, 1975). No curvilinear trends were detected, therefore transformation of the data was considered not necessary (Draper and Smith, 1966 ; Edwards, 1979).

Independent variables were then regressed against the dependent variable (self-pollination percent under bags) for each environment separately, and then pooled over all environments. Dummy variables were constructed to refine the residual by removing unmeasured genotype effects in single environments. Dummies were similarly utilised to remove unmeasured genotype, environment and interaction effects in the pool (Draper and Smith, 1966).

Estimates of standardised partial regression coefficients ($\hat{\beta}'_k$) were used to determine relative importances of each of the independent variables, in predicting Y. The functional relationship between the standardised dependent variable given by the standardised regression equation is presented in Figure 3.5. A path coefficient diagram based on this model is also shown (Figure 3.5). Standardised regression coefficients were then ranked according to magnitude. Important characters could then be identified on this basis.

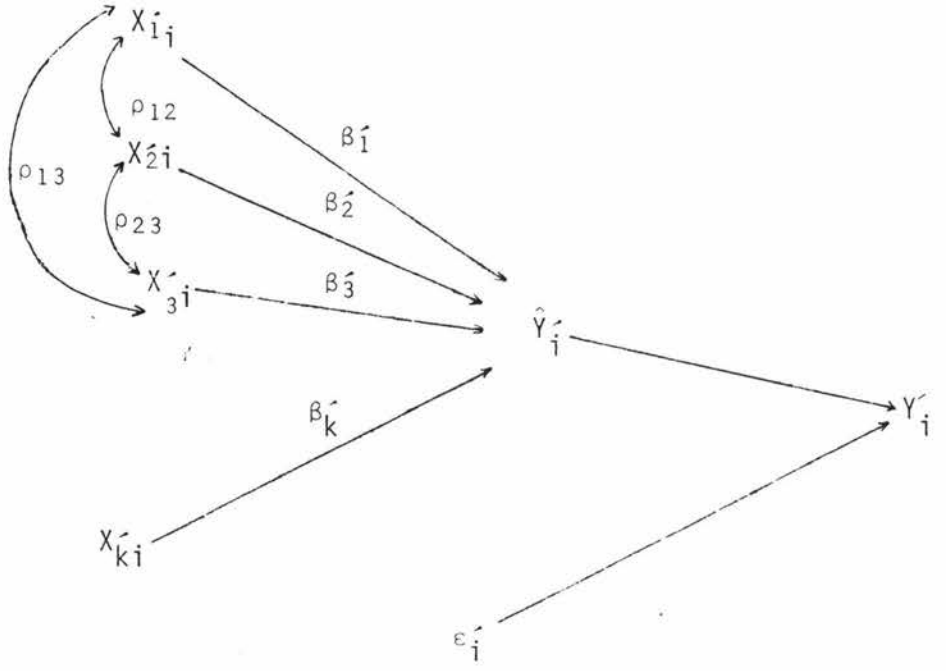
Figure 3.5 The standardised regression model, and the related path coefficient diagram

The standardised regression model:

$$Y'_i = \beta'_1 X'_{1i} + \beta'_2 X'_{2i} + \beta'_3 X'_{3i} + \ldots\ldots\ldots \beta'_k X'_{ki} + \varepsilon'_i$$

(Draper and Smith, 1966)

The path coefficient diagram



(Li, 1975)

where Y'_i is the i^{th} standardised observation of Y

$\hat{Y}'_i$ is the regression estimate of the standardised observation of Y

β'_k is the k^{th} independent variable regression coefficient

X'_{ki} is the i^{th} standardised observation of the k independent variable

ε'_i is the i^{th} observations standardised residual

ρ is the simple correlation coefficient between various independent variables.

3.5.2.3 Principal Factor Analysis

Principal factor analysis was used as an aid in determining the most important characters influencing self-pollination under bags, because no clear patterns emerged in the standardised partial regression coefficients ($\hat{\beta}_k'$) from the various environments (refer to Section 3.5.2.2). Analysis was conducted using the computer program SPSS/FACTOR (Nie *et al.*, 1975).

Absolute values of the estimates of standardised partial regression coefficients were used as a data base. Environments were used as "variables" with the independent characters as "individuals" which were to be discriminated amongst.

The most important factors were determined by the amount of variation of the vector variable (ζ) that they explained. Once determined, their factor structures were noted by observing the partial correlations of the factor concerned, with the original variables (environments). Factor scores (for the most important factors) for each independent character were examined to ordinate the characters ('pooled' across all environments) and thereby indicates their relative importance in determination of self-pollination.

3.5.2.4 Analysis of Variance

A computer program PHANIE (Gordon unpubl.) was used to conduct analysis of variance, and to estimate heritability ratios.

Each character was analysed using the random effects model for a randomised complete block design in single environments. An analysis pooled over environments was also conducted. All effects were assumed random, independent deviates with expectations equal to zero and generating variances of corresponding designation.

The populations of inference for genotypes and environments are oultined in Section 3.5.2.1.

Models on which these analyses are based, are given below.

Single environment model

$$X_{ij} = \mu + \beta_j + \gamma_i + \varepsilon_{ij}$$

where j = 1.........b blocks

i = 1.........g genotypes

and

X_{ij} is an individual observation on the i^{th} genotype in the j^{th} block

μ is the population mean for the character being considered

β_j is the j^{th} block effect

γ_i is the i^{th} genotype effect

ε_{ij} is the individual residual ("error").

Pooled environment model

$$X_{ijk} = \mu + \beta_{j(k)} + \gamma_i + \eta_k + \gamma\eta_{ik} + \varepsilon_{ijk}$$

where j = 1.......b blocks

i = 1.......g genotypes

k = 1.......e environments

and

X_{ijk} is an individual observation of the i^{th} genotype in the j^{th} block and k^{th} environment.

μ is the population mean for the character being considered

$\beta_{j(k)}$ is the jth block effect in the kth environment

γ_i is the ith genotype effect over all environments

η_k is the kth environment effect over all genotypes

$\gamma\eta_{ik}$ is the interaction effect of the ith genotype in the kth environment

ε_{ijk} is the individual residual ("error").

The expectations of mean squares and appropriate F tests are listed in Tables 3.3 and 3.4 for the two models (Gordon *et al.*,1972).

One of the assumptions underlying pooling was tested by examining the homogeneity of error variances across the four environments. Bartlett's chi-square test was used to test error variance homogeneity following the procedure of Steel and Torrie (1960). If errors proved heterogeneous data were standardized and reanalyzed. The environment means were not subtracted.

i.e. $$X'_{ijk} = \frac{X_{ijk}}{S_k}$$

where

X_{ijk} is an individual observation of the ith genotype in the jth block and kth environment

S_k is the standard deviation of data in the kth environment

X'_{ijk} is the standardised individual observation of the ith genotype in the jth block and kth environment.

This means the scale of the analysed variables is now in standard deviates.

Table 3.4 Expectations of mean squares for the single environment model

Model: $X_{ij} = \mu + \beta_j + \gamma_i + \varepsilon_{ij}$.

Source	df	MS	E(MS)	F
Blocks	(b-1)	MS1	$\sigma^2+g\sigma^2_B$	MS1/MS3
Genotypes	(g-1)	MS2	$\sigma^2+b\sigma^2_G$	MS2/MS3
Error	(b-1)(g-1)	MS3	σ^2	
Total	bg-1			

The respective variance component estimates in the E(MS) are:

σ^2_B arising from β_j the block effect

σ^2_G arising from γ_i the genotype effect

σ^2 arising from ε_{ij} the residual ("error")

Table 3.5 Expectations of mean squares for the pooled environments model

model: $X_{ijk} = \mu + \beta_{j(k)} + \gamma_i + \eta_k + \gamma\eta_{ik} + \varepsilon_{ijk}$

source	df	MS	E(MS)	F
Environments	e-1	MS1	$\sigma^2 + b\,\sigma^2_{GE} + g\sigma^2_{B(E)} + bg\sigma^2_E$	$\frac{MS1+MS5}{MS2+MS4}$
Blocks	b-1	MS2	$\sigma^2 + g\sigma^2_{B(E)}$	$MS2/_{MS5}$
Genotypes	g-1	MS3	$\sigma^2 + b\,\sigma^2_{GE} + be\,\sigma^2_{G}$	$MS3/_{MS4}$
Genot - Env	(g-1)(e-1)	MS4	$\sigma^2 + b\,\sigma^2_{GE}$	$MS4/_{MS5}$
Error	e(g-1)(b-1)	MS5	σ^2	
Total	egb-1			

The respective variance component estimates from the E(MS) are:

$\sigma^2_{B(E)}$ arising from $\beta_{j(k)}$ the block effect

σ^2_G arising from γ_i the genotype effect

σ^2_E arising from η_k the environment effect

σ^2_{GE} arising from $\gamma\eta_{ik}$ the interaction effect

σ^2 arising from ε_{ijk} the residual ("error")

Subdivision of data into sets of environments with homogeneous error variances was not attempted. Such subdivision would fragment data, with little gain in comparing environment and genotype means among homogeneous subsets.

The complex F-test of environments shown in Table 3.5 requires a weighted degree of freedom (df') estimated as

$$df' = \frac{(\sum_{n} a_n \; MS_n)^2}{\sum_{n} \frac{MSn}{dfn}}$$

where n = number of mean squares involved

a = weighting factor; which is one when whole mean squares are used.

MS and df represent means squares and their degrees of freedom.

Degrees of freedom for both demoninator and numerator were calculated (Satterthwaite, 1946).

These data could equally have been analysed using a more complex model to separate temperature, humidity and their interaction effects (Le Clerg *et al.*,1962). As only two levels of these environmental variables were used, low degrees of freedom would have resulted. Sampling of the temperature and humidities would have been severely restricted. Such a model was not used, therefore.

In a sampling experiment Balaam (1963) showed the least significant difference to be more efficient than the Ducan's procedure, in discerning differences among small numbers of means. Least significant differences L.S.D. were used in this study to place pooled genotype and single environment means into significance groups, as small numbers of genotypes and environments were involved.

Where means of genotypes pooled over environments were ranked into significance groups variance components derived from the pooled analysis were used to estimate the L.S.D. Heterogeneity of errors precluded the use of the L.S.D. in ranking environments, for some characters. In such cases individual t-tests utilising appropriate error variances, were used to place environments in significance groups. Appropriate formulas are given by Steel and Torrie (1960).

3.5.2.4.1 Heritability estimates

Two forms of broadsense heritability can be and were derived based on the variance component estimates of Table 3.5 (Gordon *et al*,,1972).

(a) A full or complete phenotypic variance definition, where the phenotypic variance contains all the variance components including block and environmental effects.

$$h_F^2 = \frac{\sigma_G^2}{\sigma^2 + \sigma_G^2 + \sigma_{GE}^2 + \sigma_{B(E)}^2 + \sigma_E^2}$$

(b) A utilitarian or restricted phenotypic variance definition, where phenotypic variance contains variance components associated with phenotypic differences.

$$h_R^2 = \frac{\sigma_G^2}{\sigma^2 + \sigma_G^2 + \sigma_{GE}^2}$$

The numerator σ_G^2 may be narrow or broad depending upon the genotypes used and their previous genetic history. Crossing experiments permit partitioning of σ_G^2 into additive, dominance and epistatic effects. It is therefore evident that h^2 may be of many different types depending on what is included on the numerator and denominator.

Standard errors of heritability estimates were estimated using the methods outlined by Gordon *et al.* (1972).

3.5.2.5 Adaptation Analysis

Where significant genotype-environment interaction variance was found in the pooled analysis of variance, adaptation analysis was conducted. The genotype-environment interaction sum of squares was partitioned according to each genotype. Such sums of squares are known as ecovalences. Such sum of squares for each genotype are given by

$$\sum_k (\overline{X}_{i.k} + \overline{X}_{...} - \overline{X}_{i..} - \overline{X}_{..k})^2$$

where $i = 1......g$ genotypes

$k = 1......e$ environments

and $\overline{X}_{i.k}$ is the i^{th} genotype mean in the k^{th} environment

$\overline{X}_{...}$ is the grand mean

$\overline{X}_{i..}$ is the i^{th} genotype mean over all environments.

$\overline{X}_{..k}$ is the mean of the k^{th} environment.

Regression methods outlined by Finlay and Wilkinson (1963) and Eberhart and Russell (1966) were used to observe the pattern of adaptability. Linear regressions of genotype mean ($\overline{X}_{i.k}$) against environment means ($\overline{X}_{..k}$) were computed. Using terms outlined for the pooled environments model in Table 3.5; the above regression in effect derives a relationship between $\gamma_i + \eta_k + \gamma\eta_{ik}$(the Y variate) and η_k as the X variate (Hill, 1975), across environments for each genotype. As a result the regression coefficient derived includes environmental variance and the portion of the genotype - environment interaction variation which is a linear function of environments. The remaining part of the genotype - environment interaction variance forms the unexplained deviations from the regression line. The coefficient of determination (R^2) for the regression line gives an index of the degree of deviation about regression. Genotypes with low coefficients of determination, indicating large deviations about the regression line have been defined as unstable by Eberhart and Russell (1966). Well adapted genotypes were defined as those with high mean yield; adaptation coefficients (syn.regression coefficient)equalling 1 and deviations from regression as small as possible (high coefficient of determination or stability coefficient). (Refer Figure 3.6). Negative regression coefficients are possible in adaptation analysis. (Owino, 1977).

Adaptation analysis was performed using the computer program PHANIE (Gordon unpubl.). The regression coefficients significance was determined by examining its departure from 0 and 1 using t-tests (Steel and Torrie, 1960). Standard errors of the genotype'sown regression coefficients were used.

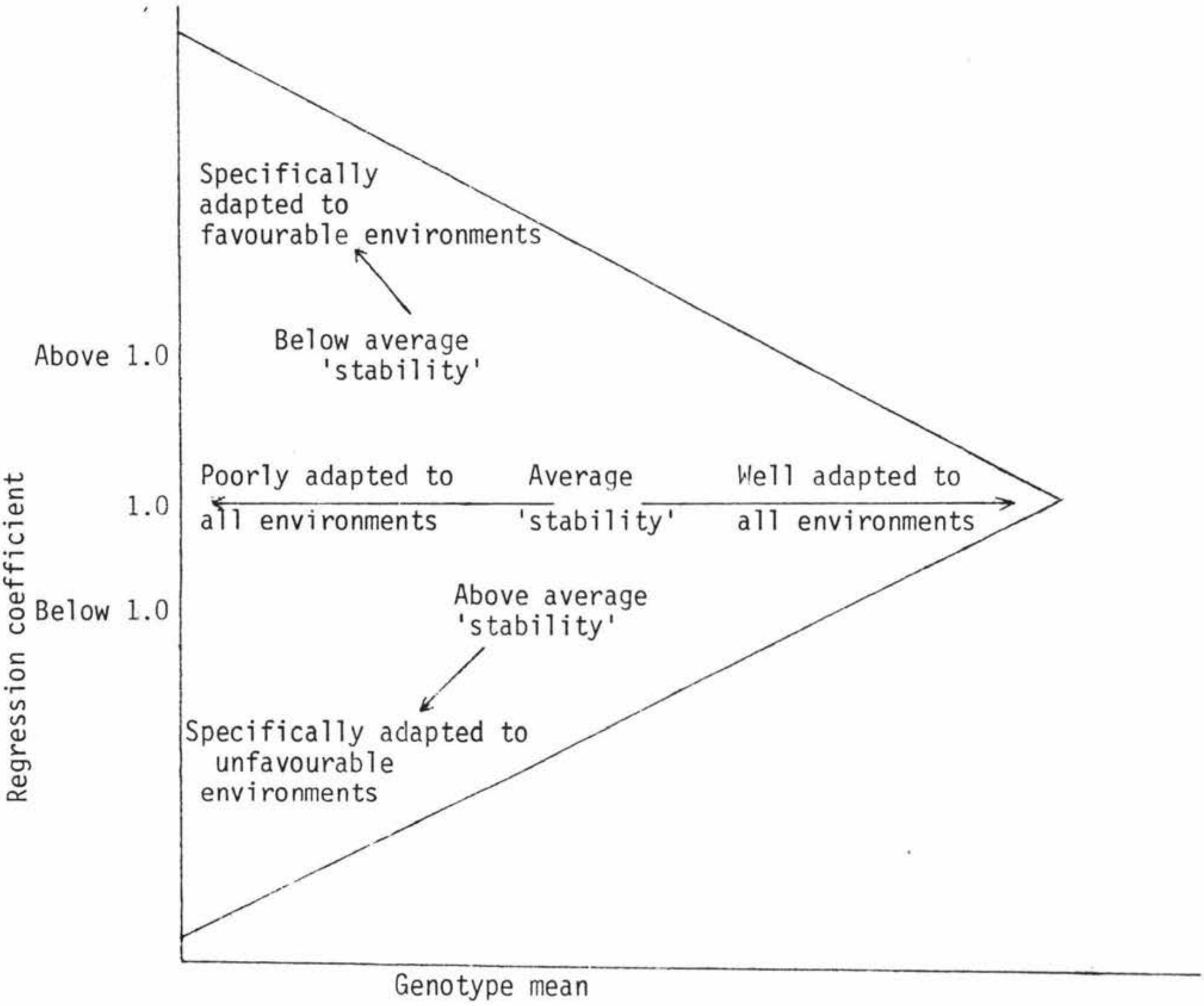


Figure 3.6 The relationship of genotype regression coefficient and genotype mean in terms of 'adaptability' (from Finlay and Wilkinson, 1963)

4. MAIN STUDY RESULTS AND ASSOCIATED DISCUSSION

4.1 Multiple Regression Analysis

In scattergrams of independent variables against the dependent variable, no curvilinear trends were detected. Transformation of the data for regression was therefore not necessary.

Coefficients of determination are presented in Table 4.1. The coefficients are high in the single environments indicating the explanation of a large portion of the total variation in the data. The considerably lower value obtained for the pooled environment may reflect heterogeneity of regression.

Summary regression statistics including the unstandardised partial regression coefficients for single and pooled environment analyses are presented in Appendix 4.

Table 4.2 gives the standardised partial regression coefficients derived from the equations for single and pooled environment analyses. Negative standardised partial regression coefficients ($\hat{\beta}'_k$) distinguish independent variables negatively associated with self-pollination percent, the dependent variable. Most independent variables resulted in standardised partial regression coefficients of small magnitude. Those variables having standardised partial regression coefficients of high absolute magnitude, were important in determining self-pollination percent.

Signs of standardised partial regression coefficients varied considerably from environment to environment, making interpretation difficult.

Table 4.3 gives the ratios of the absolute standardised regression coefficients of the independent variables to LS2 which obtained the largest value ($\hat{\beta}'_k$) in the pooled environment analysis. It can be seen that the independent characters vary greatly in relative importance between environments. A principal factor analysis (Section 4.2) was used to discriminate among characters influencing self-pollination over all environments.

Table 4.1 Total coefficients of determination (R^2) for regression equations with dummy variables present.

Environment	1	2	3	4	Pool
Total R^2	0.82392	0.90741	0.94134	0.87547	0.65866

Table 4.2 Standardised partial regression coefficients ($\hat{\beta}'_k$) for the independent characters entered into the regression equation (with dummy variables present)

	Environments				
Character	1	2	3	4	Pool
VP%1	0.71013	-0.72277	0.74543	0.77267	-0.11453
DP%	1.13525	-0.06484	-0.17659	-0.07113	0.01860
VP%2	-0.67281	1.34559	0.72852	-0.31451	0.24355
VP%3	-0.04700	2.16488	1.37389	0.26807	-0.00771
AP1	0.05089	-0.17301	0.15775	0.09874	-0.11081
AP2	0.35169	0.24686	0.28963	-0.00325	0.22928
AP3	-0.13413	1.21419	0.82196	-0.36077	0.04716
AVP1	-0.53376	2.58142	2.42807	-0.31935	0.18918
AVP2	0.08712	1.43397	3.03835	0.90067	-0.24686
AVP3	#	#	#	#	0.00005
TAVP	0.36835	-5.34149	-6.06939	-0.31323	#
LCT1	-0.74541	-3.84481	-1.45445	1.72311	-0.20467
LP2	-4.12169	-4.38696	1.73932	-3.36489	-0.14352
LS1	1.13397	1.52329	1.44064	-0.17048	0.03573
LCT2	-0.38503	2.99741	1.07247	-1.73059	0.03508
LP2	4.10963	5.49495	-0.26924	3.42899	0.43277
FREQST	0.01335	-0.34630	-1.39472	0.23232	-0.08751
LS2	-1.29884	-1.47184	-4.14637	0.98535	-0.43696
RSEXPA	0.59230	2.04620	2.58533	-0.51147	0.30158
RCTEXPA	-0.43151	-3.41354	-3.65711	1.67122	-0.37717
RPEXPA	-2.30340	-1.46776	0.65379	-1.17618	-0.07251
PPTEXT	0.62794	0.17715	0.39121	0.28175	#

Table 4.2 ctd.

Character	1	2	3	4	Pool
RSEXPO	0.43192	-0.44134	0.55005	-0.13193	0.05668
PT	-0.19954	-0.27144	0.01534	0.11133	0.02443
ROSETTE	0.17581	-0.21099	-0.24368	0.13876	0.00763
FLOW	0.66613	0.67407	-0.57760	-0.22382	-0.07108
FLMED	0.20444	-0.22193	0.12852	0.17303	0.07004
FL	-0.13267	-0.24638	0.20121	-0.11352	-0.08100
HEIGHT	-0.13198	0.93867	0.25357	0.32111	0.19660
TNH	0.02253	0.01195	-0.45205	-0.22178	0.08207
FCOL	-0.00057	-1.09677	-1.52156	-0.27780	0.09115
NCOL	-0.28791	0.44967	-0.16035	0.47754	-0.04672
DFCOL	0.35841	-0.53204	1.26184	-0.36980	-0.02277
AC	0.00125	-0.04025	-0.43315	0.36561	0.01944
NEC	-0.09369	9.42651	-0.46262	0.31273	-0.01600
FDENS	0.04038	0.91354	0.21567	-0.59439	-0.07008
FE	-1.16494	0.72982	-0.47129	-0.10323	-0.04458
AMTPOL	0.32727	-0.44974	0.49417	0.25214	0.03010
ARPOLAD	-0.15300	0.26806	0.17154	-0.18443	-0.00710
NSTIG	0.05786	-0.02775	0.14498	-0.05345	-0.02918
DEXT	-0.15594	-0.39971	1.24646	0.38735	-0.05520
PP	-0.10799	0.03375	0.15891	0.48075	-0.00346
TEXT	#	#	#	#	0.20389
ESTA	0.24952	-0.06523	0.34293	-0.07711	0.03000

Linearity with other variables was detected, and parameters were therefore not estimated.

Table 4.3 Ratios of standardised partial regression coefficients for each variable over the value for LS2 i.e. Importances relative to LS2.

	Environments				
Character	1	2	3	4	Pool
VP%1	0.54674	0.49107	0.17978	0.78416	0.26211
DP%	0.87405	0.04405	0.04259	0.07219	0.04257
VP%2	0.51801	0.91422	0.17570	0.31919	0.55737
VP%3	0.03619	1.47087	0.33135	0.27206	0.01764
AP1	0.03918	0.11755	0.03805	0.10021	0.25359
AP2	0.27077	0.16772	0.06895	0.00330	0.52472
AP3	0.10327	0.82495	0.19824	0.36613	0.10793
AVP1	0.41095	1.75387	0.58559	0.32410	0.43295
AVP2	0.06080	0.97427	0.73277	0.91406	0.56495
AVP3	#	#	#	#	0.00011
TAVP	0.28360	3.62912	1.46378	0.31789	#
LCT1	0.57390	2.61225	0.35078	1.74873	0.46840
LP1	3.17336	2.98060	0.41948	3.41492	0.32845
LS1	0.87306	1.03496	0.34745	0.17301	0.08177
LCT2	0.29644	2.03651	0.25865	1.75632	0.08028
LP2	0.31640	3.73339	0.06493	3.47997	0.99041
FREQST	0.01028	0.23528	0.33637	0.23577	0.20270
LS2	1.00000	1.00000	1.00000	1.00000	1.00000
RSEXPA	0.45602	1.39023	0.62352	0.51907	0.69018
RCTEXPA	0.33223	2.31923	0.88200	1.69607	0.86317
RPEXPA	1.77343	0.99723	0.15768	1.19367	0.16594
PPTEXT	0.48346	0.12036	0.09435	0.28594	#
RSEXPO	0.33254	0.29986	0.13266	0.13389	0.12971
PT	0.15363	0.18442	0.00370	0.11299	0.05591
ROSETTE	0.13536	0.14335	0.05870	0.14082	0.17460

Table 4.3 continued

Character	1	2	3	4	Pool
FLOW	0.51287	0.45798	0.13930	0.22715	0.16267
FLMED	0.15740	0.15078	0.03100	0.17560	0.16029
FL	0.10214	0.16740	0.04853	0.11521	0.18537
HEIGHT	0.10161	0.63775	0.06115	0.32588	0.44993
TNH	0.01735	0.00812	0.10902	0.22508	0.18782
FCOL	0.00044	0.74517	0.36696	0.28193	0.20860
NCOL	0.22167	0.30552	0.03867	0.48463	0.10692
DFCOL	0.27595	0.36148	0.30432	0.37530	0.05211
AC	0.00096	0.02735	0.10446	0.37105	0.04449
NEC	0.07213	0.28978	0.11157	0.31738	0.03662
FDENS	0.03109	0.62068	0.05201	0.60323	0.16038
FE	0.89691	0.49586	0.11366	0.10476	0.10202
AMTPOL	0.25197	0.30556	0.11918	0.25589	0.06889
ARPOLAD	0.11780	0.18213	0.04137	0.18717	0.01625
NSTIG	0.04455	0.01885	0.03497	0.05424	0.06678
DEXT	0.12006	0.27157	0.30061	0.39311	0.12633
PP	0.08314	0.02293	0.03833	0.48790	0.00792
TEXT	#	#	#	#	0.46661
ESTA	0.19211	0.04432	0.08271	0.07826	0.06866

variable did not enter regression

4.2 Principal Factor Analysis

This was conducted using the absolute values of the environment standardised partial regression coefficients as attributes in fitting the principal factors, and ordinating the characters overall on that basis.

Percentages of variation taken into account by the factors (Table 4.4) show factors 1 and 2 to be most important. Their cumulative explanation of variance of 86.7% suggests these two factors will adequately ordinate the characters. Examination of factor structure (Table 4.5) shows factor 1 to be a general factor with least empahsis on environment 3 . Factor 2 contrasts environment 3 and pool (to a lesser extent) with environments 1 and 4 respectively. The remaining factors provide other contrasts, but the percentage of variation they account for is minor.

Factor scores given in Table 4.6 indicate characters importances in the factor concerned. Factor score coefficients are listed in Appendix 5. Figure 4.1 provides a graphical representation of the factor scores for the first two factors (the most important as noted above). Examination of the ordination in Figure 4.1 reveals that the characters LCT1, RCTEXPA, LS2, AVP2, RSEXPA, AVP1 and VP%2 are most important in self-pollination, as they were positively associated with both of the most important factors. Because the ordination is based on absolute values of standardised partial regression coefficients, high factor scores reflect greater importance in prediction of self-pollination. Characters LP2, LP1, RPEXPA, LCT2 and LS1 were also important in self-pollination as they were positively associated with the single most important factor.

Examination of the factor scores (Table 4.6) together with the standardised partial regression coefficients and ratios in Tables 4.2 and 4.3 respectively revealed several unimportant characters. Some of these

Table 4.4: Percentages of variation taken into account by the successive factors

Factor	Eigen value	Percent of variation	Cumulative percent
1	3.23870	64.8	64.8
2	1.09748	21.9	86.7
3	0.34225	6.8	93.6
4	0.23095	4.6	98.2
5	0.09062	1.8	100.0

Table 4.5: Factor structure matrix

	Factor				
Environment	1	2	3	4	5
1	0.78552	-0.50119	-0.11657	0.33738	-0.06598
2	0.93005	-0.09533	0.19376	-0.23181	-0.18612
3	0.57865	0.74335	0.26275	0.20773	0.02038
4	0.90884	-0.31082	0.12183	-0.10698	0.22607
Pool	0.77191	0.43362	-0.45524	-0.09379	0.00994

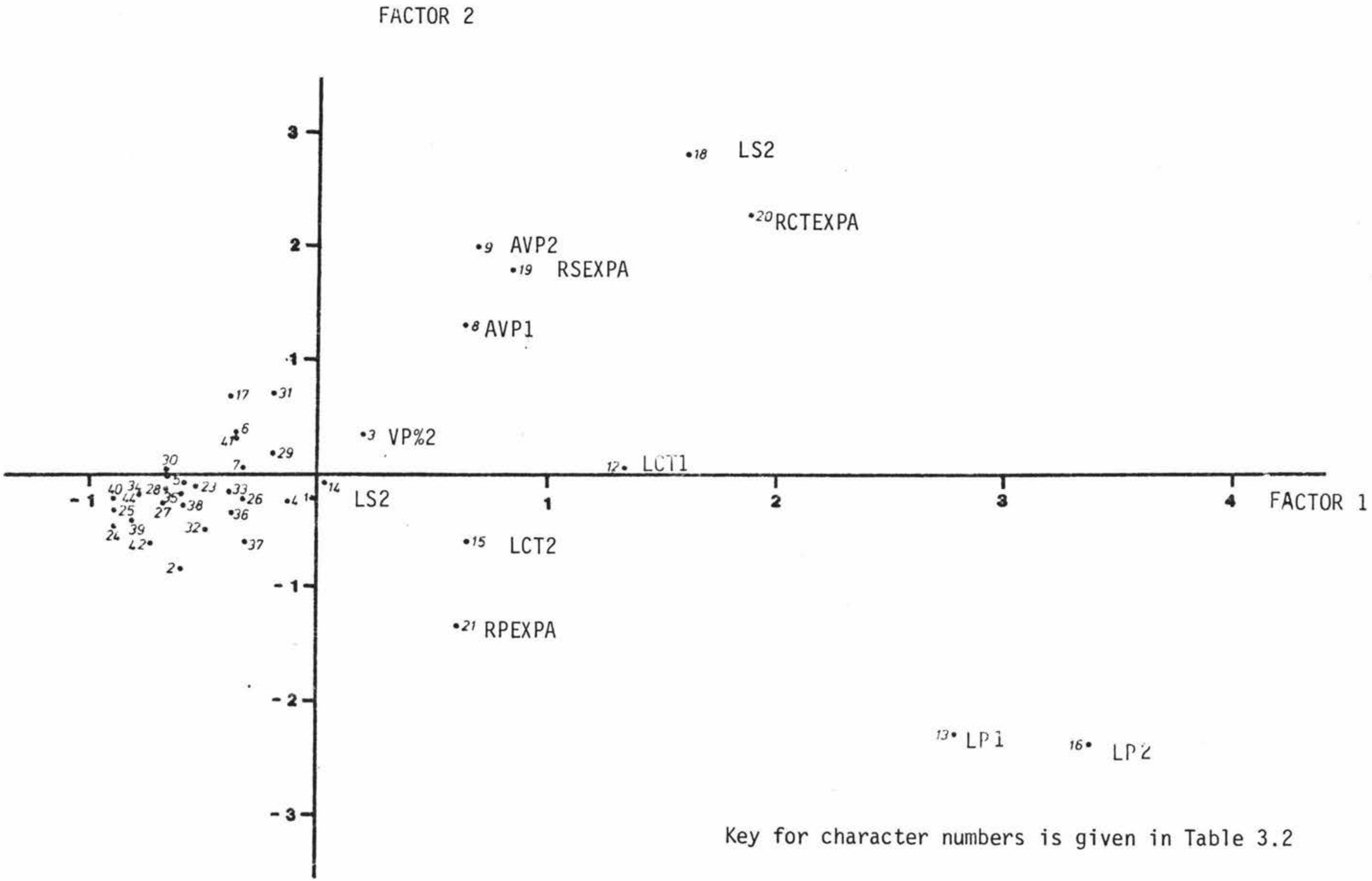
Table 4.6 Factor scores for each character

Case (original variable)	Factor 1	 2	 3	 4	 5
VP%1	-0.020141	-0.211771	-0.340723	0.191458	1.102886
DP%	-0.600325	-0.882142	-0.440326	1.588238	-0.625872
VP%2	0.203848	0.353265	-1.743790	-0.537928	-1.171701
VP%3	-0.159741	0.259913	1.991030	-0.711984	-2.193039
AP1	-0.662104	-0.024005	-1.050886	-0.532229	0.213596
AP2	-0.337416	0.348376	-2.416281	-0.358185	-0.295526
AP3	-0.330746	0.007211	0.719131	-0.535842	-0.565907
AVP1	0.632914	1.303329	0.763420	0.012570	-2.653895
AVP2	0.698987	1.995697	0.503685	0.204759	1.513918
AVP3	*	*	*	*	*
TAVP	*	*	*	*	*
LCT1	1.319997	0.007927	0.941379	-2.376112	-0.573778
LP1	2.81306	-2.269250	1.604724	1.960763	1.147179
LS1	0.014461	-0.050788	1.009084	1.487674	-2.296214
LCT2	0.630563	-0.594530	2.343989	-2.046291	0.811579
LP2	3.407347	-2.377691	-2.298292	-1.268018	-0.436078
FREQST	-0.413170	0.693032	0.310890	0.390615	0.648489
LS2	1.634729	2.765714	-1.191798	2.344297	1.210397
RSEXPA	0.855913	1.72420	-0.559347	0.151959	-1.114246
RCTEXPA	1.870521	2.279923	0.572810	-1.123166	0.837579
RPEXPA	0.595198	-1.383231	-0.007263	1.923567	-0.085199
PPTEXT	*	*	*	*	*
RSEXPO	-0.533516	-0.156081	-0.142097	0.375114	-0.359720
PT	-0.799067	-0.495184	-0.183997	-0.212195	-0.128924
ROSETTE	-0.802165	-0.391728	0.176857	0.044572	0.106196
FLOW	-0.355294	-0.250892	-0.227833	0.481780	-0.596154

Table 4.6 continued

	Factor				
Case	1	2	3	4	5
FLMED	-0.673676	-0.285831	-0.610990	-0.259414	0.207593
FL	-0.672652	-0.145115	-0.670048	-0.327516	0.063778
HEIGHT	-0.202798	0.160724	-1.551174	-1.334215	-0.245345
TNH	-0.667061	0.058444	-0.502496	-0.160935	0.915068
FCOL	-0.205920	0.731330	0.715910	-0.129055	-0.341871
NCOL	-0.536060	-0.567673	-0.116420	-0.372863	0.731849
DFCOL	-0.390274	0.155470	0.961889	0.809277	0.433416
AC	-0.746250	-0.208817	0.279486	-0.099521	1.277895
NEC	-0.658315	-0.252046	0.450683	-0.182226	0.437869
FDENS	-0.399410	-0.343741	0.003035	-1.212303	0.599753
FE	-0.330141	-0.615043	-0.218826	1.281090	-1.498762
AMTPOL	-0.580128	-0.276388	0.212779	0.177756	0.049819
ARPOLAD	-0.793300	-0.451372	0.181023	-0.124259	0.161796
NSTIG	-0.876709	-0.285776	-0.218533	-0.111886	0.213543
DEXT	-0.401954	0.355365	0.605608	0.459405	0.879774
PP	-0.760776	-0.540913	0.261179	-0.187042	1.491988
TEXT	*	*	*	*	*
ESTA	-0.773679	-0.253136	-0.118670	0.318293	0.126270

* some values were missing, so statistics were not calculated



Key for character numbers is given in Table 3.2

Figure 4.1: Graph of factor scores for factors 1 and 2

were DP%, FREQST, PPTEXT, RSEXPO, PT, ROSETTE, HEIGHT, NCOL, DFCOL, AC, NEC, ARPOLAD, NSTIG, DEXT, PP and ESTA. These have been discarded from further consideration and will not be discussed in the text. Others of possible intrinsic value were included for discussion. These included VP%1, VP%3, AP1, AP2, AP3, AVP3, TAVP, FLOW, FLMED, FL, FS, TNH, FLWID, FCOL, FDENS, FE, AMTPOL, TEXT, CROSS, SELF1 SELF2 and SELF1%.

4.3 Analysis of Variance

Characters shown to be important by the principal factor analyses as well as those of intrinsic importance are discussed in the text. Other characters not included in the discussion have summary statistics presented in Appendix 6. Variance component estimates and their significance in single environments are presented in Appendix 7. Genotype means within single environments are presented in Appendix 9. Summary statistics for analysis of variance on standardised data are presented in Appendix 10.

4.3.1 Homogeneity of Error Variances

Prior to conducting pooled analyses of the four environments a chi-square test of homogeneity of error variances was carried out (Steel and Torrie, 1960). Table 4.7 gives results of the tests; indicating whether environments had homogeneous error variance. Error variances in single environments are given in Appendix 8.

Pollen characters were mainly heterogeneous, but corolla characters were homogeneous. Other characters could not be grouped simply.

No single environment appeared to be consistently different from the others for heterogeneity. Therefore no simple transformation would be likely to overcome heterogeneity of error variances. Standardisation of data was used to homogenise the environmental error variances (refer to Section 3.5.2.4).

Table 4.8 compares analyses of variance tables for standardised and non-standardised data for character AVP1. Significance of the environmental variance at the 1% level was reduced to the 5% level as a result of

Table 4.7 Chi-square values and probabilities of tests of homogeneity of error variances among environments.

Character	χ^2	Probability	
VP%1	13.131	0.005	HET
VP%2	12.762	0.006	HET
VP%3	34.638	0.000	HET
AP1	31.689	0.000	HET
AP2	21.818	0.000	HET
AP3	33.554	0.000	HET
AVP1	12.105	0.008	HET
AVP2	6.375	0.094	HOMO
AVP3	11.275	0.011	HET
TAVP	10.727	0.014	HET
LCT1	2.895	0.590	HOMO
LP1	3.864	0.276	HOMO
LS1	3.433	0.330	HOMO
LCT2	2.040	0.568	HOMO
LP2	1.526	0.681	HOMO
LS2	0.849	0.839	HOMO
RSEXPA	11.314	0.010	HET
RCTEXPA	21.946	0.000	HET
RPEXPA	37.499	0.000	HET
FLOW	6.476	0.090	HOMO
FLMED	2.169	0.542	HOMO
FL	7.816	0.050	HET
FS	2.768	0.569	HET
TNH	9.082	0.028	HET
FLWID	19.630	0.000	HET
FCOL	67.193	0.000	HET

Table 4.7 continued

Character	χ^2	Probability	
FDENS	10.775	0.013	HET
FE	36.658	0.000	HET
AMTPOL	15.801	0.002	HET
TEXT	3.669	0.299	HOMO
CROSS	2.567	0.534	HOMO
SELF1	71.304	0.000	HET
SELF2	19.923	0.000	HET
SELF1%	88.934	0.000	HET

(5% level of significance)

HET = error variances were heterogeneous

HOMO = error variances were homogeneous

Table 4.8 Analyses of variance tables for character AVP1, for standardised data and non-standardised data.

Non Standardised data

	df	MS	Sig	$\hat{\sigma}^2$comp	Ratio to error
ENV	3	120.0341	****	1.6967	0.42
BLOCKS (within ENV)	20	4.6499	NS	0.0886	0.02
GENOTS	11	23.2563	(NS)	0.5621	0.14
G E	33	11.2067	****	1.2699	0.35
ERROR	220	3.5871		3.5871	1.00
				CV=0.4571	

$\hat{h}^2$ Full = 0.091 cv = 0.7669

$\hat{h}^2$ Rest = 0.100 cv = 0.7448

Standardised data

	df	MS	Sig	$\hat{\sigma}^2$comp	Ratio to error
ENV	3	13.1821	*	0.1350	0.13
BLOCKS (within ENV)	20	1.3109	NS	0.0259	0.03
GENOTS	11	6.7906	*	0.1516	0.15
G E	33	3.1528	****	0.3588	0.36
ERROR	220	1.0000		1.0000	1.00
				CV =0.4488	

$\hat{h}^2_{Full}$ = 0.072 cv = 0.7186

$\hat{h}^2_{Rest}$ = 0.094 cv = 0.7136

Significance NS = not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

standardising. But, genotypic variance attained significance at the 5% level. All estimates of variance were reduced as expected. No marked changes in the coefficients of variation were observed. Ratios of variance components to error variance changed little except for environmental variance which was greatly reduced in relative size. Heritability estimates reflected changes in the respective variance components used in their estimation, but changed only slightly. Coefficients of variation for heritability estimates also changed only slightly.

Standardisation slightly altered the rankings of means for character AVP1, shown in Tables 4.9 and 4.10. Changes in rankings although slight, made data conceptually difficult to interpret. It was decided not to proceed with the transformed data for all characters because of this. Therefore, remaining results are on untransformed data. Where heterogeneity of error variances has occurred, reported tests of significance and variance component estimates may be biased. Comparisons of means especially those involving genotype-environment interaction may be misleading. (Refer to Sections 1.6.7.1 and 5.2.2).

Summary statistics in the transformed scale are provided in Appendix 11.

Table 4.9 Genotype means (pooled across environments) with ranks for non-standardised and standardised data for character AVP1.

Genotype	1	2	3	4	5	6	7	8	9	10	11	12	se
non-standardised	2.2167	4.9833	2.8223	5.5112	4.7060	4.0993	4.7276	5.2573	4.4445	3.8621	4.2935	3.3936	0.6833
Standardised	1.1733	2.7597	1.4760	2.9840	2.4405	2.0941	2.3581	2.7878	2.3468	2.0617	2.3785	1.8782	0.3624

Ranks of genotypes

Genotype	1	2	3	4	5	6	7	8	9	10	11	12
Non-standardised	12	3	11	1	5	8	4	2	6	9	7	10
Standardised	12	3	11	1	4	8	6	2	7	9	5	10

Table 4.10 Environment means and standard errors (in brackets) with ranks for non-standardised data for character AVP1.

ENV	1	2	3	4	Pool
Non-standardised	5.6876 (0.2794)	2.8417 (0.2066)	4.8039 (0.2166)	3.4392 (0.1778)	3.1931 (0.1116)
Standardised	2.3994 (0.1179)	1.6207 (0.1179)	2.6132 (0.1178)	2.2795 (0.1179)	2.2282 (0.0589)

Ranks of environments

ENV	1	2	3	4
Non-standardised	1	4	2	3
Standardised	2	4	1	3

4.3.2 Coefficients of Variation

Coefficients of variation for single and pooled environments are presented in Table 4.11. The coefficients of variation range from 4.0% for FLMED to 335.6% for RPEXPA in the pooled environment.

Coefficients of variation for pollen characters, and rates of expansion of floral parts tend to be high (over 30%) compared to length characters. No consistent pattern of environmental influence on coefficients of variation was evident. The high coefficients of variation are presumably caused by high intrinsic variability, insufficient sampling, or measurement and operator techniques.

Coefficients of variation of the order 10-15% are common in agricultural experiments (Balaam, 1972). To know whether or not a particular coefficient of variation is large or small requires experience with similar data (Steel and Torrie, 1960).

4.3.3 Components of Variance

4.3.3.1 Introduction

The sources of variation in these pollination related characters can be examined by partitioning the variance into components.

Block, genotype, environment and genotype-environment interaction variance component estimates, standard errors and F-test significance level are presented in Table 4.12. Ratios to error variance of the respective variance component estimates, reflecting their importance, are presented in Table 4.13.

Table 4.11 Coefficients of variation in each environment

Character	Environments 1	2	3	4	Pool
VP%1	0.3386	0.5522	0.3300	0.4149	0.4117
VP%2	0.6288	0.4675	0.5138	0.5009	0.5226
VP%3	1.0628	0.5512	0.8552	0.7463	0.7447
AP1	0.2275	0.2506	0.1915	0.1785	0.2197
AP2	0.2211	0.2269	0.2032	0.2002	0.2180
AP3	0.2833	0.2369	0.2672	0.2504	0.2732
AVP1	0.4168	0.6170	0.3827	0.4387	0.4517
AVP2	0.7269	0.5942	0.5629	0.5752	0.6192
AVP3	1.3103	0.6513	0.9886	0.7606	0.8687
TAVP	0.4478	0.4621	0.3401	0.3888	0.4158
LCT1	0.1071	0.1168	0.0939	0.1199	0.1094
LP1	0.0500	0.0453	0.0453	0.0423	0.0447
LS1	0.0974	0.0877	0.0806	0.0819	0.0872
LCT2	0.0780	0.1012	0.0785	0.0783	0.0835
LP2	0.0411	0.0411	0.0421	0.0370	0.0404
LS2	0.0883	0.0956	0.0756	0.0805	0.0847
RSEXPA	0.5263	0.3683	0.3732	0.3516	0.4090
RCTEXPA	0.9271	0.6611	0.5365	0.5477	0.6719
RPEXPA	2.3199	#	3.8242	2.5297	3.3558
FLOW	0.0638	0.0560	0.0411	0.0410	0.0501
FLMED	0.0476	0.0447	0.0334	0.0366	0.0402
FL	0.1651	0.1230	0.1146	0.1476	0.1371
FS	0.3146	0.3358	0.2494	0.3358	0.3070
TNH	0.3328	0.5913	0.2511	0.4825	0.3919
FLWID	0.1292	0.0875	0.1053	0.0794	0.1029
FCOL	0.1584	0.0534	0.1661	0.1491	0.1401

Table 4.11 contd

Character	Environments				
	1	2	3	4	Pool
FDENS	0.2064	0.1475	0.1487	0.1192	0.1559
FE	0.1120	0.1949	0.1550	0.2330	0.1819
AMTPOL	0.2696	0.3456	0.1833	0.3173	0.2804
TEXT	0.2111	0.1701	0.1550	0.1343	0.1634
CROSS	0.3869	0.5745	0.2859	0.3006	0.3571
SELF1	0.9757	3.2856	0.6830	1.3687	1.0304
SELF2	0.4648	0.7608	0.3043	0.4565	0.4328
SELF1%	0.8584	3.1851	0.7876	1.1683	1.0740

very large value.

Table 4.12 Estimates of block, environment, genotype and genotype-environment interaction variance components together with their standard errors (in brackets) and significance in the F-test

Character	$\hat{\sigma}^2$B(within environment)	$\hat{\sigma}^2$Env	$\hat{\sigma}^2$Genotype	$\hat{\sigma}^2$GE
VP%1	-2.2308 NS (7.5225)	-9.3378 NS (4.5136)	-0.2278 NS (19.2807)	116.9262 **** (40.5916)
VP%2	-1.0012 NS (6.0761)	72.3566 **** (48.6363)	165.2332 **** (70.3896)	15.8264 (NS) (13.9416)
VP%3	2.8201 NS (7.1151)	140.9305 **** (93.2546)	57.4668 **** (29.9351)	32.3648 ** (17.6741)
AP1	-0.0471 NS (0.1042)	7.1385 **** (4.6454)	2.3761 **** (1.1934)	1.8213 **** (0.6173)
AP2	-0.0199 NS (0.1028)	5.2883 **** (3.4479)	1.1836 *** (0.6705)	1.3075 **** (0.4811)
AP3	-0.1697 NS (0.1126)	4.7593 **** (3.1102)	1.1396 ** (0.6792)	1.2189 **** (0.5425)
AVP1	0.0886 NS (0.1202)	1.4967 **** (1.0552)	0.5021 (NS) (0.3961)	1.2699 **** (0.4501)
AVP2	0.0166 NS (0.0329)	-0.0398 NS (0.0329)	1.8052 **** (0.7990)	0.4696 *** (0.2213)
AVP3	0.0738 NS (0.0800)	0.3865 *** (0.2768)	0.7668 **** (0.3466)	0.0867 NS (0.1147)
TAVP	0.6626 * (0.5266)	-0.0162 NS (0.3192)	6.0812 **** (2.8331)	2.3390 *** (1.0808)
LCT1	0.0424 NS (0.1365)	1.8996 **** (1.2613)	3.7315 **** (1.5674)	0.2596 NS (0.2608)
LP1	-0.0038 NS (0.0020)	0.1018 **** (0.0673)	0.1166 **** (0.0521)	0.0442 **** (0.0153)
LS1	-0.0113 NS (0.0136)	0.3351 **** (0.2299)	1.1826 **** (0.4997)	0.2552 **** (0.0870)
LCT2	0.0304 NS (0.1046)	5.6640 **** (3.6635)	1.0648 *** (0.5695)	0.8718 **** (0.3580)
LP 2	-0.0012 NS (0.0022)	0.1158 **** (0.0765)	0.1118 **** (0.0503)	0.0484 **** (0.0155)
LS2	0.1616 **** (0.0788)	0.5618 **** (0.4069)	1.5789 **** (0.6839)	0.4519 **** (0.1559)
RSEXPA	0.0084 NS (0.0107)	-0.0017 NS (0.0064)	0.0826 *** (0.0439)	0.0602 **** (0.0272)

Table 4.12 continued

Character	$\hat{\sigma}^{2}$B (within environment)		$\hat{\sigma}^{2}$ Env		$\hat{\sigma}^{2}$ Genotype		$\hat{\sigma}^{2}$ GE	
RCTEXPA	0.0069 (0.0061)	(NS)	0.0115 (0.0104)	*	0.0444 (0.0218)	****	0.0173 (0.0107)	*
RPEXPA	-0.0001 (0.0001)	NS	-0.0001 (0.0001)	*	-0.0002 (0.0001)	*	0.0001 (0.0002)	NS
FLOW	-0.0649 (0.2510)	NS	32.8470 (21.0736)	****	16.4077 (7.0131)	****	4.0965 (1.3964)	****
FLMED	-0.3027 (0.1312)	NS	42.4998 (27.1257)	****	28.5273 (11.7111)	****	3.9158 (1.2683)	****
FL	0.0240 (0.0181)	*	0.6188 (0.4003)	****	0.0737 (0.0413)	***	0.0505 (0.0296)	*
FS	0.0248 (0.1366)	NS	0.5318 (0.0248)	*	5.1123 (2.2342)	****	1.4729 (0.5534)	****
TNH	-0.8900 (2.3275)	NS	31.1200 (23.2340)	***	271.6690 (113.3338)	****	52.0187 (16.4136)	****
FLWID	0.4443 (0.3890)	(NS)	3.2363 (2.3926)	***	7.2640 (3.4153)	****	3.9657 (1.3490)	****
FCOL	-0.0055 (0.0160)	NS	0.0088 (0.0186)	NS	2.9588 (1.1844)	****	0.1310 (0.0589)	****
FDENS	0.0278 (0.0411)	NS	0.2411 (0.2026)	*	2.4013 (1.0295)	****	0.6705 (0.2111)	****
FE	-0.0040 (0.0220)	NS	0.0819 (0.1016)	NS	8.5316 (3.4371)	****	0.7743 (0.2205)	****
AMTPOL	0.0679 (0.1299)	NS	0.2510 (0.2621)	(NS)	3.7842 (1.6605)	****	1.0659 (0.4267)	****
TEXT	-0.0096 (0.0084)	NS	0.7471 (0.4932)	****	0.8109 (0.3592)	****	0.3411 (0.0985)	****
CROSS	3.9306 (3.7923)	(NS)	73.7304 (49.8463)	****	34.5034 (18.9808)	***	36.1174 (12.7340)	****
SELF1	1.2176 (0.8595)	*	13.5149 (9.2714)	****	10.7207 (5.3480)	****	8.0477 (2.7003)	****
SELF2	3.8775 (2.8369)	*	88.9701 (58.5758)	****	15.6359 (9.8867)	*	25.1254 (8.6378)	****
SELF1%	7.3651 (7.4998)	NS	128.3267 (87.2238)	****	76.4674 (40.2139)	***	65.8435 (24.0500)	****

Significance NS = not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$
(NS) $0.001 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

Table 4.13 Blocks, environments, genotypes and genotype-environment interaction variance components ratio to the error variance. ($\hat{\sigma}^2$)

	Variance component			
Character	Blocks	Environment	Genotype	G.E
VP%1	-0.01	-0.03	-0.00	0.38
VP%2	-0.00	0.30	0.68	0.07
VP%3	0.01	0.59	0.24	0.14
AP1	-0.01	1.60	0.53	0.41
AP2	-0.00	1.28	0.29	0.32
AP3	-0.01	0.78	0.19	0.20
AVP1	0.02	0.42	0.14	0.35
AVP2	0.01	-0.01	0.68	0.17
AVP3	0.03	0.17	0.35	0.04
TAVP	0.05	-0.00	0.48	0.19
LCT1	0.01	0.40	0.79	0.06
LP1	-0.03	0.38	1.00	0.38
LS1	-0.02	0.53	1.86	0.40
LCT2	0.01	1.56	0.29	0.24
LP2	-0.01	1.20	1.16	0.50
LS2	0.14	0.48	1.34	0.38
RSEXPA	0.03	-0.01	0.26	0.19
RCTEXPA	0.04	0.07	0.28	0.11
RPEXPA	-0.02	0.04	0.06	0.04
FLOW	-0.01	3.21	1.60	0.40
FLMED	-0.04	5.20	3.49	0.48
FL	0.06	1.47	0.18	0.12
FS	0.01	0.11	1.04	0.30
TNH	-0.01	0.32	2.77	0.53

Table 4.13 contd.

	Variance component			
Character	Blocks	Environment	Genotype	G.E.
FLWID	0.05	0.33	0.74	0.40
FCOL	-0.01	0.01	4.43	0.20
FDENS	0.02	0.19	1.92	0.54
FE	-0.00	0.09	9.71	0.88
AMTPOL	0.02	0.06	0.90	o.25
TEXT	-0.02	1.78	1.93	0.81
CROSS	0.04	0.73	0.34	0.36
SELF1	0.06	0.71	0.56	0.42
SELF2	0.06	1.38	0.24	0.39
SELF1%	0.04	0.63	0.38	0.32

4.3.3.2 Blocks (within environments) variance

Block variance was significant in only 5 of the 34 characters listed. Block effects in climate room experiments would be expected to be small, because of the evenness of conditions within the room. Lack of significance of blocks (within environments) variance for the majority of characters demonstrates this.

Ratios of the block variance estimates to error variance, being small also indicate the relative unimportance of block variance.

Where block variance is not significant it can be assumed to be zero. F-tests for the pooled environment outlined in Table 3.5 can be restructured to take this into account. Normally this would not be done, however.

4.3.3.3 Environmental variance

Twenty eight of the 34 characters had significant environmental variance. Of these 18 characters, 6 had ratios to the error variance greater than 1 (Table 4.13), including the characters LP2 and LCT2 which were shown to be important in self-pollination. Ratios greater than 1 demonstrate the importance of environmental variance for these characters.

The small environmental variance for some characters may reflect unrepresentative environment sampling. Such an assumption is not unlikely in this instance, as only four environments were used in this study. Much environmental variance was noted for the majority of characters, and the environments used were from extremes of the population they represented. It is possible that increased sampling of environments may have increased environmental variance substantially.

4.3.3.4 Genotypic variance

Significant genotypic variance was shown for 32 of the 34 characters. In terms of the analysis of variance, F values obtained had a probability of less than 5%. Hence the null hypothesis of equal genotype means was rejected.

Examination of the ratios of genotypic variance to error variance estimates indicate 10 of the characters to have a ratio greater than 1. Of these 10 characters LS2 , LS1 , LP1 and LP2 were shown to be important in self-pollination by the principal factor analysis. Such high ratios clearly demonstrate the importance of genotypic variance.

4.3.3.5 Genotype-environment interaction variance

Genotype-environment interaction variance was significant for 30 of the 34 characters. Ratios to error variance were generally low (less than 0.50 in most cases). Genotype-environment interaction variance constituted a smaller portion of total variance than environmental and genotypic variance respectively, for most characters including important ones.

Where genotype-environment interaction variance was found to be significant further analysis was performed to elucidate the patterns of response (these are discussed later).

4.3.4 Heritability Estimates

Broad-sense heritability estimates are presented in Table 4.14. Broad-sense, full heritabilities showed a similar trend to broad-sense restricted heritabilities. High heritabilities were recorded for FCOL and FE. Most characters were of moderate or low heritability. In all cases, with the exception of VP%1, heritability estimates were greater than their respective standard errors. Coefficients of variation of the heritability estimates reflected this, and were correspondingly low to moderate in value.

The negative heritability estimate obtained for VP%1 reflects negative estimates of variance components (refer to Table 3.5). Variation in sampling will occasionally give rise to negative variance component estimates.

Differences between estimates of full and restricted broad-sense heritabilities reflect the influence of environmental and block variance components. As block variance was not significant in most cases differences between the heritability estimates largely reflect environmental variance.

Heritability estimates from single environments are not provided as genotype-environment interactions bias estimates of genotypic variance upward. As such interaction effects can not be estimated in single environments, heritability estimates are similarly biased. The pooled analysis thus provides the preferable estimates.

Table 3.14 Full and restricted broadsense heritability estimates with standard errors (in brackets) and coefficients of variation, from the pooled analysis

Character	$\hat{h}^2$(full)		$\hat{h}^2$(restricted)	
VP%1	-0.001	(0.0465) #	-0.001	(0.0452) #
VP%2	0.334	(0.1018) 0.3045	0.391	(0.1043) 0.2667
VP%3	0.122	(0.6140) 0.5053	0.175	(0.0776) 0.4443
AP1	0.151	(0.0790) 0.5239	0.274	(0.1049) 0.3823
AP2	0.100	(0.0592) 0.5942	0.179	(0.0869) 0.4856
AP3	0.087	(0.5270) 0.6028	0.135	(0.0721) 0.5347
AVP1	0.072	(0.0554) 0.7669	0.094	(0.0698) 0.7448
AVP 2	0.368	(0.1061) 0.2886	0.366	(0.1062) 0.2903
AVP3	0.217	(0.0801) 0.3690	0.249	(0.0870) 0.3486
TAVP	0.280	(0.0970) 0.3459	0.289	(0.0991) 0.3431
LCT1	0.350	(0.1054) 0.3009	0.429	(0.1057) 0.2466
LP1	0.311	(0.1124) 0.3614	0.421	(0.1138) 0.2705
LS1	0.493	(0.1179) 0.2391	0.570	(0.1081) 0.1897
LCT2	0.095	(0.0556) 0.5882	0.191	(0.0859) 0.4498
LP2	0.301	(0.1146) 0.3810	0.435	(0.1163) 0.2674
LS2	0.402	(0.1143) 0.2845	0.493	(0.1131) 0.2295
RSEXPA	0.178	(0.0805) 0.4516	0.181	(0.0817) 0.4519
RCTEXPA	0.188	(0.0773) 0.4115	0.204	(0.0822) 0.4038
RPEXPA	0.052	(0.0391) 0.7472	0.053	(0.0400) 0.7477
FLOW	0.258	(0.1189) 0.4602	0.534	(0.1111) 0.2082
FLMED	0.344	(0.1462) 0.4244	0.702	(0.0898) 0.1279
FL	0.062	(0.0391) 0.6294	0.135	(0.0678) 0.5008
FS	0.424	(0.1112) 0.2623	0.445	(0.1122) 0.2525
TNH	0.601	(0.1077) 0.1791	0.644	(0.1004) 0.1558
FLWID	0.294	(0.1043) 0.3556	0.345	(0.1113) 0.3227

Table 4.14 contd.

Character	$\hat{h}^2$(full)		$\hat{h}^2$(restricted)	
FCOL	0.787	(0.0691) 0.0879	0.787	(0.0692) 0.0878
FDENS	0.523	(0.1132) 0.2165	0.555	(0.1113) 0.2005
FE	0.831	(0.0598) 0.0720	0.838	(0.0582) 0.0695
AMTPOL	0.405	(0.1095) 0.2707	0.419	(0.1109) 0.2647
TEXT	0.351	(0.1273) 0.3626	0.516	(0.1178) 0.2285
CROSS	0.139	(0.0728) 0.5245	0.202	(0.0927) 0.4596
SELF1	0.204	(0.0904) 0.4433	0.283	(0.1063) 0.3752
SELF2	0.079	(0.0523) 0.6625	0.148	(0.0837) 0.5638
SELF1%	0.159	(0.0775) 0.4874	0.221	(0.0947) 0.4278

very large coefficient of variation

4.3.5 Examination of Means and Adaptation Statistics

Environment means and standard errors, together with the significance of environmental variance, are presented in Table 4.15. Significance groups of such means derived from either the least significant difference or individual t-tests are presented in Table 4.16. Genotype means pooled across environments, standard errors and significance of genotypic variance are shown in Table 4.17. Table 4.18 gives significance groupings of such genotype means, based on the least significant difference. The regression coefficients of genotype mean within environments ($\overline{X}_{i.k}$) versus environment mean ($\overline{X}_{..k}$), their standard errors, significances from zero and one, ratio to the smallest ecovalence and coefficient of determination (R^2) values are given in Tables 4.19.1 to 4.19.12. These statistics summarise the analyses of patterns of response to environments.

Following these Tables, major groups of characters will be discussed further (Sections 4.3.5.1 to 4.3.5.6).

Table 4.15 Environment means with standard errors (in brackets) and significance of the environments F-test.

	Environments					
Character	1	2	3	4	Pool $(\bar{X}..)$	Significance
VP%1	44.90 (1.792)	40.47 (2.634)	44.09 (1.714)	41.55 (2.032)	42.75 (1.037)	NS
VP%2	21.39 (1.585)	40.39 (2.225)	23.36 (1.445)	33.32 (1.967)	29.74 (0.916)	****
VP%3	10.89 (1.364)	36.80 (2.391)	11.83 (1.193)	23.54 (2.071)	20.77 (0.911)	****
AP1	12.9043 (0.3460)	6.8288 (0.2017)	10.7194 (0.2419)	8.1202 (0.1708)	9.6432 (0.1245)	****
AP2	12.1568 (0.3168)	6.6604 (0.1781)	9.9880 (0.2392)	8.4328 (0.1989)	9.3095 (0.1196)	****
AP3	11.8797 (0.3966)	6.7197 (0.1876)	9.5213 (0.2998)	8.0044 (0.2362)	9.0313 (0.1454)	****
AVP1	5.6876 (0.2794)	2.8417 (0.2066)	4.8039 (0.2166)	3.4392 (0.1778)	4.1931 (0.1116)	****
AVP2	2.6043 (0.2231)	2.6931 (0.1886)	2.3886 (0.1585)	2.8609 (0.1939)	2.6367 (0.0962)	NS
AVP3	1.2660 (0.1955)	2.5452 (0.1954)	1.1083 (0.1291)	1.9420 (0.1741)	1.7154 (0.0878)	***
TAVP	9.5580 (0.5045)	8.0801 (0.4400)	8.3009 (0.3327)	8.2422 (0.3777)	8.5453 (0.2096)	****
LCT1	19.60 (0.248)	17.98 (0.248)	21.24 (0.235)	20.54 (0.290)	19.84 (0.128)	****
LP1	7.47 (0.044)	7.25 (0.035)	7.99 (0.043)	7.78 (0.039)	7.63 (0.020)	****
LS1	9.33 (0.107)	8.52 (0.088)	9.90 (0.094)	8.85 (0.085)	9.15 (0.047)	****
LCT2	21.78 (0.200)	20.23 (0.239)	25.42 (0.235)	24.13 (0.223)	22.84 (0.112)	****
LP2	7.59 (0.037)	7.26 (0.035)	8.06 (0.040)	7.87 (0.034)	7.70 (0.018)	****
LS2	12.27 (0.128)	12.13 (0.137)	13.89 (0.124)	12.88 (0.122)	12.79 (0.064)	****
RSEXPA	1.3335 (0.0827)	1.2516 (0.0543)	1.4518 (0.0639)	1.4421 (0.0598)	1.3698 (0.0330)	NS
RCTEXPA	0.5627 (0.0615)	0.4255 (0.0331)	0.7244 (0.0458)	0.6432 (0.0415)	0.5890 (0.0233)	*
RPEXPA	0.0340 (0.0093)	0.0024 (0.0048)	0.0131 (0.0059)	0.0156 (0.0046)	0.0163 (0.0032)	*
FLOW	59.02 (0.444)	58.67 (0.387)	68.79 (0.333)	68.89 (0.333)	63.84 (0.189)	****

Table 4.15 continued

Character	1	2	3	4	Pool ($\overline{X}$..)	Significance
FLMED	65.83 (1.278)	64.98 (0.342)	77.17 (0.304)	76.38 (0.329)	71.07 (0.169)	****
FL	3.96 (0.077)	4.17 (0.061)	5.67 (0.077)	5.09 (0.089)	4.72 (0.038)	****
FS	6.81 (0.252)	6.32 (0.250)	8.28 (0.243)	7.49 (0.296)	7.22 (0.130)	*
TNH	26.97 (1.058)	17.54 (1.223)	32.10 (0.950)	24.42 (1.389)	25.26 (0.583)	***
FLWID	30.97 (0.472)	27.61 (0.285)	31.89 (0.396)	31.42 (0.294)	30.48 (0.185)	***
FCOL	5.65 (0.106)	5.75 (0.036)	6.04 (0.118)	5.88 (0.103)	5.83 (0.048)	NS
FDENS	6.81 (0.166)	6.79 (0.118)	7.14 (0.125)	7.99 (0.112)	7.18 (0.066)	N
FE	5.28 (0.070)	4.67 (0.107)	5.06 (0.092)	5.62 (0.155)	5.15 (0.055)	NS
AMTPOL	7.49 (0.238)	6.35 (0.259)	7.73 (0.167)	7.62 (0.285)	7.30 (0.121)	(NS)
TEXT	2.86 (0.071)	3.67 (0.074)	4.83 (0.088)	4.51 (0.071)	3.97 (0.038)	****
CROSS	28.36 (1.293)	15.75 (1.067)	36.60 (1.233)	31.52 (1.117)	28.06 (0.591)	****
SELF1	4.02 (0.462)	0.60 (0.231)	9.57 (0.771)	2.76 (0.445)	4.24 (0.257)	****
SELF2	18.21 (0.997)	6.75 (0.606)	30.31 (1.087)	18.97 (1.020)	18.56 (0.473)	****
SELF1%	13.73 (1.389)	2.42 (0.908)	29.46 (2.734)	7.48 (1.029)	13.27 (0.840)	****

Significance. NS not significant * 0.050 ≥ P> 0.010 *** 0.005≥ P > 0.001

(NS) 0.100 ≥ P >0.050 ** 0.010 ≥ P> 0.001 **** P ≤0.001

Table 4.16 Significance groupings of single environment means with least significant differences given where appropriate

	Environments				#
Character	1	2	3	4	$LSD_{0.05}$
VP%1	a	a	a	a	-
VP%2	b	a	b	b	*
VP%3	c	a	c	c	*
AP1	a	d	b	c	*
AP2	a	d	b	c	*
AP3	a	d	b	c	*
AVP1	a	c	b	c	*
AVP2	a	a	a	a	-
AVP3	b	a	b	a	*
TAVP	a	a	a	a	* σ_E^2 signif
LCT1	b	c	a	a	0.6928
LP1	b	c	a	a	0.1709
LS1	b	c	a	c	0.4073
LCT2	c	d	a	b	0.8240
LP2	c	d	a	b	0.1709
LS2	c	c	a	b	0.5456
RSEXPA	a	a	a	a	-
RCTEXPA	ab	b	a	a	*
RPEXPA	a	b	ab	a	*
FLOW	b	b	a	a	1.6323
FLMED	b	b	a	a	1.5569
FL	c	c	a	b	*
FS	b	b	a	a	*
TNH	b	c	a	b	*
FLWID	a	b	a	a	*

Table 4.16 continued

Character	1	2	3	4	LSD $_{0.05}$
FCOL	a	a	a	a	NS
FDENS	b	b	b	a	*
FE	a	a	a	a	-
AMTPOL	a	a	a	a	-
TEXT	c	b	a	a	0.4341
CROSS	b	c	a	ab	4.9269
SELF 1	b	c	a	b	*
SELF 2	b	c	a	b	*
SELF 1%	b	d	a	c	*

* Based on individual t-tests using standard errors appropriate to the means being compared (error variances among environments were heterogeneous).

\# Absence of LSD values means that the F-test for environmental variance was not significant.

σ^2_E signif. The failure of individual t-tests among environment means to reflect F-test significance is a consequence of heterogeneity of error variances. The t-test result is more valid in such instances.

Means sharing any letter in common are not significantly different at the 5% level.

Table 4.17 Genotype means in the pooled environment with their standard error, and F-test significance for genotypes

Character	1	2	3	4	5	6	7	8	9	10	11	12	se	Sig
VP%1	32.80	46.80	33.67	44.14	47.35	38.46	49.71	51.56	41.06	46.58	46.20	34.63	6.492	NS
VP%2	29.46	14.56	38.12	44.71	21.84	44.61	28.47	22.44	51.13	36.73	11.72	13.09	3.745	****
VP%3	22.55	14.95	25.98	30.40	13.92	30.11	27.55	11.56	33.43	19.39	10.04	9.30	4.249	****
AP1	6.3445	11.8703	7.8834	12.4129	9.8770	10.2855	8.4756	10.2611	10.5667	8.0278	9.2176	10.4956	0.8009	****
AP2	6.2723	10.5963	8.1926	10.5648	9.4067	10.2435	8.8900	10.3278	10.0371	7.9889	9.2325	9.9618	0.7061	***
AP3	5.7685	0.6185	8.9482	10.3130	8.2436	10.1211	8.3055	10.0055	9.8685	8.2732	8.5843	10.2252	0.7473	**
AVP1	2.2167	4.9833	2.8223	5.5112	4.7060	4.0993	4.7276	5.2573	4.4445	3.8621	4.2935	3.3936	0.6833	(NS)
AVP2	1.6611	1.3593	3.2536	4.7408	1.8052	4.2990	2.3063	2.2204	5.0426	2.9361	0.8564	1.1599	0.4767	****
AVP3	1.3018	1.1944	2.3463	3.2000	0.8940	2.9268	1.9038	0.8537	3.0611	1.3656	0.7639	0.7733	0.3379	****
TAVP	5.1796	7.5370	8.4220	13.4518	7.4052	11.3253	8.9378	8.3315	12.5482	8.1639	5.9138	5.3271	1.0540	****
LCT1	17.46	21.89	17.70	17.17	21.03	20.70	19.11	21.28	18.38	18.50	22.28	22.62	0.511	****
LP1	7.10	7.42	7.73	7.76	7.11	8.19	7.46	7.45	8.26	7.50	7.69	7.84	0.126	****
LS1	8.18	10.13	7.95	7.81	9.11	9.14	8.12	9.72	9.35	8.35	10.77	11.20	0.301	****
LCT2	21.86	23.60	23.51	20.55	23.17	23.44	21.22	22.38	22.48	23.02	24.12	24.69	0.608	***
LP1	7.13	7.46	7.71	7.85	7.20	8.23	7.48	7.69	8.30	7.58	7.84	7.88	0.127	****
LS2	11.72	14.02	11.91	9.68	12.82	13.80	13.80	12.05	17.80	12.72	13.99	14.21	0.402	****
RSEXPA	1.3698	1.3981	1.7163	0.8113	1.4166	1.5916	1.7200	0.8267	1.2002	1.5211	1.1967	1.2114	0.1677	****

Table 4.17 continued

Character	1	2	3	4	5	6	7	8	9	10	11	12	se	Sig
RCTEXPA	1.0097	0.4261	1.0067	0.5195	0.5209	0.5960	0.4599	0.2385	0.6515	0.7674	0.4201	0.4533	0.1041	****
RPEXPA	0.0050	0.0095	-0.0036	0.0185	0.0208	0.0068	0.0066	0.0640	0.0088	0.0104	0.0381	0.0105	0.0125	*
FLOW	65.60	57.00	64.46	69.13	63.95	64.89	64.33	59.67	69.54	72.67	63.46	63.46	1.204	****
FLMED	71.58	63.71	71.38	76.75	69.59	71.06	68.69	67.08	72.17	84.98	69.13	66.68	1.149	****
FL	4.45	4.65	4.42	4.88	4.78	5.12	4.93	5.20	5.11	4.41	4.29	4.46	0.174	***
FS	6.08	6.71	6.91	7.63	5.63	6.17	4.37	7.42	11.62	12.31	5.67	6.13	0.757	****
TNH	12.33	23.67	18.46	21.33	14.84	17.58	15.99	20.54	37.33	75.07	27.02	18.98	4.133	****
FLWID	27.79	30.51	31.74	32.38	30.65	31.10	26.07	28.53	26.60	31.72	31.70	36.89	1.183	****
FCOL	5.04	5.04	5.00	5.36	6.34	5.37	5.17	5.04	10.00	8.69	4.83	4.10	0.246	****
FDENS	6.75	7.63	8.67	4.54	8.27	6.15	7.08	7.38	4.13	7.40	8.79	9.42	0.469	****
FE	7.33	2.33	9.63	7.42	2.80	5.37	2.08	2.13	9.13	7.94	2.50	3.19	0.480	****
AMTPOL	4.17	8.50	5.70	11.17	5.38	7.08	5.34	9.46	5.83	8.27	7.94	8.71	0.121	****
TEXT	3.54	3.00	4.88	5.67	3.40	3.75	3.52	3.21	5.25	5.04	3.19	3.15	0.321	****
CROSS	35.06	20.35	21.17	40.61	22.33	30.62	16.92	27.44	27.58	32.55	32.22	28.87	3.635	***
SELF1	11.69	2.26	3.01	4.49	2.99	1.52	0.48	6.37	0.59	10.93	3.53	2.99	1.675	****
SELF2	22.33	16.84	15.11	21.68	12.86	16.59	9.34	21.15	15.32	21.48	25.35	24.19	2.995	*
SELF1%	33.11	20.59	12.87	10.18	9.96	4.23	1.75	20.89	1.71	27.17	8.98	7.80	0.840	****

Significance. NS not significant * 0.050 ≥P >0.010 *** 0.005 ≥P >0.001

(NS) 0.100 ≥P >0.050 ** 0.010 ≥P >0.005 **** P <0.001

Table 4.18 Significance groupings of genotype means in the pooled environment, based on least significant differences

Character	1	2	3	4	5	6	7	8	9	10	11	12	LSD $_{0.05}$#
VP%1	a	a	a	a	a	a	a	a	a	a	a	a	-
VP%2	cd	ef	bc	ab	def	ab	cd	de	a	bc	f	ef	10.3795
VP%3	abcd	cde	abc	ab	de	ab	ab	de	a	bcde	e	e	11.7781
AP1	e	ab	de	a	bcd	abc	cde	abc	abc	de	cd	abc	2.2199
AP2	d	a	bcd	a	abc	a	abc	a	ab	cd	abc	ab	1.9571
AP3	b	a	a	a	a	a	a	a	a	a	a	a	2.0713
AVP1	a	a	a	a	a	a	a	a	a	a	a	a	-
AVP2	def	ef	bc	a	def	ab	cde	cde	a	cd	f	ef	1.3212
AVP3	cd	cd	ab	a	d	a	bc	d	a	cd	d	d	0.9366
TAVP	f	cdef	bcd	a	cdef	ab	bc	cd	a	cde	def	ef	2.9214
LCT1	e	abc	de	e	bc	c	de	abc	de	de	ab	a	1.4171
LP1	f	def	cd	cd	ef	ab	de	def	a	cd	cd	bc	0.3493
LS1	f	bc	f	f	de	de	f	cd	cd	ef	ab	a	0.8331
LCT2	def	abc	abcd	f	abcd	abcd	ef	cde	bcde	abcd	ab	a	1.6849
LP2	f	def	cd	c	ef	ab	de	cd	a	cd	c	bc	0.3520
LS2	c	a	c	d	bc	ab	ab	c	bc	bc	a	a	1.1154
RSEXPA	a	ab	a	c	ab	ab	a	c	bc	ab	bc	bc	0.4648

Table 4.18 contd

Character	1	2	3	4	5	6	7	8	9	10	11	12	LSD$_{0.05}$
RCTEXPA	a	de	a	bcde	bcde	bcd	de	e	bcd	ab	de	de	0.2886
RPEXPA	b	b	c	b	b	b	b	a	b	b	ab	b	0.0347
FLOW	bc	g	cd	ab	cde	bcd	cd	efg	def	a	cde	def	3.3384
FLMED	cd	f	cd	b	cde	cd	de	e	c	a	cde	ef	3.1841
FL	de	bcde	de	abcd	abcd	ab	abc	a	ab	de	e	cde	0.4810
FS	bc	b	b	b	bc	bc	c	b	a	a	bc	bc	2.0983
TNH	d	cd	cd	cd	d	cd	cd	cd	b	a	bc	cd	11.4585
FLWID	de	bcd	bc	b	bcd	bc	e	cde	e	bc	bc	a	3.2813
FCOL	d	d	d	d	c	d	d	d	a	b	d	e	0.6823
FDENS	ef	bcde	abc	g	abcd	f	def	cdef	g	cdef	ab	a	1.2996
FE	c	e	a	c	e	d	e	e	ab	bc	e	e	1.3298
AMTPOL	e	bc	de	a	de	cd	de	ab	de	bc	bc	bc	1.8404
TEXT	b	b	a	a	b	b	b	b	a	a	b	b	0.8886
CROSS	ab	de	cde	a	cde	bc	e	bcd	bc	ab	ab	bcd	10.0758
SELF1	a	cd	cd	cd	cd	d	d	bc	d	ab	cd	cd	4.6435
SELF2	abc	bcde	cde	abc	de	bcde	e	abcd	cde	abc	a	ab	8.3018
SELF1%	a	ab	bc	bc	bc	c	c	ab	c	a	bc	bc	13.8389

Absence of LSD values means that the F-test for genotypic variance was not significant.

Means sharing any letter in common are not significantly different at the 5% level

Table 4.19.1 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 1. Statistics were derived from adaptation analyses. F-test significance of genotype-environment interaction is also given

Character	$\hat{\beta}$	se of β	Sig(0)	Sig(1)	Ratio to least ecovalence	R^2	Signif
VP%1	3.049	1.131	NS	NS	2.22	0.784	****
VP%2	1.192	0.066	***	NS	1.00	0.994	(NS)
VP%3	0.270	0.130	NS	*	11.99	0.684	**
AP1	0.656	0.495	NS	NS	12.72	0.468	****
AP2	0.603	0.564	NS	NS	19.40	0.364	****
AP3	0.618	0.318	NS	NS	3.83	0.653	****
AVP1	0.773	0.370	NS	NS	1.71	0.686	****
AVP2	-0.200	1.711	NS	NS	1.48	0.007	***
AVP3	-0.195	0.142	NS	*	157.06	0.485	NS
TAVP	0.238	1.601	NS	NS	1.35	0.011	***
LCT1	1.511	0.414	(NS)	NS	8.30	0.870	NS
LP1	1.904	0.452	*	NS	22.40	0.899	****
LS1	1.848	0.564	(NS)	NS	227.68	0.843	****
LCT2	1.435	0.356	(NS)	NS	14.38	0.891	****
LP2	2.062	0.371	*	NS	21.12	0.939	****
LS2	1.939	0.310	*	NS	14.06	0.951	****
RSEXPA	0.573	3.203	NS	NS	57.60	0.016	****
RCTEXPA	1.627	1.900	NS	NS	20.64	0.268	*
RPEXPA	0.513	1.291	NS	NS	7.25	0.073	NS
FLOW	1.222	0.157	*	NS	5.38	0.988	****
FLMED	1.096	0.062	***	NS	1.00	0.994	****
FL	1.197	0.502	NS	NS	11.62	0.740	*
FS	0.811	1.371	NS	NS	12.52	0.149	****
TNH	0.348	0.318	NS	NS	16.71	0.374	****
FLWID	1.700	1.150	NS	NS	16.64	0.522	****

Table 4.19.1 continued

Character	$\hat{\beta}$	se of β	Sig(0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
FCOL	-0.357	0.245	NS	*	16.31	0.516	****
FDENS	1.498	2.194	NS	NS	19.92	0.189	****
FE	2.955	0.984	(NS)	NS	59.13	0.818	****
AMTPOL	2.044	1.309	NS	NS	5.97	0.550	****
TEXT	0.835	0.111	*	NS	1.00	0.966	****
CROSS	0.327	0.298	NS	NS	25.52	0.377	****
SELF1	1.604	0.214	*	NS	46.87	0.966	****
SELF2	0.642	0.438	NS	NS	14.53	0.518	****
SELF1%	0.942	0.089	**	NS	1.00	0.982	****

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

Table 4.19.2 Regression coefficients, their standard errors; significance from 0 and 1;ratio to least ecovalence; and coefficient of determination for genotype 2. Statistics were derived from adaptation analyses. F-test significance of genotype-environment interaction is also given.

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least covalence	R^2	Signif
VP%1	-4.973	4.930	NS	NS	27.79	0.336	****
VP%2	0.882	0.364	NS	NS	6.10	0.746	(NS)
VP%3	0.690	0.518	NS	NS	13.39	0.470	**
AP1	1.918	0.192	**	*	19.18	0.980	****
AP2	0.953	0.349	NS	NS	6.00	0.789	****
AP3	0.814	0.513	NS	NS	6.16	0.557	****
AVP1	0.461	0.843	NS	NS	9.01	0.130	****
AVP2	3.155	0.370	*	*	1.00	0.973	***
AVP3	0.933	0.712	NS	NS	108.90	0.462	NS
TAVP	-1.209	1.625	NS	NS	2.39	0.217	***
LCT1	0.748	0.068	**	(NS)	1.00	0.984	NS
LP1	0.886	0.387	NS	NS	5.71	0.724	****
LS1	1.981	0.356	*	NS	204.24	0.939	****
LCT2	0.762	0.060	***	(NS)	2.08	0.988	****
LP2	0.849	0.416	NS	NS	5.54	0.676	****
LS2	2.304	0.246	**	*	23.86	0.978	****
RSEXPA	4.078	1.697	NS	NS	42.39	0.743	****
RCTEXPA	1.306	0.673	NS	NS	2.71	0.653	*
RPEXPA	0.387	0.308	NS	NS	1.15	0.442	NS
FLOW	0.882	0.050	***	NS	1.03	0.994	****
FLMED	0.792	0.147	*	NS	5.12	0.936	****
FL	1.072	0.183	*	NS	1.54	0.954	*
FS	0.624	0.978	NS	NS	6.77	0.169	****
TNH	0.626	0.773	NS	NS	35.54	0.247	****
FLWID	0.573	1.137	NS	NS	14.68	0.113	****

Table 4.19.2 continued

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least covalence	R^2	Signif
FCOL	0.412	0.197	NS	(NS)	3.51	0.687	****
FDENS	2.260	0.788	NS	NS	5.71	0.804	****
FE	0.744	0.127	*	NS	1.00	0.945	****
AMTPOL	0.849	1.690	NS	NS	5.79	0.431	****
TEXT	0.259	0.161	NS	*	11.53	0.565	****
CROSS	0.058	0.606	NS	NS	65.71	0.005	****
SELF1	0.465	0.303	NS	NS	48.41	0.540	****
SELF2	0.406	0.457	NS	NS	21.88	0.282	****
SELF1%	2.501	0.351	*	*	130.27	0.962	****

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.0005$ **** $P \leq 0.001$

Table 4.19.3 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 3. Statistics were derived from adaptation analyses. F-test significance of genotype-environment interaction is also given.

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
VP%1	2.230	3.585	NS	NS	8.96	0.162	****
VP%2	-0.280	0.412	NS	(NS)	43.33	0.188	(NS)
VP%3	0.149	0.378	NS	NS	21.40	0.072	**
AP1	0.484	0.151	(NS)	(NS)	6.53	0.837	****
AP2	0.807	0.043	***	*	1.00	0.994	****
AP3	0.755	0.125	*	NS	1.00	0.948	****
AVP1	0.830	0.532	NS	NS	3.13	0.549	****
AVP2	-0.454	4.208	NS	NS	7.63	0.006	***
AVP3	-0.542	0.415	NS	(NS)	291.63	0.460	NS
TAVP	3.953	0.522	*	*	2.18	0.966	***
LCT1	0.639	0.196	(NS)	NS	2.85	0.842	NS
LP1	0.939	0.264	(NS)	NS	2.62	0.863	****
LS1	0.493	0.468	NS	NS	116.87	0.357	****
LCT2	1.233	0.127	**	NS	2.82	0.979	****
LP2	1.010	0.182	*	NS	1.00	0.939	****
LS2	0.240	0.139	NS	*	8.08	0.597	****
RSEXPA	0.568	1.381	NS	NS	11.13	0.078	****
RCTEXPA	1.603	0.051	****	***	1.00	0.998	*
RPEXPA	1.546	0.488	(NS)	NS	1.57	0.834	NS
FLOW	0.995	0.096	**	NS	1.00	0.982	****
FLMED	1.072	0.127	*	NS	2.23	0.973	****
FL	0.708	0.038	***	*	1.88	0.994	*
FS	1.622	0.361	*	NS	2.14	0.910	****
TNH	1.075	0.126	*	NS	1.00	0.973	****
FLWID	0.624	0.551	NS	NS	3.97	0.391	****

Table 4.19.3 contd.

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
FCOL	0.770	0.183	*	NS	1.00	0.898	****
FDENS	1.180	0.615	NS	NS	1.59	0.648	****
FE	0.211	0.419	NS	NS	9.99	0.113	****
AMTPOL	0.719	0.582	NS	NS	1.00	0.433	****
TEXT	1.280	0.467	NS	NS	9.87	0.790	****
CROSS	0.705	0.502	NS	NS	23.94	0.497	****
SELF1	0.724	0.291	NS	NS	25.25	0.756	****
SELF2	0.878	0.101	**	NS	1.00	0.974	****
SELF1%	1.140	0.262	*	NS	8.17	0.905	****

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

Table 4.19.4 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 4. Statistics were derived from adaptation analyses. F-test significance of genotype-environment interaction is also given.

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least ecovalence	R^2	Signif.
VP%1	1.120	2.984	NS	NS	5.87	0.666	****
VP%2	0.544	0.574	NS	NS	18.99	0.310	(NS)
VP%3	1.068	0.470	NS	NS	9.44	0.721	**
AP1	1.186	0.129	**	NS	1.42	0.977	****
AP2	0.800	0.092	**	NS	1.39	0.974	****
AP3	0.289	0.187	NS	(NS)	6.32	0.544	****
AVP1	1.047	0.431	NS	NS	1.97	0.747	****
AVP2	-1.710	2.027	NS	NS	3.16	0.262	***
AVP3	1.787	1.002	NS	NS	281.27	0.614	NS
TAVP	-1.296	1.426	NS	NS	2.20	0.292	***
LCT1	0.512	0.103	*	*	3.57	0.926	NS
LP1	0.410	0.230	NS	NS	8.30	0.614	****
LS1	0.081	0.189	NS	*	154.09	0.083	****
LCT2	0.738	0.214	(NS)	NS	5.21	0.856	****
LP2	0.320	0.098	(NS)	*	7.25	0.841	****
LS2	0.487	0.416	NS	NS	7.99	0.406	****
RSEXPA	0.381	1.490	NS	NS	13.42	0.032	****
RCTEXPA	0.528	0.912	NS	NS	5.11	0.144	*
RPEXPA	1.693	0.488	(NS)	NS	1.94	0.858	NS
FLOW	0.891	0.183	*	NS	4.28	0.922	****
FLMED	0.863	0.168	*	NS	4.46	0.930	****
FL	1.096	0.307	(NS)	NS	4.21	0.865	*
FS	0.984	0.877	NS	NS	5.07	0.386	****
TNH	0.615	0.097	*	(NS)	4.44	0.953	****
FLWID	0.683	0.210	(NS)	NS	1.00	0.841	****

Table 4.19.4 continued

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
FCOL	-0.619	1.973	NS	NS	86.49	0.047	****
FDENS	-0.631	0.123	*	***	5.43	0.930	****
FE	1.689	1.329	NS	NS	41.17	0.447	****
AMTPOL	0.310	0.890	NS	NS	2.74	0.054	****
TEXT	2.185	0.264	*	*	26.64	0.972	****
CROSS	1.996	0.460	*	NS	57.38	0.904	****
SELF1	0.679	0.283	NS	NS	26.99	0.743	****
SELF2	1.620	0.214	*	NS	13.50	0.966	****
SELF1%	0.260	0.307	NS	NS	38.36	0.264	****

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

Table 4.19.5 Regression coefficients, their standard errors; significance from 0 and 1 ratio to least ecovalence; and coefficient of determination for genotype 5. Statistics were derived from adaptation analyses. F-test significance of genotype-environment interaction is also given.

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
VP%1	-1.482	3.613	NS	NS	10.62	0.078	****
VP%2	1.637	0.434	(NS)	NS	17.12	0.877	(NS)
VP%3	1.310	0.354	(NS)	NS	7.35	0.872	**
AP1	1.221	0.351	(NS)	NS	6.19	0.858	****
AP2	1.409	0.131	**	(NS)	4.92	0.983	****
AP3	1.257	0.265	*	NS	2.27	0.918	****
AVP1	1.234	0.944	NS	NS	9.68	0.461	****
AVP2	4.926	0.240	***	***	3.16	0.995	***
AVP3	1.078	0.262	(NS)	NS	15.36	0.894	NS
TAVP	2.650	2.114	NS	NS	2.75	0.440	***
LCT1	1.351	0.223	*	NS	3.06	0.946	NS
LP1	0.481	0.631	NS	NS	19.46	0.225	****
LS1	1.745	0.463	(NS)	NS	165.47	0.877	****
LCT2	0.825	0.368	NS	NS	9.80	0.715	****
LP2	0.578	0.539	NS	NS	11.41	0.365	****
LS2	0.455	1.087	NS	NS	34.87	0.080	****
RSEXPA	-2.793	2.041	NS	NS	63.20	0.484	****
RCTEXPA	-0.095	1.157	NS	NS	10.51	0.003	*
RPEXPA	0.637	0.564	NS	NS	1.56	0.389	NS
FLOW	0.922	0.104	**	NS	1.52	0.975	****
FLMED	0.966	0.164	*	NS	3.26	0.946	****
FL	0.669	0.085	*	(NS)	2.65	0.969	*
FS	1.256	0.552	NS	NS	2.23	0.721	****
TNH	1.163	0.414	NS	NS	9.84	0.798	****
FLWID	1.261	0.331	(NS)	NS	1.52	0.879	****

Table 4.19.5 continued

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
FCOL	6.384	3.302	NS	NS	422.29	0.651	****
FDENS	1.201	0.577	NS	NS	1.42	0.685	****
FE	0.016	0.661	NS	NS	18.92	0.000	****
AMTPOL	0.737	1.566	NS	NS	6.58	0.100	****
TEXT	0.858	0.211	(NS)	NS	2.10	0.892	****
CROSS	1.137	0.171	*	NS	3.14	0.957	****
SELF1	1.146	0.190	*	NS	9.57	0.948	****
SELF2	1.108	0.312	(NS)	NS	5.86	0.863	****
SELF1%	1.118	0.127	**	NS	2.39	0.975	****

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

4.19.6 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 6. Statistics were derived from adaptation analyses. F-test significance of genotype-environment interaction is also given.

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
VP% 1	4.274	3.175	NS	NS	10.16	0.475	****
VP% 2	1.269	0.231	*	NS	3.93	0.938	(NS)
VP% 3	1.446	0.157	**	NS	5.24	0.977	**
AP 1	1.005	0.154	*	NS	1.00	0.955	****
AP 2	1.026	0.517	NS	NS	13.08	0.663	****
AP 3	0.826	0.313	NS	NS	2.48	0.777	****
AVP1	1.661	0.428	(NS)	NS	4.23	0.883	****
AVP2	2.652	1.791	NS	NS	1.86	0.523	***
AVP3	1.689	0.471	(NS)	NS	98.18	0.866	NS
TAVP	2.774	0.740	(NS)	NS	1.00	0.875	***
LCT1	1.427	0.306	*	NS	5.08	0.916	NS
LP1	1.553	0.484	(NS)	NS	14.17	0.887	****
LS1	1.052	0.526	NS	NS	93.43	0.667	****
LCT2	1.061	0.116	**	NS	1.00	0.977	****
LP2	1.661	0.237	*	NS	8.25	0.961	****
LS2	0.746	0.078	**	(NS)	1.00	0.979	****
RSEXPA	-0.448	0.878	NS	NS	10.12	0.115	****
RCTEXPA	0.352	0.364	NS	NS	1.86	0.319	*
RPEXPA	0.510	1.049	NS	NS	4.96	0.106	NS
FLOW	0.440	0.144	(NS)	(NS)	19.28	0.824	****
FLMED	0.671	0.120	*	NS	8.16	0.939	****
FL	0.898	0.158	*	NS	1.29	0.942	*
FS	2.114	0.508	(NS)	NS	5.79	0.897	****
TNH	1.290	0.304	*	NS	7.17	0.900	****
FLWID	0.882	0.634	NS	NS	4.45	0.485	****

Table 4.19.6 continued

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio of least ecovalence	R^2	Signif
FCOL	-1.164	1.003	NS	NS	55.67	0.403	****
FDENS	1.793	1.189	NS	NS	6.97	0.532	****
FE	-0.049	2.632	NS	NS	153.57	0.000	****
AMTPOL	1.557	0.500	(NS)	NS	1.07	0.829	****
TEXT	0.937	0.388	NS	NS	5.86	0.744	****
CROSS	1.509	0.136	**	(NS)	11.97	0.984	****
SELF1	0.516	0.058	**	*	24.74	0.976	****
SELF2	1.374	0.397	(NS)	NS	12.89	0.857	****
SELF1%	0.439	0.033	***	***	16.51	0.989	****

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

Table 4.19.7 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 7. Statistics were dericed from adaptation analyses. F-test significance of genotype-environment interaction is also given.

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
VP%1	7.942	3.855	NS	NS	25.64	0.680	****
VP%2	1.572	0.393	(NS)	NS	13.95	0.889	(NS)
VP%3	1.914	0.437	*	NS	27.75	0.906	**
AP 1	1.231	0.243	*	NS	3.60	0.928	****
AP 2	1.330	0.500	NS	NS	14.87	0.780	****
AP 3	1.207	0.351	(NS)	NS	3.17	0.856	****
AVP 1	2.459	0.655	(NS)	NS	15.73	0.876	****
AVP 2	0.839	2.842	NS	NS	3.29	0.042	***
AVP 3	1.990	0.487	(NS)	NS	155.64	0.893	NS
TAVP	3.527	1.836	NS	NS	3.09	0.649	***
LCT 1	1.006	0.544	NS	NS	8.14	0.631	NS
LP 1	0.691	0.671	NS	NS	18.19	0.347	****
LS1	1.191	1.010	NS	NS	348.55	0.410	****
LCT 2	1.036	0.324	(NS)	NS	6.86	0.887	****
LP2	0.741	0.593	NS	NS	11.59	0.438	****
LS2	1.357	0.320	*	NS	4.35	0.900	****
RSEXPA	3.455	1.202	NS	NS	24.81	0.805	****
RCTEXPA	1.757	0.458	(NS)	NS	2.69	0.880	*
RPEXPA	-0.077	0.330	NS	(NS)	2.80	0.026	NS
FLOW	1.080	0.238	*	NS	6.53	0.911	****
FLMED	0.895	0.192	*	NS	5.02	0.916	****
FL	0.970	0.265	(NS)	NS	3.02	0.870	*
FS	0.182	1.390	NS	NS	14.95	0.009	****
TNH	1.286	0.884	NS	NS	43.78	0.514	****
FLWID	0.508	0.967	NS	NS	11.20	0.121	****

Table 4.19.7 continued

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
FCOL	0.110	0.809	NS	NS	17.46	0.009	****
FDENS	1.703	1.110	NS	NS	5.97	0.541	****
FE	0.127	0.146	NS	*	13.49	0.277	****
AMTPOL	0.754	1.429	NS	NS	5.48	0.122	****
TEXT	0.598	0.258	NS	NS	5.64	0.730	****
CROSS	0.563	0.747	NS	NS	52.94	0.221	****
SELF1	0.096	0.079	NS	**	85.35	0.425	****
SELF2	0.619	0.571	NS	NS	22.60	0.370	****
SELF1%	0.127	0.083	NS	**	40.43	0.538	****

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.05 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

Table 4.19.8 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 8. Statistics were derived from adaptation analyses. F-test significance of genotype-environment interaction is also shown.

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
VP%1	-1.875	2.160	NS	NS	5.79	0.274	****
VP%2	1.364	0.846	NS	NS	34.27	0.565	(NS)
VP%3	0.842	0.124	*	NS	1.18	0.959	**
AP1	1.227	0.121	**	NS	1.69	0.981	****
AP2	1.333	0.429	(NS)	NS	11.71	0.828	****
AP3	1.885	0.394	*	NS	12.02	0.919	****
AVP1	1.023	0.308	(NS)	NS	1.00	0.847	****
AVP2	-1.250	4.594	NS	NS	9.61	0.036	***
AVP3	0.961	0.221	*	NS	10.60	0.904	NS
TAVP	0.624	1.879	NS	NS	1.70	0.052	***
LCT1	1.112	0.400	NS	NS	4.58	0.794	NS
LP1	0.788	0.070	**	(NS)	1.00	0.984	****
LS1	1.191	1.010	NS	NS	348.55	0.644	****
LCT2	0.819	0.205	(NS)	NS	3.80	0.889	****
LP2	0.891	0.261	(NS)	NS	2.23	0.853	****
LS2	0.442	0.075	*	*	4.22	0.946	****
RSEXPA	0.771	0.392	NS	NS	1.00	0.659	****
RCTEXPA	0.623	0.584	NS	NS	2.24	0.363	*
RPEXPA	4.975	0.810	*	*	34.75	0.950	NS
FLOW	1.196	0.166	*	NS	5.10	0.963	****
FLMED	1.001	0.176	*	NS	3.69	0.942	****
FL	1.000	0.153	*	NS	1.00	0.955	*
FS	-0.380	0.873	NS	NS	11.31	0.087	****
TNH	0.729	0.242	(NS)	NS	5.07	0.819	****
FLWID	0.923	0.365	NS	NS	1.45	0.761	****

Table 4.19.8 continued

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
FCOL	0.729	0.720	NS	NS	9.23	0.339	****
FDENS	-0.388	0.475	NS	(NS)	4.80	0.250	****
FE	0.084	0.278	NS	(NS)	13.65	0.044	****
AMTPOL	1.878	1.559	NS	NS	7.45	0.421	****
TEXT	1.019	0.260	(NS)	NS	2.60	0.885	****
CROSS	0.510	0.172	(NS)	NS	12.12	0.815	****
SELF1	1.635	0.419	(NS)	NS	77.48	0.884	****
SELF2	0.684	0.255	NS	NS	6.53	0.782	****
SELF1%	1.616	0.404	(NS)	NS	36.76	0.889	****

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

Table 4.19.9 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 9. Statistics were derived from adaptation analyses. F-test significance of genotype-environment interaction is also given.

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
VP%1	1.959	1.059	NS	NS	1.00	0.644	****
VP%2	0.523	0.215	NS	NS	1.02	0.747	(NS)
VP%3	1.557	0.131	***	*	7.30	0.986	**
AP1	0.932	0.370	NS	NS	5.85	0.760	****
AP2	1.210	0.197	*	NS	2.97	0.950	****
AP3	1.275	0.161	*	NS	1.40	0.969	****
AVP1	1.151	0.480	NS	NS	2.55	0.742	****
AVP2	-1.188	4.727	NS	NS	10.06	0.031	***
AVP3	1.470	0.504	(NS)	NS	78.03	0.810	NS
TAVP	3.054	0.897	(NS)	NS	1.37	0.853	***
LCT1	0.913	0.616	NS	NS	10.55	0.524	NS
LP1	1.253	0.507	NS	NS	10.57	0.753	****
LS1	0.221	0.603	NS	NS	224.27	0.517	****
LCT2	1.101	0.661	NS	NS	28.78	0.581	****
LP2	0.971	0.570	NS	NS	9.80	0.592	****
LS2	1.967	0.389	NS	NS	10.34	0.930	****
RSEXPA	1.735	1.494	NS	NS	13.92	0.403	****
RCTEXPA	0.562	1.152	NS	NS	7.72	0.106	*
RPEXPA	0.468	0.724	NS	NS	2.71	0.173	NS
FLOW	1.147	0.138	*	NS	3.23	0.972	****
FLMED	1.236	0.038	****	*	3.48	0.998	****
FL	0.844	0.337	NS	NS	5.36	0.759	*
FS	1.357	1.205	NS	NS	10.00	0.388	****
TNH	0.006	0.914	NS	NS	70.70	0.000	****

Table 4.19.9 continued

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
FLWID	0.447	0.961	NS	NS	11.42	0.098	****
FCOL	1.265	0.922	NS	NS	14.71	0.485	****
FDENS	0.873	0.490	NS	NS	1.00	0.614	****
FE	0.481	0.659	NS	NS	11.67	0.211	****
AMTPOL	-1.084	0.502	(NS)	*	11.06	0.866	****
TEXT	1.095	0.153	*	NS	1.07	0.962	****
CROSS	1.155	0.263	*	NS	6.60	0.906	****
SELF1	0.135	0.050	NS	***	77.40	0.786	****
SELF2	0.828	0.292	(NS)	NS	3.15	0.894	****
SELF1%	0.093	0.061	NS	***	42.28	0.537	****

Significance NS not significant $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

Table 4.19.10 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 10. Statistics were derived from adaptation analyses. F-test significance of genotype-environment interaction is also given.

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
VP%1	7.264	1.368	*	*	14.14	0.934	****
VP%2	0.872	0.709	NS	NS	22.37	0.431	(NS)
VP%3	1.204	0.423	NS	NS	8.46	0.802	**
AP1	0.396	0.428	NS	NS	15.33	0.299	****
AP2	0.371	0.458	NS	NS	19.96	0.246	****
AP3	0.613	0.555	NS	NS	8.41	0.379	****
AVP1	1.242	0.545	NS	NS	3.44	0.722	****
AVP2	-1.549	3.977	NS	NS	7.75	0.071	***
AVP3	0.744	0.334	NS	NS	30.81	0.714	NS
TAVP	-0.523	2.206	NS	NS	2.84	0.027	***
LCT1	1.421	0.901	NS	NS	24.78	0.554	NS
LP1	1.183	0.299	(NS)	NS	3.88	0.887	****
LS1	0.221	0.603	NS	NS	224.27	0.063	****
LCT2	1.291	1.550	*	NS	4.32	0.972	****
LP2	1.273	0.121	**	NS	1.56	0.982	****
LS2	0.302	0.389	NS	NS	10.34	0.232	****
RSEXPA	0.730	2.905	NS	NS	47.15	0.031	****
RCTEXPA	1.488	1.439	NS	NS	11.86	0.349	*
RPEXPA	-0.844	0.698	NS	NS	8.88	0.422	NS
FLOW	1.138	0.113	**	NS	2.44	0.981	****
FLMED	1.369	0.131	**	NS	10.10	0.982	****
FL	1.136	0.271	*	NS	3.54	0.898	*
FS	2.191	1.999	NS	NS	31.03	0.375	****
TNH	4.130	0.565	*	*	277.68	0.964	****
FLWID	2.103	0.524	(NS)	NS	9.37	0.889	****

Table 4.10.10 continued

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least covalence	R^2	Signif
FCOL	3.924	2.010	NS	NS	138.31	0.656	****
FDENS	1.666	0.271	*	NS	1.19	0.950	****
FE	1.097	1.907	NS	NS	74.81	0.142	****
AMTPOL	2.577	0.118	***	***	3.33	0.996	****
TEXT	1.149	0.769	NS	NS	23.12	0.527	****
CROSS	1.657	0.241	*	NS	22.18	0.959	****
SELF1	3.061	0.094	****	***	438.78	0.998	****
SELF2	1.416	0.038	****	**	4.99	0.999	****
SELF1%	2.292	0.094	***	***	87.88	0.997	****

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

Table 4.19.11 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 11. Statistics were derived from adaptation analyses. F-test significance of genotype-environment interaction is also given.

Character	$\hat{\beta}$	s e of β	Sig (0)	Sig (1)	Ratio to least covalence	R^2	Signif
VP% 1	-3.583	3.360	NS	NS	14.34	0.362	****
VP% 2	1.214	0.288	*	NS	4.64	0.899	(NS)
VP% 3	0.759	0.094	*	NS	1.60	0.971	**
AP 1	0.523	0.108	*	*	5.26	0.921	****
AP 2	1.015	0.194	*	NS	1.85	0.932	****
AP 3	0.917	0.381	NS	NS	3.26	0.744	****
AVP 1	-0.003	0.407	NS	NS	7.05	0.000	****
AVP 2	3.262	0.962	(NS)	NS	1.42	0.852	***
AVP 3	1.019	0.067	***	NS	1.00	0.991	NS
TAVP	-0.876	1.621	NS	NS	2.07	0.127	***
LCT 1	0.591	0.280	NS	NS	4.46	0.690	NS
LP 1	0.949	0.454	NS	NS	7.59	0.686	****
LS 1	0.926	0.016	****	*	1.00	0.999	****
LCT 2	0.651	0.311	NS	NS	10.25	0.687	****
LP 2	0.572	0.300	NS	NS	5.46	0.645	****
LS 2	0.763	0.813	NS	NS	18.04	0.306	****
RSEXPA	1.580	3.379	NS	NS	64.48	0.099	****
RCTEXPA	0.808	1.003	NS	NS	5.55	0.245	*
RPEXPA	1.669	1.728	NS	NS	13.03	0.318	NS
FLOW	1.250	0.654	NS	NS	49.91	0.646	****
FLMED	1.161	0.503	NS	NS	31.54	0.727	****
FL	0.954	0.192	*	NS	1.62	0.925	*
FS	-0.146	1.048	NS	NS	11.57	0.010	****
TNH	0.186	0.938	NS	NS	64.42	0.019	****
FLWID	0.267	0.366	NS	NS	4.27	0.210	****

Table 4.19.11 continued

Character	$\hat{\beta}$	$\hat{s}e$ of β	Sig (0)	Sig (1)	Ratio to least covalence	R^2	Signif
FCOL	0.316	0.529	NS	NS	8.54	0.151	****
FDENS	1.341	0.731	NS	NS	2.39	0.627	****
FE	0.762	0.346	NS	NS	3.05	0.708	****
AMTPOL	1.264	1.337	NS	NS	4.82	0.309	****
TEXT	0.395	0.244	NS	NS	9.32	0.566	****
CROSS	1.089	0.092	***	NS	1.00	0.986	****
SELF1	0.970	0.066	***	NS	1.00	0.991	****
SELF2	1.120	0.373	(NS)	NS	8.32	0.818	****
SELF1%	0.735	0.099	*	NS	4.68	0.965	****

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

Table 4.19.12 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 12. Statistics were derived from adaptation analyses. F-test significance of genotype-environment interaction is also given.

Character	$\hat{\beta}$	s e of β	Sig (0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
VP% 1	-3.926	3.054	NS	NS	14.12	0.453	****
VP% 2	1.212	0.221	*	NS	3.12	0.938	(NS)
VP% 3	0.792	0.045	***	*	1.00	0.993	**
AP 1	1.222	0.127	**	NS	1.70	0.979	****
AP 2	1.143	0.122	**	NS	1.23	0.978	****
AP 3	1.543	0.244	*	NS	4.55	0.952	****
AVP 1	0.122	0.360	NS	NS	5.42	0.054	****
AVP 2	3.516	1.425	NS	NS	2.11	0.753	***
AVP 3	1.066	0.099	**	NS	2.57	0.983	NS
TAVP	-0.916	1.447	NS	NS	1.85	0.167	***
LCT 1	0.769	0.288	NS	NS	3.01	0.781	NS
LP 1	0.963	0.410	NS	NS	6.16	0.734	****
LS 1	1.199	0.672	NS	NS	158.56	0.614	****
LCT 2	1.048	0.171	*	NS	1.98	0.949	****
LP 2	1.073	0.312	(NS)	NS	3.01	0.855	****
LS 2	0.997	0.297	(NS)	NS	2.31	0.849	****
RSEXPA	1.370	2.300	NS	NS	28.83	0.151	****
RCTEXPA	1.441	1.151	NS	NS	7.71	0.439	*
RPEXPA	0.523	0.364	NS	NS	1.00	0.508	NS
FLOW	0.836	0.166	*	NS	4.47	0.927	****
FLMED	0.878	0.108	*	NS	2.26	0.971	****
FL	1.455	0.246	*	NS	7.01	0.946	*
FS	1.386	0.278	*	NS	1.00	0.926	****
TNH	0.546	0.267	NS	NS	9.27	0.677	****
FLWID	2.028	0.308	*	(NS)	6.61	0.956	****

Table 4.19.12 continued

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
FCOL	0.231	0.828	NS	NS	16.32	0.037	****
FDENS	-0.496	0.256	NS	*	4.78	0.652	****
FE	4.305	2.664	NS	NS	257.86	0.586	****
AMTPOL	2.822	1.068	NS	NS	7.41	0.777	****
TEXT	1.390	0.415	(NS)	NS	9.52	0.849	****
CROSS	1.294	0.401	(NS)	NS	16.50	0.839	****
SELF1	0.969	0.149	*	NS	4.65	0.955	****
SELF2	1.304	0.230	*	NS	5.62	0.941	****
SELF1%	0.738	0.113	*	NS	4.92	0.955	****

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

4.3.5.1 Pollen Characters

Pollen viabilities and amounts of pollen are examined in characters VP%1, VP%2, VP%3, AVP1, AVP2, AVP3, TAVP, AP1 AP2 and AP3.

Pollen viabilities were highest in the higher humidity environments regardless of temperatures (Table 4.15). Lower humidities gave lowest pollen viabilities. Numbers of viable pollen grains in time period 1 (AVP1) (at dawn) were highest at the lower humidity. However 3 hours later the higher humidity gave greatest amounts of viable pollen. The general decline in both amounts of viable pollen and of viability percent with time were significant (Tables 4.20 and 4.21) in all environments. Most genotypes behaved similarly (Tables 4.23 and 4.24). The cumulative amount of viable pollen (TAVP) was greatest in the higher temperature and higher humidity environment (Tables 4.15 and 4.16). The decline in pollen viability from dawn may indicate a short life in safflower pollen. The rate of decline was greater in lower humidity conditions. Some genotypes did record slight increases in pollen viability (Table 4.17) however these were not significant in most cases. (Table 4.23).

Lack of significance for genotypic and environmental variance in VP%1 (Table 4.12) indicated a high degree of stability for this character, in the species over a range of environments. Variances became significant as the pollen aged (in later time periods) possibly suggesting that levels in time one are critical for reproduction, but later levels of viability are specific to environments i.e. genotype-environment interaction was expressed as extension of pollen viability.

Table 4.20 Significance groupings across times of pollen viability percentages within each environment (based on individual t-tests)

Env	1	2	3	4	Pool
VP%1	a	a	a	a	a
VP%2	b	a	b	b	b
VP%3	c	a	c	c	c

Means having any letters in common are not significantly different at the 5% level

Table 4.21 Significance groups across times of amounts of viable pollen within each environment (based on individual t-tests)

Env	1	2	3	4	Pool
AVP1	a	a	a	a	a
AVP2	b	a	b	ab	b
AVP3	c	a	c	b	c

Means having any letters in common are not significantly different at the 5% level

Table 4.22 Significance groupings across times of amounts of pollen within each environment (based on individual t-tests)

Env	1	2	3	4	Pool
AP1	a	a	a	a	a
AP2	a	a	ab	a	ab
AP3	a	a	b	a	b

Means having any letters in common are not significantly different at the 5% level

Table 4.23 Significance groupings across times for pollen viability percentages in each genotype mean in the pooled environment (based on individual t-tests)

	Genotype											
	1	2	3	4	5	6	7	8	9	10	11	12
VP% 1	a	a	a	a	a	a	a	a	ab	a	a	a
VP% 2	a	b	a	a	b	a	b	b	a	a	b	b
VP% 3	a	b	a	a	b	a	b	b	b	b	b	b

Means sharing any letter in common are not significantly different from each other at the 5% level

Table 4.24 Significance groupings across times for amounts of viable pollen in each genotype mean in the pooled environment (based on individual t-tests)

	Genotype											
	1	2	3	4	5	6	7	8	9	10	11	12
AVP1	a	a	a	a	a	a	a	a	ab	a	a	a
AVP2	a	b	a	a	b	a	b	b	a	ab	b	ab
AVP3	a	b	a	a	b	a	b	b	b	b	b	b

Means sharing any letter in common are not significantly different from each other at the 5% level.

The characters VP%2 and AVP3 did not display significant genotype-environment interaction (Table 4.12). Remaining pollen characters showed significant genotype-environment interaction. Analyses of response to environment suggested the general trend to be towards specific adaptation to higher humidity environments for pollen viabilities and amounts of viable pollen. (Tables 4.19.1 and 4.19.12). Genotypes with specific adaptation may serve as useful sources of germplasm for plant breeders. Significant regression coefficients were in all cases associated with moderate to high R^2 values; indicating that regression explained a large portion of that genotype's genotype-environment interaction variance. Most genotypes contributed to genotype-environment interaction in a similar manner, as shown by the ratios of ecovalences to the least ecovalence. (Tables 4.19.1 to 4.19.12).

Greater amounts of pollen were produced in lower humidity environments (Tables 4.15 and 4.16). Such overall amounts of pollen did not differ significantly across time periods (Table 4.22), indicating that wind within the climate rooms did not cause significant pollen removal from the florets (except perhaps in environment 3). Such production of greater amounts of pollen may be compensatory for the lower viabilities at the lower humidity, as by time 3 amounts of viable pollen were highest in the low humidity environments.

4.3.5.2 Corolla Characters

4.3.5.2.1 Lengths: The characters LCT1, LP1, LS1, LCT2, LP2, LS2

Significant genotypic and environmental variance was observed for these characters (Table 4.12).

Corolla tube and petal lengths were greatest in low temperature environments, at both dawn and full extrusion (Tables 4.15 and 4.16). Style-stigma length from the neck of the corolla tube was not consistent in reaction to environments (Tables 4.15 and 4.16). Table 4.25 demonstrates that in each environment corolla tubes and style-stigma lengths underwent significant increases between dawn and full extrusion, in each environment. All genotypes displayed significant increases in style-stigma length between dawn and full extrusion, suggesting it is a critical part of the pollination mechanism. (Table 4.26). Petal lengths were statistically the same at both sampling times, for each environment, and each genotype, indicating that petal size was fixed before floret opening (Tables 4.25 and 4.26). Corolla tube growth occurred only in some of the genotypes. Percentages of style-stigma length from the base of the corolla tube, exposed above the anther column are given in Table 4.27. The similarity of values suggests the relative positioning of floral parts is about the same in the different environments. Therefore differences in length of style-stigma above the anther column are purely physical length differences rather than positional changes.

Table 4.25 Comparisons of time differences between floral length measurements (using individual t-tests) for each environment

Env means compared	1	2	3	4	Pool
LCT1/LCT2	*	*	*	*	*
LP1/LP2	NS	NS	NS	NS	NS
LS1/LS2	*	*	*	*	*

* = significant at the 5% level

NS = not significant at the 5% level

Table 4.26 Comparison among genotype means for floral lengths at the two times in the pooled environment (based on individual t-tests) and the genotype means of pollen presence in the pooled environment.

	genotypes											
Comparison	1	2	3	4	5	6	7	8	9	10	11	12
$\mathrm{LCT1}/_{\mathrm{LCT2}}$	*	NS	*	*	NS	*	NS	NS	*	*	NS	NS
$\mathrm{LP1}/_{\mathrm{LP2}}$	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
$\mathrm{LS1}/_{\mathrm{LS2}}$	*	*	*	*	*	*	*	*	*	*	*	*
PP	0.2	0.0	1.2	1.4	0.2	0.6	0.9	0.3	0.7	0.8	0.0	0.0

* significant at the 5% level

NS not significant at the 5% level

Table 4.27 Percentage of the total style-stigma length exposed above the anther column

Time	Environment				
	1	2	3	4	Range
At dawn	6.4%	4.9%	6.2%	3.6%	2.8%
At full extrusion	13.8%	15.1%	14.8%	13.5%	1.7%

(derived from environment means presented in Table 4.15).

Significant genotype-environment interaction variance was recorded for these characters , except for LCT1. Analysis of response to environment revealed that corolla tube and petal length responded in a similar manner with regression coefficients (average) approximately one. R^2 values were moderate to high in most cases, although low values occurred for petal lengths. Contributions to the genotype-environment interaction variance were relatively similar, excepting the character LS1 which had considerable variation in contribution by the various genotypes.

4.3.5.2.2 Rates of floral part expansion

RSEXPA, RCTEXPA, RPEXPA, TEXT, AMTPOL

Environmental variance for characters RSEXPA and AMTPOL and genotype-environment interaction variance for RPEXPA were not significant (Table 4.12). Environments did not influence rates of floral part expansion in a consistent manner (Table 4.15). RCTEXPA was fastest at low temperatures. A similar trend was noted for RSEXPA although differences were non-significant (Table 4.16). RPEXPA was fastest at high temperatures. Times taken for full extrusion (TEXT) were shortest in the higher temperature environments. Humidities did not display consistent effects on this character. The faster rates recorded for RSEXPA and RCTEXPA in lower temperature environments must reflect greater style-stigma and corolla tube lengths occurring in these environments, with a less proportionate increase in the values of TEXT. High values of RPEXPA in the hot environments must reflect shorter time periods of expansion as lengths are proportionately similar.

Analysis of response to environments revealed few significant regression coefficients, for these characters. R^2 values were low. Ecovalence ratios were relatively similar for most genotypes within characters, except for RSEXPA.

4.3.5.3 Days to: flowering; flowering median. The length of flowering within heads, and the spread of flowering. Total number of heads and the width of heads FLOW, FLMED, FL, FS, TNH, FLWID.

Ratios of variance components to error in Table 4.13 suggest genotypic variance to be most important. Environmental variance and genotype-environment interaction variance although smaller in magnitude were still significant.

These characters behaved similarly. Lower temperatures resulted in longer periods before flowering (Table 4.15). The length of flowering within heads was similarly longest at the lower temperature, but at the higher temperature was enhanced by the higher humidity. Genotype differences were significant, but no pattern emerged (Table 4.18). Cooler environments increased the spread of flowering, while higher humidities tended to decrease it. Total number of heads and head width were greatest in the lower temperature, lower humidity environment.

Most genotypes showed average response to environment. R^2 values varied considerably, between genotypes and characters (Tables 4.19.1 to 4.19.12). Most genotypes contributed in a similar manner to the genotype-environment interaction variance, as shown by the relatively narrow range of ecovalence ratios.

4.3.5.4 Flower colour; Floret density; Floret emergence: FCOL, FDENS, FE.

Environmental variance was not significant for FCOL and FE (Table 4.12). Environment differences in FDENS showed cooler environments to have higher values, indicating florets to be at a higher density. Genotype differences for FDENS were not distinct, unlike those for FCOL and FE which were relatively clear cut.

Few significant adaptation coefficients occurred. R^2 values were low for FE and FCOL but moderate to high for FDENS. Ecovalences were variable for FE and FCOL but relatively similar for FDENS.

4.3.5.5 Self-pollination under bags, and other seed set characters. SELF1%, CROSS, SELF1, SELF 2.

SELF1% was significant for genotypic, environment and genotype-environment interaction variances (Table 4.12). Environmental variance was greatest, with genotypic and genotype-environment interaction variances ranking approximately equally. The lower humidity and temperature conditions favoured self-pollination (Table 4.15). Genotype differences were large and significant (Tables 4.17 and 4.18).

Both specific and average response to environments were shown by the regression coefficients. Ratios to least ecovalence were highly variable. R^2 values were high for most genotypes.

Environment means and significance groups for CROSS, SELF 1 , SELF 2 (Tables 4.15 and 4.16) show the higher humidity, and higher temperature conditions to depress all seed set characters. The depression of SELF1 heads when compared with CROSS heads in all environments(Table 4.15) may indicate the presence of a mild incompatibility system. Genotype means and significance groupings across the seed treatments (Table 4.28) also suggest this. SELF 1 was lowest in all environments, and for all genotypes (Tables 4.15 and 4.16). Genotypes having high CROSS values tended to have high SELF 1 and SELF2 values.

4.3.5.6 Stigma turgidity and esterase activity

Stigma turgidities were not subjected to analysis of variance because many genotypes had constant values within and between environments; so they had no variance, which would cause computational difficulties. The most likely reason for this occurrence was insufficient sampling. Heads were only sampled once a day for this character.

Slight differences occur in the means of emasculated and non-emasculated florets, shown in Tables 4.29 and 4.30. Such differences are possibly carry over effects from difficulties in determining wilting in emasculated florets. Non-emasculated floret turgidity was easily determined, as the moment stigmas commenced wilting they were no longer vertical to the florets. After emasculation the style and stigma were no longer restrained by the corolla tube, and followed random 'tracks'. Loss of turgidity in the style and stigma on these florets had to be more pronounced to be detected. Observations recorded do suggest the presence of both environmental and genotypic differences. Stigma turgidity was in all cases associated with appreciable esterase activity, indicating stigma receptivity. Esterase activity may vary from day to day (Appendix 11).

Table 4.28 Significance groupings of genotype means in the pooled environment across seed set treatments (based on individual t-tests)

	Genotypes											
	1	2	3	4	5	6	7	8	9	10	11	12
CROSS	a	a	a	a	a	a	a	a	a	a	a	a
SELF1	a	a	a	b	ab	a	ab	a	a	a	a	a
SELF2	b	b	b	c	b	b	b	b	b	b	b	b

Means having any letter in common are not significantly different at the 5% level.

Table 4.29 Environment means of duration of stigma turgidity for emasculated and non-emasculated florets

	Environments				
	1	2	3	4	P
Non-emasculated	2	1.90	2.05	2.08	2.01
Emasculated	2	1.88	2.19	2.43	1.12

Table 4.30 Genotype means of duration of stigma turgidity for emasculated and non-emasculated florets.

	Genotypes											
	1	2	3	4	5	6	7	8	9	10	11	12
Non-emasculated	2.00	2.21	2.00	2.08	2.00	2.00	2.00	1.75	2.08	2.00	2.00	2.00
Emasculated	2.05	2.25	2.00	2.25	2.05	2.21	2.15	1.75	2.21	2.27	2.08	2.25

5. GENERAL DISCUSSION

5.1 Experimental Objectives

Experiments were designed to investigate factors influencing pollination in safflower. Basic studies on pollination are necessary if the crop is to develop in the New Zealand environment. Efficient use of breeding procedures in crops is dependent upon knowledge of pollination pattern. Pollination patterns affect the genetic structure of the species. Self-pollinated populations tend to consist of many lines of homozygous individuals. Nevertheless over the whole population a considerable degree of heterogeneity exists. Cross-pollinated populations tend to consist of heterozygous individuals. Breeding programs can be divided into those applicable to self-pollinated crops; and those for cross-pollinated crops (Poehlman, 1979). Methods applicable to cross-pollinated species allow for slower rates of inbreeding, and may utilize heterosis.

It was conjectured that the major factors influencing pollination in safflower would have been the plant, environment and insect pollinators. These factors were investigated. Characters studied indicated the presence of much variation in morphological development; although the basic pattern was the same across all genotypes. Environmental influences on floret morphology were revealed. Genotypic variation in rates of self-pollination were significant, as was insect pollination in the field. The most important characters influencing self-pollination, in this study, were determined (Section 4.2).

5.2 Experimental Design

5.2.1 Field Experiments

The field experimental study of insect behaviour on safflower constituted a small part of this study. Pollination by insects on safflower is potentially a very important area. Significant increases in seed set were noted with insect pollination of safflower. Insect visitation to the crop was frequent.

The size of these experiments, or amounts of data collected, were largely limited by prevailing weather conditions. With poor weather conditions, insect visitation was poor and data collection not justifiable.

Variation in day to day climatic conditions make behavioural experiments in open environments, unreplicable. Lack of replication results in difficulty with statistical analysis of results, thus placing undue interpretational restraints on the data.

Presence of diseases in the field resulted in the loss of some experimental data.

5.2.2 Controlled Environment Study

Common sources of variability in the field result from soil heterogeneity, poor sampling or measurement techniques; plant variability:- heterogeneity within genotypes; competition and border effects. Methods of overcoming these sources of variability include use of replication, plot size and shape.

Soil heterogeneity between plots and environments was effectively eliminated by use of standard size pots of a uniform soil mix. Nutrients were supplied as required, and should never have been a limiting factor. Interplot competition for aerial space and light may have been considerable. The use of a germplasm collection in this study introduced considerable variation. A more uniform set of genotypes may have reduced aerial competition, but would have lowered the inferential value of the experiment. Reducing plant numbers in each room would have had the same effect. Growth differences occurring in the different rooms would have resulted in differing degrees of competition depending on environment. Border effects around the perimeter of experiments within each room may have existed. It was considered that variation within the controlled environment rooms was sufficiently small as to not warrant control of border effects. High coefficients of variation for a few characters do not support this.

As genotype populations appeared reasonably homogeneous, single plants were considered sufficient to produce a representative sample. The large number of blocks used, was originally aimed at eliminating the effects of using single plants as plots. If more than one plant had been used per plot, within plot variance might have occurred. Larger samples from multiple plant plots would have been necessary to estimate this. By spreading the single plants over blocks, so decreasing plot size but increasing block numbers, a part of within plot variance due to the different plants becomes part of the plot variance. Increased replication of small plots has been found to be a more efficient means of obtaining a high degree of accuracy, than use of the same amount of land with larger plots and less replication (Le Clerg *et al.*, 1962).

The lack of significant block variance suggests that smaller numbers of blocks would have sufficed. It also implies that room conditions were sufficiently uniform that a completely random design would have been just as efficient as the randomised complete block design, for most characters. However, use of the completely random design may have resulted in slightly larger error variances, and thus some mean squares may have lost significance. As replication is still necessary the blocking structure is a realistic, and "safe" approach.

Use of single plants as plots for this type of study where samples are of a small nature, may have increased precision of estimates. Where possible samples for any one test were taken from a single capitulum, randomly chosen. Variation among capitula on individual plants has been noted by Yermanos and Francois (1963), and Williams (1962). Such variation would have led to loss of precision of estimates obtained. It was decided to take samples from individual heads, as some genotypes only had one or a few flowers open at any time. As much as possible the single heads used for any single character test were from the same capitulum category (i.e. primary, secondary or tertiary). This overcame the problem of genotypic variance being confounded by sampling differences (resulting from sampling of different head categories). If such control had not been possible covariance adjustment (Steel and Torrie,1960) could have been used to correct for differences in the category of head sampled.

In the hot-wet environment, where general plant vigour was low, some genotypes produced fewer heads than normal. In a few cases this meant, sample sizes had to be reduced or characters dropped. Some plants failed to grow. In such cases it was necessary to use missing data estimates.

The heterogeneity of error variances noted for many characters across the environments is a difficult but common problem; and could not be overcome. (Time constraints prevented the testing of other transformations which may have overcome the problem, without distorting the data).

Significant variance components for genotype, environment, and genotype - environment interaction showed that these sources of variation had been examined by the sample. Greater sampling of environments and/or genotypes may have increased the magnitude of variance components, and led to more reliable estimation of these parameters in the population of inference. The resources required would have been considerable. Low error variance intrinsically implies that a reasonable degree of precision in measurement has been obtained. If such precision of measurement did not exist error variances would be so large that other variances partitioned out might be masked,if their variability was not larger than that of the error.

Variance components estimated in this study may be of use to future researchers in designing their experiments. Methods of estimating optimum plot allocation have been oultined by Jones *et al*. (1960). Abel (1976a) used such techniques based on the variance of varietal means to recommend numbers of locations and years that should be sampled in the screening of safflower. Evaluation of optimum plot allocation was not a goal of this study.

5.3 Experimental Methods

Methods of measurement appeared satisfactory in most cases, as indicated in the following.

Differences observed in viable pollen percentages and amounts of viable pollen indicate that measurement was sufficient to show such differences. The low values obtained might reflect poor measurement. In many instances pollen was released prior to dawn. It may be assumed that pollen release was more influenced by increasing temperatures in the early morning, than light. Release prior to testing at dawn, combined with short pollen longevity could result in the low pollen viability percentages observed. Ideally counts of germinated pollen grown on compatible stigmas would have been conducted but this requires large resources. Pollen tube growth on artificial media would also have been useful, could it have been induced.

Measurements of corolla characters also appeared sufficient. More accurate measurements would have been desirable in obtaining rates of expansion of various floral parts, but time constraints prevented this.

Scoring systems were satisfactory in detecting differences. With more time available and/or less material to screen, intensive measurement techniques might have been useful. It is doubtful whether extra information important to this study would have been gleaned.

The initial test involving esterase activity was satisfactory in determining the receptive area of the stigma. More faith would be placed in the test if crossing experiments using emasculated florets revealed the same results as the combined esterase activity score, and stigma turgidity. Scores of esterase activity may not have been sufficiently definitive, as many genotypes displayed constant high values. This problem of constancy made analysis of variance impractical. Attempts at artificial crossing of safflower prior to the main study met with poor results. The non-specific esterase activity in the pellicle of the stigma may not necessarily reflect receptivity, but it was the best index available in view of poor artificial crossing results.

Seed set measurements may have been biased. Ideally knowledge of whether or not a plant is self-pollinated should be gained by isolating a single plant in space. Isolation by bags or cages introduces the possibility of imposing environmental conditions adverse to seed production (Allard, 1960). Such effects were noted by Howard *et al.* (1915) on safflower. Failure of seed set in isolation is an almost certain indication that a species is cross-pollinated; although genotypic variation for this might occur within a species. Other methods of estimating out-crossing, based on genetic markers, are listed by Jain (1979). Useful genetic markers are present in safflower (Abel, 1976b, Zimmerman 1976, Claassen, 1952, Dillé and Knowles 1975, Ebert and Knowles 1966.) Time constraints prevented use of these techniques in assessing pollination. Estimation of crossed seed set may be biased also. Pollination by insects is very likely to be different in its effects than the pollination techniques used in this experiment.

Statistical techniques utilized appear satisfactory, within the constraints already discussed in Sections 1.7, 3.5 and 5.2.2.

The analysis of adpatation was performed knowing that the small number of environments and genotypes would lead to few significant results. Any significant results could well be biased by sampling of environments. Normally such analyses would be performed on data sets comprising many genotypes and environments.

5.4 Experimental Results

5.4.1 Pollination Mechanism

Results of this study confirmed the basic pollination mechanism reported by Howard *et al.* (1915), involving anther dehiscence about the time of stigma extrusion. Variations in timing of dehiscence relative to timing of stigmatic extrusion reported by Ebert and Knowles (1966) and Claassen (1950) were also confirmed. Genotype means of the number of stigmas with pollen present, and the positioning of pollen adhesion are given in Appendix 9 to verify this. In most instances variations in timing of anther dehiscence in relation to stigma extrusion occurred in only a few florets, on the capitulum. The general tendency was for anthers to dehisce before stigma extrusion, in both the field and the all controlled environments. Timing of anther dehiscence relative to stigma extrusion may reflect old cultivar versus new cultivar differences. Older cultivars reported by Howard *et al.* (1915) with anther dehiscence delayed till after stigma extrusion, may have had greater opportunity to cross. No difference in the timing of anther dehiscence was observed between the modern cultivars and wild types sampled in this experiment (Appendix 9). Howard *et al.* (1915) had also reported that some lines used by farmers in two Indian provinces were mainly selfed as indexed by progeny uniformity of individual parents. More modern cultivars used by Claassen (1950) and Ebert and Knowles (1966) may reflect trends toward greater self-pollination. Selection by man has resulted in switches from cross-pollination to self-pollination in many crop species e.g. wheat and tomatoes (Simmonds, 1979; Simmonds, 1976). Genotypic variation in rates of self-pollination were observed in this experiment. In unbagged heads allowed to "self-pollinate", modern cultivars were superior in self-pollination, however when bags were applied many of the wild genotypes had superior self-pollination. Wild genotypes may thus respond better to bagging. Despite self-pollination occurring, cross-pollination is still possible. Cross-fertilization would have much greater chance of occurring if self-incompatibility mechanisms were functioning.

During the flowering period of safflower in New Zealand much variation in day to day climatic conditions occurs. Genotypes might therefore pollinate quite differently from day to day as plants respond to differing environmental influences. Significant differences between self-pollination percent in the environments used in this study, and wide day to day variation in pollinator numbers under field conditions tend to support this. The complex interaction of plant-pollinator-environment can not be fully understood, but presumably modifies plant factors to ensure some form of pollination.

5.4.2 Dynamics of the Pollination Mechanism.

The most crucial factors in pollination are undoubtedly the presence of viable pollen, and receptivity of the stigma.

Results of this study suggest that safflower has short lived pollen. Consideration of results obtained leads to two hypotheses by which the plant can maintain the presence of viable pollen for as long as possible.

1. Variability in emergence of florets within single capitulum. Fresh florets would be opening at different times, so viable pollen would be present over a long period. Uniform floret emergence would lead to a large amount of viable pollen being present at one time.

2. Lengthening the period of stigmatic extrusion. This could be accomplished by slower rates of stigmatic extrusion, or longer stigmas to be extruded. Longer periods of stigmatic extrusion means that the resource of viable pollen within the anther column is being gradually depleted, and made available to pollinating agents. Short stigmatic extrusion periods would mean that viable pollen would be exposed all at once.

Both hypotheses assume that anther dehiscence has occurred prior to any style-stigma growth. Modifications in the rates of corolla tube growth, and style-stigma growth may vary placement position of pollen on the stigma. Even style-stigma, and corolla tube growth rates, would prolong the period that the stigma was enclosed within the anther column in intimate contact with viable pollen. Differences in the rates of corolla tube growth and style-stigma expansion would shorten this period of contact. The position of the stigma prior to dehiscence would also influence amounts of pollen collected on the stigmatic hairs during extrusion. It is not known whether all five anthers dehisce simultaneously or otherwise. Variability in the timing of dehiscence among the anthers may alter the pollen coating along the length of the stigma, depending on the number of anthers dehisced.

Rapid rates of style-stigma extrusion were recorded in higher temperature environments in this study. According to the hypothesis outlined above, this would be associated with a short period of exposed viable pollen. Higher insect activity is known to occur in warmer environments, and thus pollination by insects in such conditions could be important.

Significant genotype differences in petal segment length and corolla tube length were noted. Larger petals may serve as attractants to insects. The longer corolla tubes (reflecting bract size) would contain large nectar reserves compared to shorter corolla tubes. Significant genotypic differences in style-stigma length were observed. This may play a part in pollen tube growth. Should pollen from the parent plant have slower growth rate, foreign pollen with faster growth rate would have a competitive advantage. Stigmas themselves may serve as a visual cue to insects. Pollen attached to stigmas may have a similar function. Should the odour of safflower arise from pollen, pollen coverage of the stigma may have a role in dispersal of scent.

Variability in the spread of flowering in the plant, and the length of flowering within heads was observed. Longer spreads of flowering likely to allow greater cross-pollination, as there is more chance of other genotypes flowering and then crossing. Short lengths of flowering within heads may promote selfing, as other genotypes flowering at the same time could be restricted. Both factors differed with environment.

Receptivity of safflower stigma was found to last a few days. Those genotypes with short receptivity may be reliant on the plant's self-pollination mechanism.

In New Zealand safflower has been grown as a summer crop in the Manawatu region. About flowering time (late January to early March, depending on genotype and planting date), weather conditions can be variable. This study suggests that on cooler days there may be greater overlap of pollen viability and stigma receptivity, than on warmer days. Self-pollination is therefore more likely on cooler days. Greater insect activity on warmer days is likely to promote crossing, and possibly improve seed set.

5.5 Implications for Plant Breeding

5.5.1 Germplasm

Taxonomic classification systems which emphasize genetical relationships and discontinuities have advantages for plant breeders working with cultivated plants and their wild relatives. It should be clear where gene-exchange can occur, so that appropriate steps can be taken to conserve as broader germplasm as possible (Baker, 1970). Such germplasms serve as source of genes or genetic variation, which if not conserved would otherwise be lost (Harlan, 1965, 1976; Wu and Jain, 1977). Knowles (1977) has discussed the value of safflower germplasm present in the U.S.A.

The most common form of storing germplasm is as seeds. Bass *et al.* (1963) and Bass and Clark (1974) have outlined seed storage conditions promoting longevity in safflower. Alternatives to seed storage include pollen storage (Stanley and Linksens 1974) or tissue cultures. Pollen germplasms require good methods for extended storage. Methods of extended storage have not been developed for safflower.

Collection and maintenance of germplasm assumes a knowledge of pollination pattern. Evaluation of lines may occur at any stage of the project. Selection of lines for collection, may involve some form of evaluation in the field.

5.5.1.1 Collection

Field sampling procedures in plant exploration are aimed at the fullest possible recovery of genetic variation from the species centres of diversity. Such centres of diversity in safflower have been oultined by Knowles (1969). Sampling procedures should reflect knowledge of the distribution of genetic variance within and between populations (Frankel and Bennett, 1970).

Results of this study suggested that safflower was a self-pollinating species with a capacity for crossing. The high degree of uniformity among individuals within lines also suggests this. Variability in some genotypes (1 and 5) suggested that crossing had occurred in the past. Differences in the rates of self-pollination among lines used in this study, may reflect regional variation in pollination pattern as noted by Howard *et al.* (1915). Such differences in the origins of lines, might be used to reflect broader geographical differences in pollination pattern, and population structure. Thus influencing sampling strategy.

5.1.1.2 Seed Increase and Maintenance

Self-pollinated species can be easily increased by harvesting all seed produced in nursery rows adjacent to other introductions of the same species. Chance crosses are minimal in most cases, and so are acceptable. This is not a satisfactory way of increasing seed of cross-pollinated species. Most of the harvested seed would be hybrids of unknown male parentage, and would not be representative of the introduction. Seed multiplication is the prime objective of maintenance. Collections must be grown in suitable environments, and might be required to meet quarantine regulations. Evaluation of genotypes present in the collection may accompany maintenance. Variability in safflower's pollination requirements make recommendations for maintenance difficult. Genotypes having reasonable self-fertility, could be grown in environments without pollinators, so as to preclude the use of bags to prevent crossing. Lack of crossing among the lines implies that the integrity of the line would be maintained. Maintenance of such homozygosity allows expression of recessive characters, some of which might be useful to plant breeders (Creech & Reitz, 1971).

Safflower lines with low self-fertility (i.e. very little or no seed set under bags), require cross-pollination for maintenance. Several systems of intercrossing have been outlined by Burton (1979) for germplasm maintenance. They include increasedisolation, single crossing and random mating. Splitting a germplasm into sections outlined above with differing maintenance systems assumes prior knowledge of pollination requirements. It is unlikely that these would be known, and the method itself is relatively impractical.

As noted in Section 1.3.8.8 some of safflower's wild relatives are self-incompatible. Such relatives might be included in the collection. Results of this study suggested the presence of a mild form of self-incompatability, or inhibitory effect of bagging. Selfing can not be used to multiply seed of fully self-incompatible species. Intercrossing is required to maintain the frequency of self-incompatible alleles in the line (Burton, 1979). Thus there may be some validity in treating all safflower lines as requiring cross-fertilization, and so allow free or restricted intercrossing. Restricted intercrossing is more likely to uncover recessive genes. Sufficient pollinators would have to be present to accomplish crossing.

Pooling germplasm by mixing together seeds from the many introductions and growing the mixture in an isolated field allows free intercrossing. Bulk seed is harvested from the field. Such a method of maintenance breaks linkages, increases gene interchange and may improve adaptation to the environment in which the collection is grown. Pooling germplasm leads to natural selection and thus changes in gene frequency. Some genes may be lost from the collection. This method appears acceptable for safflower, but immediate utility of the germplasm is reduced as considerable screening is necessary to isolate genes of any use from such a highly heterogeneous population.

Sampling from one generation to the next during maintenance also poses a problem. Constraints on storage space mean only limited amounts of seed can be stored. When lines are planted out only a limited number of seeds can be planted, as a result sampling bias might occur. With self-pollinated lines this problem is not as great; as within line variance is minimal. Cross-pollinated lines however have large within line variance and thus poor sampling may bring about genetic changes in the line. Restricted population size will also result in inbreeding and possibly fixation of genes in the introduction.

5.5.2 Recommendations for Artificial Crossing

Controlled crosses in safflower are difficult, this being a consequence of the structure of the flower and the fact that it will yield only one seed. Claassen (1950) has reported poor seed setting rates with artificial crossing of safflower. Poor results were obtained in trial crosses prior to this study.

Peripheral florets have been reported as having rudimentary ovaries in many of the wild species (Schank and Knowles, 1964). In all lines of safflower *(C. tinctorius)* examined in the main experiment, some degree of peripheral female sterility was present. No literature reviewed has commented on this fact. Both Claassen (1950) and Knowles (1958) have recommended the use of the peripheral whorl of florets in artificial crossing. This may have resulted in the poor results obtained, to date. Experiments were not conducted to test this hypothesis.

Allowing peripheral florets to elongate also removes much of the guess work involved in choosing capitula which are about ready to open.

Prior to eamsculation of non-elongated florets, bracts surrounding the capitulum are removed to eliminate spines (making the job more pleasant) and to expose the unopened florets. Karve *et al.* (1976) have reported that bract removal has no effect on seed set. Removal of peripheral florets and emasculation of the outer two whorls of unopened florets follows. This should give better efficiency in crossing programs, as part of the uncertainty as to whether or not florets were going to elongate is removed.

Techniques of emasculation have been reviewed by Wiess (1971). All involved removal of the anther column the afternoon prior to the day in which the florets are due to elongate. Methods used by Claassen (1950) and Chavan (1961) (after Wiess, 1971) involve splitting the corolla and anther column then removing them with sterile forceps. Knowles (1958) simplified the process by squeezing the floret just below the attachment of the anthers, then bending the floret to break the corolla tube. The corolla tube could then be slipped off without releasing pollen. A number of styles break with this technique. Claassen (1950) and Chavan (1961) (after Wiess, 1971) used a 57% alcohol rinse to remove any escaped pollen. The relatively rapid decline in pollen viability after dehiscence, most likely precludes the necessity of such a practice. Any pollen escaping onto the stigma during emasculation is most likely not mature, and would probably have died before stigmas became receptive.

Pollination of emasculated florets is conducted in the morning while styles are elongating. In this experiment whole heads were used as a pollen source. Freshly elongating styles should be carrying viable pollen with them. Should viability outside the floret be very short, some viable pollen would still be present on such heads. On lines where delayed dehiscence occurs removing fresh anthers using forceps and dehiscing them on to elongating or receptive stigmas may be of some use. Alternatively, plants could be placed in a controlled temperature environment, with a view to causing earlier dehiscence, and then whole heads could be used in crossing. If whole heads are in short supply, individual freshly elongating florets could be removed and used as a pollen source.

Pollinations could be repeated on days when the stigma is turgid. Fresh pollen would thus be applied to the emasculated stigma each morning that it is turgid. There is no evidence of repeated pollination leading to increased seed set in safflower.

Difficulty arises in suggesting an ideal environment in which to conduct crossing. As already noted environmental differences between characters exist. Seed sets were highest in the cool-dry environment. Viable pollen percentage and amounts of viable pollen were highest in hot-humid environments; stigma turigidities tended to be slightly longer in cool environments.

Several approaches to this problem are possible:

1. Plants could be grown under conditions where seed set is optimal, in the hope that such conditions result in optimal levels of crossed seeds.
2. Male and female parents could be grown in separate environments providing optimal conditions for each. After crossing female parents might be grown on, under conditions of optimal seed set.
3. With cooler conditions insects are not as active and plants have high selfed seed set. Co-evolution of safflower with pollinators may have led to a greater reliance on crossing in warmer more humid environments. Insect activity is normally considered to improve with warmer temperatures. Perhaps plant growth characteristics in

such environments add to the crossing potential and therefore improve crossed seed set.

Controlled pollination could also be accomplished using caged insects. Inbred parental lines could be placed within the cage and bees used to perform the crossing. Screening of progeny would show those plants which were selfed. Young bees would have to be removed from the hive before their first flight, and placed in the cage. Foraging behaviour would then be more normal. Such a crossing technique could not be used with heterozygous parents, as difficulties would arise in determining which progeny resulted from self-pollination or cross-pollination.

5.5.3 Breeding Plans for Safflower

Breeding plans exploit genetic variance to achieve phenotypic gains. This study clearly demonstrated the presence of genetic variance for most characters. Sahai and Dalal (1974) have artificially induced genetic variation using mutation. Use of germplasm collections should provide ample genetic variance, to meet most breeding objectives. Genetic variance can be partitioned into additive, dominance and epistatic components. Genetic partioning experiments (Griffing, 1956; Hayman, 1958; Mather and Jinks, 1977) can be used to study the nature of gene action for any character. Several authors have conducted such studies in safflower (Abel, 1976b; Kotecha, 1980; Ehdaie and Ghaderi, 1978; Zimmerman, 1978). Population structure will influence expression of the variance components. Self-fertilized species could be expected to largely express additive variance. Dominance and epistatic effects could only be separated from the additive effects after crossing (Mather, 1973).

Breeding plans commonly used, fall into two categories, those with the prime objective of utilizing additive genetic variance, and those utilising dominance and epistatic effects in addition to the basic additive effects. Such breeding plans have been outlined and discussed by Allard, (1960) Simmonds (1979) and Poehlman (1979).

As an oil crop safflower has given a good account of itself, when it is considered that for many centuries it was grown and utilised for its flowers (Knowles, 1958). Breeding plans used by modern plant breeders to accomplish this vary as do objectives.

Desirable characteristics or breeding objectives will differ according to the wishes of local growers. Recent history shows safflowers past importance as a dye. Usage has now largely changed, and high yield of unsaturated oil from the seed is the prime objective (Wiess, 1971). Other modern day objectives include cold tolerance, seed dormancy and resistance to various pests and diseases.

5.5.3.1 Breeding Plans Utilising Additive Genetic Variance

Many breeding advances and potential advances in safflower, originate from introductions which may be used directly, or as parents (Claassen 1952; Knowles,1955, 1958, 1960b; Zimmer, 1963, 1967; Zimmer and Leininger, 1965; Ashri, 1971, Zimmerman 1972, 1976, 1978; Zimmerman and Buck, 1977).

The majority of commercial cultivars of safflower are known somewhat loosely as pure lines (Wiess, 1971). Commercial cultivars in the U.S.A. have been selected from introductions obtained directly from Africa or South West Asia (Knowles, 1955) . After introducing material (the basic germplasm for the program), selfing is allowed or forced to occur, resulting in rapid inbreeding and the development of line structure within the breeding program. Increasing line structure is accompanied by redistribution of genetic variance from within lines to amongst lines (Falconer, 1960). Selection in early generations to reduce numbers of lines in the program, might be based on highly heritable characters e.g. height, or some disease. Most intense selection is likely to occur when line structure is well developed, during the 4th to 6th generation of selfing (Rubis 1970a). With-holding selection till these later selfed generations ensures that maximum additive genetic variance is being utilized.

Response to selection will be dependent upon intensity of selection applied and the level of predictive heritability, for the character concerned. The expected genetic advance might be expressed as $\Delta G = i \sigma p h^2$ where i is the standardised selection differential, σp is the phenotypic standard deviate and h^2 is a predictive form of heritability estimate for a particular selection system (Falconer, 1960). Expected genetic advance formulae for different selection procedures have been presented by Shelbourne (1969) and Falconer (1960).

The uniformity of the lines utilised in this study would tend to suggest that line structure was already well developed in safflower, and as a consequence line selection could commence early in the program. Presence of heterozygosity evidenced by non uniformity within a line, would invalidate such a statement.

Claassen (1952) suggested that improvement might be possible through hybridization and selection. Pedigree breeding programs accomplish this. Backcrossing techniques might be useful in incorporating genes into one of the parents involved in a pedigree program (Allard, 1960). Pedigree breeding programs exploit variation expressed in the F_2 after a cross. Selection strategies will change with the redistribution of within line and amongst line variance accompanying inbreeding.

Both pure line and pedigree breeding plans are applicable to self-pollinated species. Other methods could be used, but no mention of them has been made in the safflower literature reviewed.

In the application of either breeding program it would be desirable to select for all characters considered important in the breeding objectives. Hazel and Lush (1942) suggested the use of a selection index as being the most efficient means of accomplishing this.

5.5.3.2 Breeding Plans Utilising Dominance and Epistatic Variances

Dominance and epistatic effects are manifested as heterosis, in the progeny resulting from crosses. Several authors have reported on the presence or absence of inbreeding depression and heterosis in safflower (Varisai-Muhammad *et al.*,1969; Yazdi-Samadi *et al.*,1975; Deokar and Patil, 1979; Barbier, 1975; Rubis, 1970b; Urie and Zimmer, 1970a). Yazdi-Samadi *et al.* (1975) observed inbreeding depression in only 10-11% of cases. Rubis (1970b) found 30% of hybrid lines to exceed yield of commercial check cultivars.

Hybrid and synthetic breeding plans are the two methods normally used to utilise heterosis for practical gains. Both methods normally apply to cross-pollinated species with utilizable levels of heterosis. Effective pollination controls are essential for commercial utilization of such methods.

Rubis *et al.* (1966) and Ebert and Knowles (1968) have reported on fucntional male sterility caused by delayed anther dehiscence. Rubis (1970b) used this gene to develop hybrid cultivars. Factors influencing the production of hybrid seed using insect pollination were also studied. Urie and Zimmer (1970a) found yield reduction caused by female selfs, as a result of functional male sterility breakdown. Discovery of genetic male sterility as noted by Heaton *et al.* (1979) may improve production of hybrid seed in the presence of insects.

Transfer of self-incompatibility mechanisms from wild relatives, and further use of male sterility may allow synthetics to be developed.

Continued improvement of parental inbred lines involved with these plans, might be achieved using methods utilising additive genetic variance. Alternatively recurrent selection methods might be used. Types of recurrent selection most applicable to the development of hybrid or synthetic cultivars are:

1. recurrent selection for general combining ability;
2. recurrent selection for specific combining ability;
3. reciprocal recurrent selection.

All these techniques involve progeny testing. If the tester has a broad genetic base, general combining ability or additive genetic variance is being accessed. Narrow genetically based testers assess specific combining ability, largely aimed at utilizing dominance and epistatic variance.

5.5.3.3 Induced Polyploidy

Investigative work has been carried out on the induction of polyploidy using colchicine in safflower (Krijthe (1942) after Schank and Knowles, 1961). Schank and Knowles (1961) suggested that as the genus as a whole seems to have benefitted from polyploidy (namely alloploidy) safflower might benefit. Autotetraploid plants were produced which had larger stomata, pollen grains and seeds, than the diploid. All failed to set selfed seed in the first generation. Seed set improved with increasing generations. Diversity of germplasm has been advantageous in improving fertility (Burnham, 1966). Low oil content of the seed was a serious limitation of autotetraploids. Triploids have also been produced (Estilai and Knowles, 1980). These are useful tools in assigning genes to chromosomes.

Chromosome manipulations can result in useful transfer of genes between non-crossable species. Studies of taxonomic relatedness (as mentioned in Section 1.1.0) may provide bridging species for interspecific crossing. Ashri (1974) has suggested that introgression may occur between species in the genus, despite differences in chromosome number.

CONCLUSIONS

1. Characters most important in determining pollination pattern of safflower were: the length of style-stigma at full extrusion; the rate of corolla tube expansion; the rate of style-stigma expansion and amounts of viable pollen on the floret during expansion. Synchronized rates of style-stigma and corolla tube growth may promote selfing by maintaining the stigma in close proximity to freshly released pollen for an extended period. Shorter style-stigma lengths at full extrusion achieve the same result (self-pollination). Poor synchronization or long style-stigmas would promote cross-pollination.

2. Pollen viability periods were short, with stigma turgidity and receptivity lasting a few days in all environments. Release of pollen was generally prior to stigma extrusion in most genotypes. Self-pollination was the general pattern with the possibility of cross-pollination in the presence of insects. Should fertilization controls exist, self- or cross-fertilization may not necessarily follow.

3. Activity of daytime active pollinating insects (mostly the honey bee) accounted for some cross-pollination in safflower. Variation in insect activity under field conditions was noted, being due to complex interactions of insect, plant and environment. Insect activity on all genotypes was at the same level, indicating that variability in plant characters normally associated with influencing insects were having little or no effect.

4. Genotypic differences were present for most plant characters involved in pollination. Out of the characters most important in self-pollination, only one the amount of viable pollen at time 2 did not have significant genotypic differences. Uniformity of plants within lines used, indicated previous selfing history, and the probability of largely additive gene action.

5. Environmental influences were pronounced. Selfed and crossed seed sets were highest in the cooler drier environment, and poorest in the warmer humid environment. Higher humidities adversely affected seed set, but promoted pollen viability, and had little effect on stigma turgidity duration. Lower humidity and temperature conditions did favour self-pollination. Insects may thus be important pollinators under warm humid conditions.

6. Considerable genotype-environment interaction was present for most characters. Of the most important characters influencing self-pollination only the percentage of viable pollen at time 2 did not display significant genotype-environment interaction. The general trend among genotypes was to specific adaptation to high humidity environments for pollen viabilities, and amounts of viable pollen. Both specific and average responses to environment were noted in self-pollination percent, pollen characters and some of the corolla characters.

7. Broad-sense heritability estimates were moderate to high most for characters, but ranged from -0.001 to 0.838. Use may be made of genetic variance by selection with reasonably optimistic expectations for such characters as floret emergence and flower colour with broad-sense full heritability estimates of 0.831 and 0.787, respectively. Most characters shown to be most important in self-pollination of safflower had moderate heritability estimates.

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APPENDICES

APPENDIX 1.

Counts of insects visiting 135 m of safflower commencing at 7.30 a.m. standard time for days on which observations were made.

APPENDIX 1. Counts of insects visiting safflower during day 1 commencing at 7.30 a.m. std time

	Humenoptera			Lepidoptera		Diptera		
Time category	Nectar collectors	Pollen collectors	Bumble bees	Butterflies	Moths	Hoverflies	Small flies	Dung flies
1					3			3
2					1		10	16
3					1		36	29
4							63	50
5						1	96	60
6						2	64	62
7	2		1		1	2	54	40
8	19	2	4	1	1	10	12	38
9	25	8	2	3		3	7	21
10	28	23	4	1	1	5	3	21
11	21	45		2		1	5	8
12	26	27	3	1		3	1	12
13	29	38	2	1		8	1	11
14	26	14	1	2	1	2	3	13
15	40	6	2	1	2	3	3	10
16	27	5	1	4	2	3	3	7
17	23	8	1	1		6	4	4
18	16	3	3	2	2	3		7
19	2		2	1	1	2	1	9
20			2	1	2	2	3	12
21	6					1	6	8
22	6				1	1	1	7
23								2
24								1
25								
26								

APPENDIX 1 (ctd) Counts of insects visiting safflower during day 2, commencing at 7.30 a.m. std time

	Hymenoptera			Lepidoptera		Diptera		
Time category	Nectar collectors	Pollen collectors	Bumble bees	Butterflies	Moths	Hoverflies	Small flies	Dung flies
1								2
2							12	11
3							28	16
4							36	26
5	1				1		49	24
6	1		1		1	1	69	27
7	14	9	2			1	31	19
8	3		1				15	23
9	15	22	1	2		2	13	26
10	29	49	1	3		6	8	9
11	33	55	4	2		8	1	20
12	48	45	4	3	1	6	3	13
13	62	23	2	4	4	5	2	12
14	59	26	2	3		11	3	13
15	68	12	7	3	1	8	4	9
16	65	6	4	6	1	16	3	10
17	64	8	3	5	3	12	2	8
18	58	4	4	10		10	3	9
19	57		1	7	1	10	1	13
20	38	1		5	1	5		16
21	18		2	3	2	5		15
22	6			2		4	3	10
23	6		2	3	4	1	3	13
24	5		2			2	2	18
25					1	1	14	22
26						1	28	14

APPENDIX 1 (ctd) Counts of insects visiting safflower during day 3, commencing at 7.30 a.m. std time.

	Hymenoptera			Lepidoptera		Diptera		
Time category	Nectar collectors	Pollen collectors	Bumble bees	Butterflies	Moths	Hover-flies	Small flies	Dung flies
1								
2								
3							31	51
4							48	49
5							61	72
6							59	57
7			1		2	1	55	46
8	3			1		2	40	51
9	7	1	1			3	34	47
10	11	9	1	1		4	52	52
11	19	23		6		3	53	49
12	4	3	2	3	2		42	40
13	19	26	2			5	33	27
14	37	59	4	2		2	31	32
15	49	34	5		2	1	10	9
16	46	29	4				17	23
17	40	9	2	2	2	1	20	20
18	37	4	2	1		2	12	19
19	32	6	2		1	1	13	11
20	57	11	3			1	7	13
21	52	11	5				9	17
22	8	3	2		1	2	15	15
23	9	1	2			1	7	11
24	2		1			1	7	9
25	2		1			1	14	15
26			1				20	12

APPENDIX 1(ctd) Counts of insects visiting safflower during day 4, commencing at 7.30 a.m. std time.

	Hymenoptera			Lepidoptera		Diptera		
Time category	Nectar collectors	Pollen collectors	Bumble bees	Butterflies	Moths	Hoverflies	Small flies	Dung flies
1								
2					1		5	8
3							21	33
4					2	1	35	50
5	1				1		42	44
6	17		1			2	12	31
7	42	2		6		6	14	26
8	57	15	1			3	10	29
9	62	26	2	1		5	1	24
10	48	36	2	3		7	3	21
11	42	19	2	2		2	4	16
12	27	7	1			2	3	18
13	11	2	2			1	9	16
14	10	3				2	4	24
15	21	1	1			1	2	15
16	26	5	4			2	5	10
17	28	9	1			1	2	11
18	35	5	1				2	9
19	9	1	1			2	6	10
20	8					1	6	3
21	9					1	1	2
22	6					1		
23						1	1	6
24			1				4	6
25					1	1	1	3
26						1	2	3

APPENDIX 1 (ctd) Counts of insects visiting safflower during day 5,
commencing at 7.30 a.m. std time

	Hymenoptera			Lepidoptera		Diptera		
Time category	Nectar collectors	Pollen collectors	Bumble bees	Butterflies	Moths	Hoverflies	Small flies	Dung flies
1								
2								
3			1				2	
4							10	1
5	1					2	15	5
6	10			1		3	20	5
7	25		1	1		5	7	8
8	67	1	2			3	5	6
9	83	16			1	1	3	8
10	53	38	1			4	4	2
11	58	28				2	6	4
12	38	27	2	2		4	3	1
13	34	23				1	1	4
14	40	27		1		4		1
15	31	23	1	2		6		1
16	37	18		1		3		
17	38	7		1		7	2	4
18	30	5	1		1	1	1	4
19	30	5		1		4	1	3
20	21	1	1	4		3		7
21	15	4	1	4		3	2	3
22	8		2	2	1	3		3
23			1	1		1		
24	3		2		1	1	3	1
25			2				1	3
26			1				8	8

APPENDIX 1 (ctd) Counts of insects visiting safflower, during day 6, commencing at 7.30a.m. std time

	Hymenoptera			Lepidoptera		Diptera		
Time category	Nectar collectors	Pollen collectors	Bumble bees	Butterflies	Moths	Hoverflies	Small flies	Dung flies
1								
2								3
3							2	7
4			1				4	9
5							6	12
6	7					1	3	5
7	16	10		1		2	4	7
8	24	12	2	1			1	3
9	26	15	1			2	7	1
10	23	16	2	1			4	5
11	19	12	3		1	3	2	6
12	4	1	5				1	4
13	7	3	4		1	1	4	2
14	14	7	1				2	4
15	31	7	1	1				
16	29	5	2			1	2	5
17	30	1	1	1		3		5
18	21	6	4					5
19	7	1	2			2	2	4
20	13	2	2			2		2
21	18		1	1		1		3
22	6		2			2	1	
23		1	1			2		2
24	1			1		1		1
25								3
26								1

APPENDIX 1 (ctd) Counts of insects visiting safflower during day 7, commencing at 7.30 a.m. std time

	Hymenoptera			Lepidoptera		Diptera		
Time category	Nectar collectors	Pollen collectors	Bumble bees	Butterflies	Moths	Hoverflies	Small flies	Dung flies
1								
2								
3								
4								
5						1	4	5
6	5					3	2	3
7	13					2	4	2
8	22	2	1			1	4	4
9	32	8	3	2		1		
10	35	15	2			2		3
11	39	18	1		1	1		3
12	39	14	1	1			1	4
13	30	12	3		1	4	8	2
14	34	8	3	2		6	6	10
15	35	5	1	3		8	1	12
16	40	18		1		5	1	4
17	33	6	3	3	1	7		1
18	22	6	1	3		13		3
19	9	1		3	1	3		7
20	23	1	1	1		4		4
21	18	1	1	1		3		1
22	14		1	1		2		1
23	6		2	1		1		1
24	3		2	1	1	2		2
25						1	1	3
26						1		4

APPENDIX 1 (ctd) Counts of insects visiting safflower during day 8, commencing at 7.30 a.m. std time

	Hymenoptera			Lepidoptera			Diptera	
Time category	Nectar collectors	Pollen collectors	Bumble-bees	Butterflies	Moths	Hoverflies	Small flies	Dung flies
1								
2							3	3
3							1	13
4							5	14
5	2		3			2	4	4
6	12	3	1	2		6	1	5
7	24	11	1			5	1	3
8	40	22	4	4		5		5
9	43	26	4	2		4		5
10	41	29	3			6		3
11	38	20		2		4		3
12	27	14	2					1
13	40	15		1		2		2
14	36	10	1			2		
15	26	6	2			3	1	1
16	21	4	1	3		1		1
17	25	3				2	1	
18	16	3				2		1
19	7					3		3
20	11		3			2	1	1
21	11		1			1		2
22	6		1			1		
23	4							2
24	3					2		1
25						2		2
26								2

APPENDIX 1 (ctd) Counts of insects visiting safflower during day 9, commencing at 7.30 a.m. std time

	Hymenoptera			Lepidoptera		Diptera			
Time category	Nectar collectors	Pollen collectors	Bumble-bees	Butterflies	Moths	Hoverflies	Small flies	Dung flies	
1									
2									
3									
4	1		1				1	5	19
5	7		2					6	15
6	16		1				2	5	11
7	31		3	2			2	8	14
8	42	2	2	3			1	1	9
9	46	9	2	1			1		4
10	51	8		2			1	1	2
11	69	15							1
12	67	8					1		
13	60	5		3			2		3
14	62		3		1		2		2
15	64		3	1			1		
16	50		1				2		1
17	56			1					5
18	33		1						3
19	42		1				2		1
20	30		3	1			1		9
21	6		1	1	1		1		1
22	2		1		1				9
23	2								4
24	1								2
25									3
26									2

APPENDIX 2 Climate lab - modified half-strength Hoagland's nutrient

		grams/litre			
	Molecular Wt. (g)	Conc.	Final soln.		PPM
Stock solution A:					
Calcium nitrate $Ca\ (NO_3)_2 \times 4H_2O$	236.15	295.19	.59038	Ca N	100.20 70.04
Sequestrene 330 10% DTPA NaFe	468.20	10.4	.0208	Fe Na	2.08 1.02
Stock solution B:					
Potassium phosphate KH_2PO_4	136.08	34.02	.06804	P K	19.55 15.49
Potassium nitrate KNO_3	101.11	126.39	.25278	K N	97.75 35.02
Magnesium sulfate $MgSO_4 \times 7H_2O$	246.5	123.24	.24648	Mg S	24.32 32.06
Boric acid H_3BO_3	61.82	0.715	.00143	B	0.250
Manganese chloride $MnCl_2 \times 4H_2O$	197.92	0.4525	.000905	Mn Cl	9.251 0.324
Zinc sulfate $ZnSO_4 \times 7H_2O$	287.55	0.055	.000110	Zn S	0.025 0.012
Copper sulfate $CuSO_4 \times 5H_2O$	249.68	0.020	.00004	Cu S	0.010 0.005
Sodium molybdate $Na_2MoO_4 \times 2H_2O$	241.93	0.0067	.0000134	Na Mo	0.003 0.005
Potassium chloride KCl	74.56	1.575	.00315	K Cl	1.652 1.498

Nutrient	PPM	Nutrient	PPM
N	105.06	B	0.250
P	15.49	Mn	0.251
K	118.95	Cu	0.010
S	32.08	Zn	0.025
Ca	100.20	Mo	0.005
Fe	2.08	Cl	1.822
Mg	24.32	Na	1.023

APPENDIX 3 Insect vision of safflower

Introduction

The most study of insect vision has centred on the honey bee, which has visual capacity to see wavelengths from 300 nm to 650 nm compared to man with a range from 400 nm to 800 nm (Von Frisch, 1950). Honey bees have been shown to be significant visitors to safflower, and it was decided to attempt to elucidate what they see on safflower, as this may be markedly different from what humans see. Kevan (1972) found variation in reflectance patterns with changes in wavelength of light illuminating flowers.

Method

Safflower heads falling into the six scores outlined in Section 3.4.6 were photographed under direct sunlight using the window filters listed in Table A1. Ilford HP-5 film was used. The window filters allow restricted wavelengths to pass through. Filters available did not allow the full range of insect vision to be studied. A commercially available Kodak gray scale was included on each photograph so as to be able to gauge flower brightness at the different wavelengths. Kevan *et al.* (1973) recommended use of a calibrated gray scale, but this was not used in this study.

Table A1. Window filters used to photograph safflower heads

Filter	Transmission Range (nm)
Kodak 35	350-450 nm
Kodak 48	400-500 nm
Kodak 61	500-600 nm
Kodak 25	600-

Results

Intereptational difficulties of such studies have been exhaustively outlined by Kevan *et al.* (1973) and Kevan, (1972). Plate A1 shows photographs of the florets through the filters and without a filter. All petals appear white (indicating reflectance of light) under unscreened sunlight. Some slight colouration of petals occurs with white flowers in the wavelength range 350-400 nm. This is slightly more pronounced at the next range of 400-500nm. No other flower colours display any reflectance in these ranges. All flower colour categories show a moderate degree of reflectance at 500-600 nm. Reflectance is greater at over 600 nm.

Discussion

It would appear that insects should be able to clearly discern the white flowered genotypes of safflower. Other flower colours may not be so easily discerned. This exercise did not investigate the far ultraviolet range within insect vision. Differences in the flower colours may vary there.

Results suggest that white flowers are likely to have more ultraviolet. reflectance than other flower colours.

It is not known whether flowers within the same colour category for humans have differing patterns discernable by insects.

(Refer to Bibliography for references)

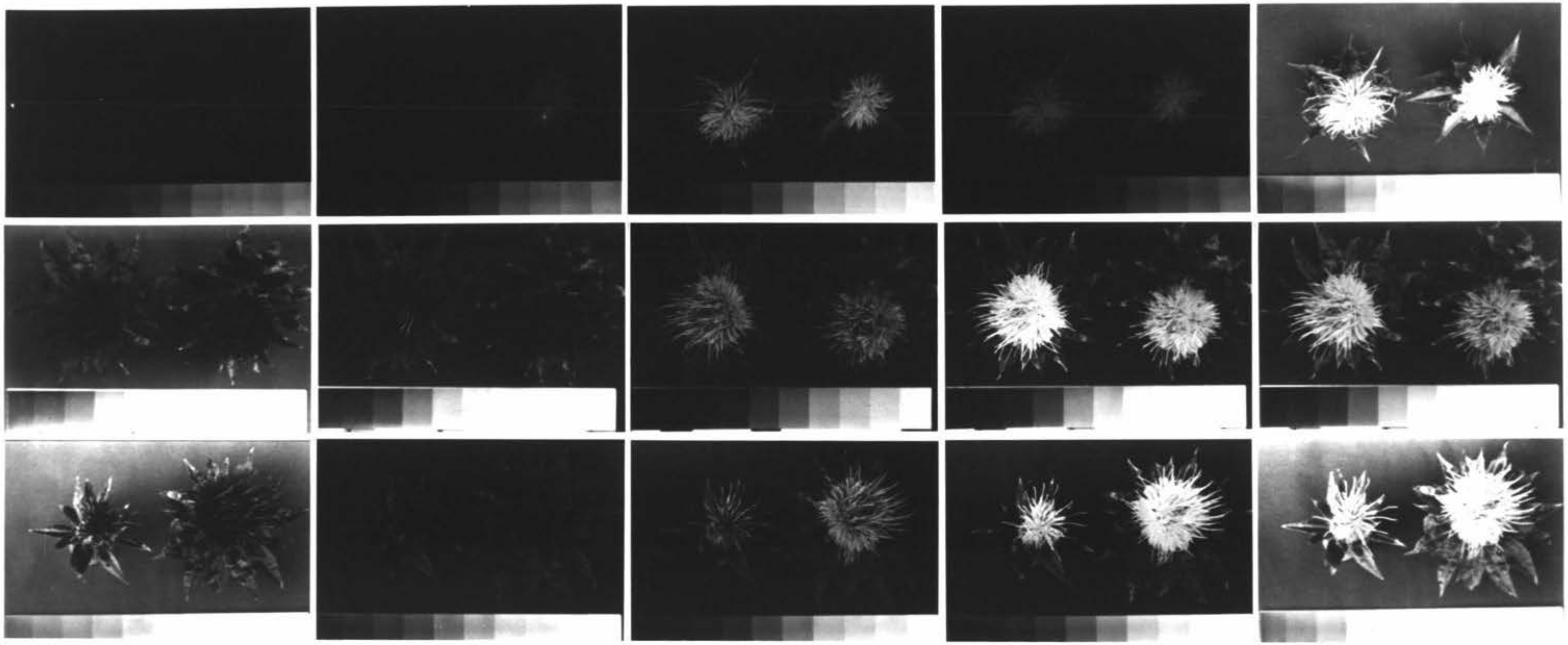

Plate A1. Safflower heads of various colours photographed through various window filters. White colouration of the florets indicates that light within the specified wavelength ranges, is being reflected by pigments in the floret. The grey scale gives some indication of the intensity of light (of the specified wavelength) passing through the filter.

APPENDIX 4

Summary statistics for the regression of SELF1% with independent variables including dummy variables (G,E,GE) for the single and pooled environments. Statistics given include the regression coefficient ($\hat{\beta}_k$) its standard error (se β), the standardised regression coefficient ($\hat{\beta}^*_k$), F values and R^2 change for each independent variable. The simple correlations of the independent variables with SELF1% are given for the pooled environment.

APPENDIX 4.1 Summary statistics for the regression of SELF1% with independent variables including dummies. Environment 1

$\hat{\mu} = -171.7567$

Character	$\hat{\beta}_k$	se β	$\hat{\beta}'_k$	F	R^2 change
G1	48.044	44.7164	0.92991	1.154	0.14451
G2	8.495	20.3800	0.16443	0.174	0.00977
G3	21.873	44.3440	0.42336	0.243	0.02654
G4	-8.736	32.8078	-0.16910	0.071	0.01064
G5	-11.312	21.2771	-0.21894	0.283	0.00008
G6	9.310	31.0664	0.18019	0.090	0.01607
G7	-28.388	19.1375	-0.54946	2.200	0.02938
G8	-0.988	18.3039	-0.01913	0.096	0.00081
G9	16.110	51.9978	0.31181	0.022	0.08730
G10	7.495	50.0553	0.14506	0.019	0.06493
G11	-40.957	18.6791	-0.79272	4.808	0.01727
VP%1	0.523	0.5746	0.71013	0.828	0.06090
DP%	1.268	0.2676	1.13525	1.248	0.00194
VP%2	-0.510	0.8671	-0.67281	0.346	0.00911
VP%3	-0.051	1.0715	-0.04700	0.002	0.00012
AP1	0.173	2.0481	0.05089	0.007	0.00116
AP2	1.436	1.8899	0.35169	0.578	0.00617
AP3	-0.495	1.1695	-0.13413	0.179	0.00083
AVP1	-2.674	8.3610	-0.53376	0.102	0.00327
AVP2	0.474	11.3565	0.08712	0.002	0.00002
TAVP	0.949	6.8741	0.36835	0.019	0.00258
LCT1	-3.639	8.9936	-0.74541	0.164	0.02506
LP1	-133.570	63.4402	-4.12169	4.433	0.00152
LS1	10.920	15.0696	1.13397	0.525	0.00559
LCT2	2.632	8.7112	0.38503	0.091	0.02081
LP2	141.144	61.3284	4.10963	5.297	0.04373
FREQST	0.099	1.9982	0.01335	0.002	0.01521

APPENDIX 4.1 ctd

Character	$\hat{\beta}_k$	se β	$\hat{\beta}'_k$	F	R^2 change
LS2	-10.476	14.8957	-1.29884	0.495	0.01904
RSEXPA	9.948	53.3584	0.59230	0.035	0.01786
RCTEXPA	-9.757	72.8754	-0.43151	0.018	0.01453
RPEXPA	-390.083	205.8412	-2.30340	3.591	0.01376
PPTEXT	14.008	9.2989	0.62794	2.269	0.02942
RSEXPO	8.564	20.8208	0.43192	0.169	0.00302
PT	-1.825	2.3240	-0.19954	0.616	0.00044
ROSETTE	0.906	1.8507	0.17581	0.240	0.01244
FLOW	1.677	1.5403	0.66613	1.186	0.00256
FLMED	0.532	1.7056	0.20444	0.097	0.00325
FL	-2.303	4.9578	-0.13267	0.216	0.00170
HEIGHT	-0.102	0.2907	-0.13198	0.123	0.00218
TNH	0.015	0.3507	0.02253	0.002	0.00013
FCOL	-0.005	4.9973	-0.00057	0.000	0.00229
NCOL	-2.888	6.5900	-0.28791	0.192	0.00010
DFCOL	1.943	2.0448	0.35841	0.902	0.00435
AC	0.004	0.7328	0.00125	0.000	0.00029
NEC	-0.677	1.5014	-0.09369	0.203	0.00082
FDENS	0.296	1.9020	0.04038	0.024	0.00002
FE	-5.451	4.4479	-1.16494	1.502	0.00929
AMTPOL	1.499	1.2384	0.32727	1.465	0.02243
ARPOLAD	-1.383	3.1769	-0.15300	0.189	0.01302
NSTIG	0.781	3.5110	0.05786	0.049	0.00662
DEXT	-1.001	2.0232	-0.15594	0.245	0.02409
PP	-3.443	12.7027	-0.10799	0.073	0.00119
ESTA	1.976	1.4532	0.24952	1.850	0.01375

APPENDIX 4.2 Summary statistics for the regression of SELF1% with independent variables including dummies. Environment 2.

$\hat{\mu} = -216.4298$

Character	$\hat{\beta}_k$	se β	$\hat{\beta}'_k$	F	R^2 change
G1	61.187	13.3052	1.74151	21.148	0.46993
G2	30.825	11.7764	0.87734	6.851	0.00002
G3	24.093	17.4628	0.68573	1.903	0.00017
G4	-2.136	19.1296	-0.06080	0.012	0.00174
G5	47.589	14.8029	1.35450	10.335	0.00008
G6	29.750	15.3546	0.84676	3.754	0.00012
G7	21.849	13.5132	0.62188	2.614	0.00017
G8	34.958	18.0278	0.99499	3.760	0.00000
G9	34.583	35.2297	0.98431	0.964	0.00034
G10	17.259	34.1884	0.49124	0.255	0.00000
G11	11.050	12.3617	0.31452	0.799	0.00394
VP%1	-0.315	0.1912	-0.72277	2.729	0.00554
DP%	-0.780	1.4794	-0.06484	0.278	0.00011
VP%2	0.615	0.2557	1.34559	5.788	0.04171
VP%3	0.922	0.3297	2.16488	7.823	0.00000
AP1	-0.747	1.3659	-0.17301	0.299	0.02914
AP2	1.225	1.3665	0.24686	0.803	0.00967
AP3	5.403	1.7882	1.21419	9.128	0.02121
AVP1	13.666	5.6351	2.58142	5.882	0.02256
AVP2	7.756	5.6049	1.43397	1.915	0.00985
TAVP	-12.368	4.0548	-5.34149	9.304	0.00427
LCT1	-13.188	5.7279	-3.84481	5.301	0.00000
LP1	-88.713	45.7882	-4.38696	3.754	0.01597
LS1	10.699	5.6899	1.52329	3.535	0.00101
LCT2	11.705	5.8202	2.99741	4.045	0.01632
LP2	105.072	44.5797	5.49495	5.555	0.04808
FREQST	-1.918	1.5666	-0.34630	1.499	0.01558

APPENDIX 4.2 ctd

Character	$\hat{\beta}_k$	se β	$\hat{\acute{\beta}}_k$	F	R^2 change
LS2	-8.764	5.6624	-1.47184	2.396	0.00213
RSEXPA	38.604	24.7693	2.04620	2.429	0.00094
RCTEXPA	-107.397	42.9285	-3.41354	6.259	0.00053
RPEXPA	-330.973	183.6623	-1.46776	3.247	0.00861
PPTEXT	1.771	4.6134	0.17715	0.147	0.01136
RSEXPO	-4.958	4.0960	-0.44134	1.465	0.00936
PT	-1.633	1.1361	-0.27144	2.066	0.01549
ROSETTE	-1.080	1.0263	-0.21099	1.108	0.00076
FLOW	1.247	0.7326	0.67407	2.897	0.02607
FLMED	-0.375	0.7899	-0.22193	0.225	0.01852
FL	-4.220	2.4562	-0.24638	2.952	0.02731
HEIGHT	0.438	0.1384	0.93867	10.035	0.00000
TNH	0.008	0.1735	0.01195	0.002	0.00183
FCOL	-6.408	6.2115	-1.09677	1.064	0.00043
NCOL	3.173	2.1956	0.44967	2.085	0.00398
DFCOL	-2.123	1.6489	-0.53204	1.658	0.00672
AC	-0.131	0.6464	-0.04025	0.041	0.00651
NEC	1.785	1.0361	0.42651	2.967	0.00052
FDENS	4.242	1.2706	0.91354	11.145	0.00826
FE	2.493	2.9107	0.72982	0.733	0.00026
AMTPOL	-1.465	0.7187	-0.44974	4.155	0.00853
ARPOLAD	0.998	0.7963	0.26806	1.572	0.00000
NSTIG	-0.094	0.6944	-0.02775	0.018	0.00444
DEXT	-1.828	1.3194	-0.39971	1.920	0.02488
PP	0.515	6.7441	0.03375	0.006	0.00200
ESTA	-0.352	0.6813	-0.06523	0.267	0.00044

APPENDIX 4.3 Summary statistics for the regression of SELF1% with independent variables including dummies. Environment 3

$\hat{\mu} = -468.9228$

Character	$\tilde{\beta}_k$	se β	$\hat{\beta}'_k$	F	R^2 change
G1	24.145	36.7759	0.22081	0.431	0.03594
G2	-15.014	22.5413	-0.13731	0.444	0.12879
G3	35.844	54.2277	0.32780	0.437	0.00268
G4	-113.568	42.3464	-1.03859	7.192	0.01544
G5	12.928	24.2463	0.11823	0.284	0.00097
G6	-86.556	30.0999	-0.79156	8.269	0.02003
G7	-30.514	38.6755	-0.27906	0.622	0.06853
G8	9.314	26.8785	0.08518	0.120	0.02597
G9	-1.414	61.3368	-0.01293	0.001	0.08999
G10	110.440	66.2464	1.00998	2.779	0.09065
G11	13.615	23.0865	0.12451	0.348	0.00670
VP%1	1.255	0.8646	0.74543	2.105	0.00466
DP%	-5.795	5.1604	-0.17659	1.261	0.00002
VP%2	1.082	0.9044	0.72852	1.430	0.00891
VP%3	2.894	1.1535	1.37389	6.294	0.00876
AP1	1.843	3.8153	0.15775	0.233	0.00008
AP2	3.896	2.5185	0.28963	2.393	0.03126
AP3	9.215	3.5842	0.82196	6.609	0.00424
AVP1	31.233	12.6074	2.42807	6.137	0.00338
AVP2	42.427	17.8016	3.03835	5.680	0.01851
TAVP	-42.207	13.9243	-6.06939	9.188	0.01738
LCT1	-16.136	6.8454	-1.45445	5.557	0.00007
LP1	117.143	71.4428	1.73932	2.689	0.00539
LS1	28.372	15.1108	1.44064	3.525	0.01608
LCT2	14.964	6.4564	1.07247	5.372	0.03737
LP2	-19.059	70.6608	-0.26924	0.073	0.00363
FREQST	-21.418	5.2733	-1.39472	16.496	0.00764

APPENDIX 4.3 ctd

Character	$\hat{\beta}_k$	se β	$\hat{\beta}'_k$	F	R^2 change
LS2	-63.416	14.9132	-4.14637	18.082	0.03758
RSEXPA	117.959	109.5866	2.58533	1.159	0.00363
RCTEXPA	-234.486	129.1178	-3.65711	3.298	0.09282
RPEXPA	421.461	379.2724	0.65379	1.235	0.00002
PPTEXT	10.500	10.6173	0.39121	0.978	0.00745
RSEXPO	27.166	43.1756	0.55005	0.396	0.00130
PT	0.274	2.6715	0.01534	0.011	0.00334
ROSETTE	-2.510	1.8899	-0.24368	1.764	0.00133
FLOW	-3.398	1.8920	-0.57760	3.226	0.01638
FLMED	0.613	1.6718	0.12852	0.135	0.00027
FL	7.794	6.0989	0.20121	1.633	0.00231
HEIGHT	0.393	0.4249	0.25357	0.858	0.01820
TNH	-0.590	0.4643	-0.45205	1.614	0.00274
FCOL	-22.059	8.3337	-1.52156	7.007	0.00302
NCOL	-2.521	4.3287	-0.16035	0.339	0.00192
DFCOL	11.283	4.6161	1.26184	5.975	0.00764
AC	-2.661	1.1794	-0.43315	5.089	0.00001
NEC	-6.245	3.1701	-0.46262	3.880	0.00024
FDENS	3.247	3.6693	0.21567	0.783	0.01180
FE	-4.564	4.5959	-0.47129	0.986	0.00759
AMTPOL	5.668	2.6178	0.49417	4.688	0.01714
ARPOLAD	5.879	4.3157	0.17154	1.856	0.02247
NSTIG	14.414	12.9953	0.14498	1.230	0.00056
DEXT	18.409	4.3634	1.24646	17.800	0.00890
PP	7.455	15.3523	0.15891	0.236	0.00009
ESTA	2.636	0.8896	0.34293	8.778	0.01953

APPENDIX 4.4 Summary statistics for the regression of SELF1% with independent variables including dummies. Environment 4

$\hat{\mu}$ = -135.8507

Character	$\hat{\beta}_k$	se β	$\hat{\beta}_k'$	F	R^2 change
G1	64.817	21.7806	1.53513	8.856	0.24198
G2	14.657	18.5643	0.34713	0.623	0.01466
G3	21.758	27.1359	0.51532	0.643	0.00949
G4	7.298	33.9471	0.17284	0.046	0.01725
G5	25.051	16.1699	0.59331	2.400	0.02012
G6	-6.154	15.8933	-0.14575	0.150	0.02525
G7	24.330	22.2597	0.57623	1.195	0.04860
G8	40.334	19.7951	0.95526	4.152	0.08481
G9	4.693	35.2341	0.11115	0.018	0.01455
G10	24.527	34.1956	0.58090	0.514	0.06911
G11	9.500	13.7042	0.22502	0.481	0.00032
VP%1	0.425	0.5125	0.77267	0.689	0.00333
DP%	-0.940	1.6866	-0.07113	0.310	0.00011
VP%2	-0.185	0.4671	-0.31451	0.157	0.00036
VP%3	0.160	0.4080	0.26807	0.153	0.00009
AP1	0.621	3.7290	0.09874	0.028	0.00066
AP2	-0.018	2.0994	-0.00325	0.000	0.00229
AP3	-1.863	1.5599	-0.36077	1.427	0.02141
AVP1	-1.879	8.0166	-0.31935	0.055	0.00171
AVP2	5.191	8.0483	0.90067	0.416	0.00288
TAVP	-0.924	4.9663	-0.31323	0.035	0.04850
LCT1	6.564	6.7984	1.72311	0.932	0.00370
LP1	-61.387	40.1709	-3.36489	2.335	0.01784
LS1	-1.758	7.2884	-0.17048	0.058	0.00001
LCT2	-8.039	7.3412	-1.73059	1.199	0.00316
LP2	67.490	42.1459	3.42899	2.564	0.00090
FREQST	1.625	2.4255	0.23232	0.449	0.03920

APPENDIX 4.4 ctd

Character	$\hat{\beta}_k$	se β	$\hat{\beta}'_k$	F	R^2 change
LS2	6.729	5.7798	0.98535	1.356	0.00099
RSEXPA	-9.904	31.9476	-0.51147	0.096	0.00009
RCTEXPA	50.239	37.1507	1.67122	1.829	0.00008
RPEXPA	-350.073	228.4594	-1.17618	2.348	0.01980
PPTEXT	2.785	5.5046	0.28175	0.256	0.00025
RSEXPO	-1.766	7.0035	-0.13193	0.064	0.00198
PT	0.872	1.8054	0.11133	0.233	0.00172
ROSETTE	0.600	1.0679	0.13876	0.315	0.00279
FLOW	-0.483	0.8796	-0.22382	0.302	0.00157
FLMED	0.294	0.8966	0.17303	0.108	0.00000
FL	-1.732	2.7026	-0.11352	0.411	0.00035
HEIGHT	0.175	0.1820	0.32111	0.925	0.03407
TNH	-0.132	0.1554	-0.22178	0.724	0.00088
FCOL	-1.632	6.3048	-0.27780	0.067	0.00618
NCOL	2.132	4.2597	0.47753	0.251	0.00515
DFCOL	-1.435	2.3400	-0.36980	0.376	0.00067
AC	0.966	0.9114	0.36561	1.124	0.00599
NEC	1.493	1.1122	0.31273	1.801	0.00454
FDENS	-3.426	2.1158	-0.59439	2.621	0.07119
FE	-0.373	1.5236	-0.10323	0.060	0.00114
AMTPOL	0.983	1.0451	0.25214	0.884	0.00643
ARPOLAD	-1.357	1.6947	-0.18443	0.642	0.00024
NSTIG	-0.298	1.1389	-0.05345	0.068	0.00104
DEXT	2.301	2.4403	0.38735	0.889	0.00468
PP	7.968	9.0664	0.48075	0.772	0.00864
ESTA	-0.199	0.7821	-0.07711	0.065	0.00272

APPENDIX 4.5 Summary statistics for the regression of SELF1% with independent variables including dummies. Pooled environment $\hat{\mu}$ = -32.5683.

Character	$\hat{\beta}_k$	se of β	$\hat{\beta}_k'$	F	R^2 change	r
E1	8.397	13.6202	0.17328	0.380	0.00030	
E2	16.524	13.3068	0.34096	1.542	0.09465	
E3	27.484	12.4167	0.56713	4.899	0.14026	
G1	28.130	11.9837	0.37050	5.510	0.07990	
G2	7.885	12.4515	0.10386	0.401	0.01678	
G3	-4.477	13.1144	-0.05896	0.117	0.00099	
G4	-25.775	15.9050	-0.33949	2.626	0.00002	
G5	6.949	12.4790	0.09152	0.310	0.00006	
G6	-7.761	11.0458	-0.10222	0.494	0.00894	
G7	5.264	13.7583	0.06934	0.146	0.02260	
G8	15.971	12.1806	0.21035	1.719	0.01215	
G9	-24.531	18.2935	-0.32310	1.798	0.02668	
G10	-3.851	20.0194	-0.05072	0.037	0.04000	
G11	10.109	10.9385	0.13314	0.854	0.00054	
E1G1	-1.650	15.9031	-0.01123	0.011	0.00010	
E1G2	2.793	16.2671	0.01901	0.029	0.00106	
E1G3	10.932	16.7613	0.07441	0.425	0.00241	
E1G4	5.213	15.8716	0.03548	0.108	0.00210	
E1G5	-4.140	16.0206	-0.02818	0.067	0.00013	
E1G6	-3.763	16.5451	-0.02562	0.052	0.00008	
E1G7	-19.912	16.7318	-0.13553	1.416	0.00067	
E1G8	-15.342	15.9890	-0.10442	0.921	0.00188	
E1G9	-4.939	17.4500	-0.03361	0.080	0.00002	
E1G10	7.194	17.3278	0.04897	0.172	0.00005	
E1G11	-18.987	15.2291	-0.12923	1.552	0.00090	
E2G1	-21.082	15.2079	-0.14349	1.922	0.00034	
E2G2	-20.389	15.7225	-0.13878	1.682	0.00841	
E2G3	-6.568	15.3297	-0.04471	0.184	0.00003	
E2G4	-20.872	14.5006	-0.14206	2.074	0.00095	
E2G5	-11.169	15.3694	-0.07602	0.528	0.00004	
E2G6	-9.221	15.4223	-0.06276	0.357	0.00342	
E2G7	-24.406	15.6947	-0.16612	2.418	0.00964	
E2G8	-30.070	15.2228	-0.20467	3.902	0.00676	
E2G9	-12.205	15.6504	-0.08307	0.608	0.00894	
E2G10	-23.298	16.2048	-0.15857	2.067	0.01386	
E2G11	-20.024	14.6646	-0.13629	1.865	0.00090	

APPENDIX 4.5 ctd

Character	$\hat{\beta}'_k$	se of β	$\hat{\beta}'_k$	F	R^2 change	r
E3G1	-5.213	15.0221	-0.03548	0.120	0.00000	
E3G2	33.292	15.5055	0.22660	4.610	0.04266	
E3G3	0.929	15.0792	0.00633	0.004	0.00207	
E3G4	-29.365	16.3569	-0.19987	3.223	0.00794	
E3G5	-6.179	16.4033	-0.04205	0.142	0.00191	
E3G6	-20.864	14.9842	-0.14201	1.939	0.00167	
E3G7	-30.198	16.1990	-0.20553	3.475	0.00809	
E3G8	-4.220	14.6898	-0.02873	0.083	0.00062	
E3G9	-17.631	15.3729	-0.12001	1.315	0.01665	
E3G10	15.940	17.0895	0.10849	0.870	0.01003	
E3G11	-11.577	15.2766	-0.07879	0.574	0.00308	
VP%1	-0.118	0.1656	-0.11453	0.509	0.00044	0.067
DP%	0.224	0.6547	0.01860	0.117	0.00009	-0.020
VP%2	0.238	0.2032	0.24355	1.372	0.00152	-0.153
VP%3	-0.008	0.1967	-0.00771	0.002	0.00065	-0.197
AP1	-0.628	0.9647	-0.11081	0.423	0.00180	0.127
AP2	1.491	0.8432	0.22928	3.126	0.00424	0.129
AP3	0.289	0.6650	0.04716	0.189	0.00074	0.109
AVP1	1.559	1.7843	0.18918	0.763	0.00130	0.141
AVP2	-2.376	1.9796	-0.24686	1.441	0.00157	-0.103
AVP3	0.425	2.0718	0.03716	0.042	0.00005	-0.165
LCT1	-1.369	2.1424	-0.20467	0.408	0.00156	0.063
LP1	-5.175	16.4696	-0.14352	0.099	0.00328	0.053
LS1	0.504	3.2639	0.03573	0.024	0.00227	0.105
LCT2	0.236	2.2195	0.03508	0.011	0.00290	0.207
LP2	15.763	16.4189	0.43277	0.922	0.00425	0.080
FREQST	-0.971	1.0340	-0.08751	0.881	0.00022	-0.078
LS2	-4.808	3.1837	-0.43696	2.281	0.00703	0.034
RSEXPA	9.390	15.1438	0.30158	0.384	0.00013	0.088
RCTEXPA	-16.542	19.0455	-0.37717	0.754	0.00206	0.182
RPEXPA	-26.474	70.9322	-0.07251	0.139	0.00005	0.037
RSEXPO	1.515	4.4265	0.05668	0.117	0.00012	-0.124
PT	0.313	0.8044	0.02443	0.152	0.00077	0.046
ROSETTE	0.051	0.6519	0.00763	0.006	0.00000	0.231
FLOW	-9.203	0.5141	-0.07108	0.156	0.00000	0.231

APPENDIX 4.5 ctd

Character	$\hat{\beta}_k$	se of β	$\hat{\beta}'_k$	F	R^2 change	r
FLMED	0.176	0.5566	0.07004	0.100	0.00078	0.276
FL	-1.681	1.6260	-0.08100	1.069	0.00138	0.133
HEIGHT	0.172	0.1021	0.19660	2.840	0.00718	0.263
TNH	0.084	0.1157	0.08207	0.527	0.00089	0.272
FCOL	1.021	1.6889	0.09115	0.366	0.00051	0.016
NCOL	-0.509	1.5391	-0.04672	0.109	0.00017	-0.007
DFCOL	-0.164	0.9575	-0.02277	0.029	0.00023	0.047
AC	0.876	0.3545	0.01944	0.061	0.00004	0.116
NEC	-0.146	0.5865	-0.01600	0.062	0.00016	-0.127
FDENS	-0.708	0.9418	-0.07008	0.565	0.00101	-0.000
FE	-0.303	1.1264	-0.04458	0.073	0.00008	0.048
AMTPOL	0.211	0.5670	0.03010	0.139	0.00022	0.103
ARPOLAD	-0.081	0.8304	-0.00710	0.010	0.00002	0.040
NSTIG	-0.322	0.7876	-0.02918	0.167	0.00037	0.006
DEXT	-0.548	0.8513	-0.05520	0.414	0.00453	-0.089
PP	-0.115	3.3953	-0.00346	0.001	0.00034	-0.107
TEXT	2.990	2.7053	0.20389	1.222	0.00214	0.033
ESTA	0.182	0.4139	0.03000	0.194	0.00003	-0.026

APPENDIX 5 Factor score coefficients

	Factors				
	1	2	3	4	5
1	0.24254	-0.45668	-0.34060	1.46082	-0.72812
2	0.28717	-0.08686	0.56615	-1.99371	-2.05391
3	0.17867	0.67732	0.76770	0.89944	0.22488
4	0.28062	-0.28322	0.35596	-0.46320	2.49483
Pool	0.23834	0.39510	-1.33012	-0.40612	0.10967

APPENDIX 6

Coefficients of variation, estimates of variances components, and their ratios to error variance, heritability estimates, environment means, genotype means in the pool and adaptation statistics for characters studied but not presented in the text.

APPENDIX 6.1 Coefficients of variation in each environment

	Environments				
Character	1	2	3	4	Pool
DP%	1.9371	1.3078	1.3701	2.3596	2.1361
FREQST	0.4577	0.4358	0.5082	0.3074	0.4205
PPTEXT	0.2255	0.2302	0.1909	0.1787	0.2042
RSEXPO	0.5024	0.4820	0.4187	0.5053	0.4851
PT	0.2351	0.2304	0.2116	0.2276	0.2258
ROSETTE	0.1016	0.0649	0.0795	0.0767	0.0816
HEIGHT	0.0750	0.0993	0.0708	0.0788	0.0802
NCOL	0.1229	0.1293	0.1182	0.1572	0.1346
DFCOL	0.1829	0.1219	0.1770	0.1494	0.1617
AC	0.2467	0.1735	0.2041	0.1505	0.2002
NEC	0.2551	0.2311	0.2997	0.2708	0.2632
ARPOLAD	0.1404	0.2661	0.0768	0.1367	0.1627
NSTIG	0.0991	0.2877	0.0286	0.1906	0.1725
DEXT	0.2146	0.1723	0.1259	0.1228	0.1610
PP	1.1612	0.6195	0.7954	0.4908	0.7008
ESTA	5.0200	*	1.9898	1.0523	2.0440
SEC	0.2192	0.3041	0.2413	0.3231	0.2711
TERT	0.3033	0.5728	0.3566	0.4105	0.3957
QUART	0.8038	1.5164	0.4322	1.3392	0.9359
QUIN	1.4586	2.5915	3.2742	2.5308	2.7521

* extremely large value

APPENDIX 6.2 Estimates of block, environment, genotype and genotype-environment interaction variance components together with their standard errors (in brackets) and significance in the F-test

Character	$\hat{\sigma}^2$B (within environment)		$\hat{\sigma}^2$ Env		$\hat{\sigma}^2$ Genotype		$\hat{\sigma}^2$GE	
DP%	0.1646 (0.1169)	*	0.1925 (0.1666)	*	0.0870 (0.0877)	NS	0.0604 (0.1251)	NS
FREQST	0.0443 (0.0652)	NS	0.2036 (0.1786)	*	0.9936 (0.4743)	****	0.5048 (0.2023)	****
PPTEXT	0.0031 (0.0139)	NS	0.5510 (0.3670)	****	0.2981 (0.1521)	****	0.2621 (0.0827)	****
RSEXPO	0.0142 (0.0126)	(NS)	0.0080 (0.0140)	NS	0.2157 (0.0981)	****	0.0803 (0.0324)	****
PT	0.2267 (0.1049)	****	0.1215 (0.1226)	(NS)	0.8658 (0.3782)	****	0.1482 (0.0952)	*
ROSETTE	0.2443 (0.1483)	**	3.6763 (2.4380)	****	2.9055 (1.3048)	****	1.1635 (0.3963)	****
HEIGHT	-0.6771 (2.9514)	NS	224.7849 (145.5576)	****	266.0440 (110.8499)	****	45.6674 (15.7875)	****
NCOL	0.0061 (0.0174)	NS	0.0902 (0.0806)	(NS)	2.8701 (1.1776)	****	0.4260 (0.1258)	****
DFCOL	0.0288 (0.0513)	NS	0.0941 (0.1171)	NS	6.5871 (2.6821)	****	0.7256 (0.2398)	****
AC	0.4816 (0.3770)	*	3.0722 (2.2737)	***	6.9006 (3.2365)	****	3.7547 (1.2625)	****
NEC	0.1017 (0.1656)	NS	0.0811 (0.1079)	NS	0.8704 (0.5156)	**	1.1426 (0.4039)	****
ARPOLAD	-0.0277 (0.0525)	NS	0.2123 (0.1756)	*	0.5524 (0.3011)	***	0.4381 (0.1994)	****
NSTIG	0.0024 (0.0686)	NS	0.1570 (0.1508)	(NS)	0.4182 (0.2636)	*	0.5128 (0.2312)	****
DEXT	0.1134 (0.0748)	*	0.0552 (0.0802)	NS	2.6419 (1.0954)	****	0.3346 (0.1449)	****
PP	0.0022 (0.0042)	NS	0.0229 (0.0186)	*	0.2177 (0.0925)	****	0.0497 (0.0173)	****
ESTA	-0.2237 (0.1185)	NS	1.3214 (1.1166)	*	-0.1412 (0.6039)	NS	4.5195 (1.3586)	****
SEC	-0.0458 (0.0586)	NS	0.6434 (0.4485)	****	0.6677 (0.3513)	***	0.4184 (0.2128)	***

APPENDIX 6.2 contd.

Character	$\hat{\sigma}^2$B (within environment)		$\hat{\sigma}^2$ Env		$\hat{\sigma}^2$Genotype		$\hat{\sigma}^2$GE	
TERT	-0.2277 (0.5704)	NS	8.6441 (6.3751)	***	25.9247 (11.9295)	****	13.4698 (4.1984)	****
QUART	-0.0113 (0.7697)	NS	2.3498 (2.3987)	(NS)	93.0545 (38.1619)	****	11.9335 (4.0484)	****
QUIN	0.0187 (0.0630)	NS	0.0180 (0.0380)	NS	1.7002 (0.7086)	****	0.0562 (0.1064)	NS

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

APPENDIX 6.3 Blocks, environments, genotypes and genotype-environment interaction variance components ratio to the error variance ($\hat{\sigma}^2$)

Character	Blocks	Variance component Environments	Genotype	GE
DP%	0.06	0.07	0.03	0.02
FREQST	0.02	0.10	0.50	0.25
PPTEXT	0.01	1.11	0.60	0.53
RSEXPO	0.04	0.02	0.67	0.25
PT	0.16	0.08	0.61	0.10
ROSETTE	0.08	1.27	1.00	0.40
HEIGHT	-0.01	1.88	2.23	0.38
NCOL	0.01	0.15	4.84	0.72
DFCOL	0.02	0.06	4.04	0.45
AC	0.05	0.34	0.77	0.42
NEC	0.03	0.03	0.27	0.36
ARPOLAD	-0.01	0.09	0.24	0.19
NSTIG	-0.00	0.06	0.16	0.19
DEXT	0.07	0.04	1.68	0.21
PP	0.02	0.17	1.63	0.37
ESTA	-0.03	0.19	-0.02	0.66
SEC	-0.02	0.24	0.25	0.15
TERT	-0.01	0.36	1.07	0.56
QUART	-0.00	0.08	3.17	0.41
QUIN	0.01	0.01	0.78	0.03

APPENDIX 6.4 Full and restricted broadsense heritability estimates with standard errors (in brackets) and coefficients of variation, from the pooled analysis

Character	$\hat{h}^2$ (full)		$\hat{h}^2$ (restricted)	
DP%	0.028	(0.0279) 0.9960	0.032	(0.0315) 0.9944
FREQST	0.266	(0.0970) 0.3643	0.285	(0.1012) 0.3548
PPTEXT	0.185	(0.0894) 0.4825	0.283	(0.1092) 0.3862
RSEXPO	0.337	(0.1051) 0.3117	0.349	(0.1073) 0.3071
PT	0.310	(0.0966) 0.3117	0.354	(0.1029) 0.2907
ROSETTE	0.267	(0.1073) 0.4022	0.417	(0.1142) 0.2740
HEIGHT	0.406	(0.1357) 0.3341	0.617	(0.1026) 0.1663
NCOL	0.720	(0.0876) 0.1216	0.738	(0.0839) 0.1137
DFCOL	0.727	(0.0842) 0.1159	0.737	(0.0825) 0.1120
AC	0.298	(0.1052) 0.3531	0.352	(0.1121) 0.3187
NEC	0.161	(0.0834) 0.5173	0.167	(0.0862) 0.5163
ARPOLAD	0.159	(0.0756) 0.4748	0.168	(0.0791) 0.4701)
NSTIG	0.113	(0.0650) 0.5778	0.117	(0.0676) 0.5763
DEXT	0.560	(0.1054) 0.1883	0.580	(0.1044) 0.1799
PP	0.511	(0.1117) 0.2187	0.542	(0.1100) 0.2028
ESTA	-0.011	(0.0488) *	-0.013	(0.0535) *

APPENDIX 6.4 contd.

Character	$\hat{h}^2$ (full)		$\hat{h}^2$ (restricted)	
SEC	0.152	(0.0710) 0.4683	0.175	(0.0787) 0.4488
TERT	0.360	(0.1143) 0.3173	0.408	(0.1173) 0.2873
QUART	0.681	(0.0929) 0.1364	0.693	(0.0910) 0.1314
QUIN	0.427	(0.1044) 0.2445	0.431	(0.1049) 0.2434

* extremely large value

APPENDIX 6.5 Environment means with standard errors (in brackets) and significance of the environments F-test

Character	1	2	3	4	Pool($\overline{X}$..)	Significance
DP%	1.5039	0.6281	0.5275	0.3616	0.7552	*
	(0.3433)	(0.0968)	(0.0852)	(0.1006)	(0.0951)	
FREQST	3.4167	3.4681	2.6250	3.8958	3.3514	*
	(0.1843)	(0.1781)	(0.1572)	(0.1412)	(0.0830)	
PPTEXT	2.5833	3.0708	4.2847	3.8361	3.4438	****
	(0.0687)	(0.0833)	(0.0964)	(0.0808)	(0.0414)	
RSEXPO	1.1242	1.3512	1.0003	1.1980	1.1684	NS
	(0.0666)	(0.0761)	(0.0493)	(0.0713)	(0.0334)	
PT	4.7818	5.4054	5.8293	5.1786	5.2988	(NS)
	(0.1325)	(0.1467)	(0.1454)	(0.1389)	(0.0705)	
ROSETTE	19.3611	18.9861	22.5000	22.6250	20.8681	****
	(0.2319)	(0.1453)	(0.2108)	(0.2045)	(0.1003)	
HEIGHT	33.4444	115.9361	148.7014	146.9667	136.2622	****
	(1.1797)	(1.3561)	(1.2411)	(1.3650)	(0.6439)	
NCOL	5.5278	5.4431	5.6667	6.2569	5.7236	(NS)
	(0.0801)	(0.0831)	(0.0789)	(0.1159)	(0.0454)	
DFCOL	8.4444	7.5917	8.0139	7.5236	7.8934	NS
	(0.1820)	(0.1091)	(0.1671)	(0.1325)	(0.0752)	
AC	15.4737	12.1615	16.3427	15.8331	14.9527	***
	(0.4499)	(0.2487)	(0.3932)	(0.2809)	(0.1764)	
NEC	7.1250	7.0472	6.0467	6.9750	6.7985	NS
	(0.2142)	(0.1920)	(0.2136)	(0.2226)	(0.1054)	
ARPOLAD	9.4444	8.5417	9.7361	9.5056	9.3069	*
	(0.1563)	(0.2678)	(0.0881)	(0.1532)	(0.0892)	
NSTIG	9.6389	8.8125	9.9306	9.2444	9.4066	(NS)
	(0.1126)	(0.2988)	(0.0334)	(0.2077)	(0.0956)	
DEXT	7.3611	7.8764	7.7361	8.2111	7.7962	NS
	(0.1862)	(0.1599)	(0.1147)	(0.1188)	(0.0740)	
PP	0.2778	0.6000	0.5417	0.6694	0.5222	*
	(0.0380)	(0.0438)	(0.0508)	(0.0387)	(0.0216)	
ESTA	0.3333	0.1278	1.6944	2.9750	1.2826	*
	(0.1972)	(0.2213)	(0.3973)	(0.3689)	(0.1545)	
SEC	6.1389	5.1139	7.1597	5.9292	6.0854	****
	(0.1586)	(0.1833)	(0.2036)	(0.2258)	(0.0972)	
TERT	13.0390	8.4028	16.1042	12.1083	12.4135	***
	(0.4661)	(0.5673)	(0.6768)	(0.5858)	(0.2894)	
QUART	6.8972	3.2639	7.6458	5.3444	5.7878	(NS)
	(0.6533)	(0.5833)	(0.3895)	(0.8435)	(0.3192)	
QUIN	0.3167	0.6667	0.3611	0.8056	0.5375	NS
	(0.0544)	(0.2036)	(0.1393)	(0.2403)	(0.0872)	

Significance NS not significant * $0.050 > P > 0.010$ *** $0.005 > P > 0.001$
(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

APPENDIX 6.6 Genotype means in the pooled environment with their standard error and F-test significance for genotypes

Character	1	2	3	4	5	6	7	8	9	10	11	12	se	signif	LSD $_{0.05}$
DP	0.3740	1.3073	0.6925	0.5771	0.4739	0.4871	1.1433	0.6975	1.8783	0.3384	0.5068	0.5869	0.3515	NS	-
FREQST	3.1667	1.4167	4.3750	5.0000	2.7583	3.8125	2.2417	4.3333	4.3333	3.8958	2.3750	2.5083	0.4571	****	-
PPTEXT	3.3333	3.0000	3.6667	4.3500	3.2083	3.1458	2.5917	2.9167	4.5833	4.2917	3.1875	3.1500	0.2935	****	0.8134
RSEXPO	1.1403	1.2969	1.2247	0.4608	1.2777	1.5531	2.4563	0.7633	0.7460	1.0832	0.9862	1.0327	0.1829	****	0.5071
PT	5.5902	3.7761	3.8353	5.7389	5.2090	5.1911	4.6772	5.2515	7.2083	6.5659	4.9647	5.5770	0.3110	****	0.8619
ROSETTE	20.5833	19.7500	24.8333	21.0000	22.2917	19.5417	19.6667	20.5833	17.5417	22.4583	21.5417	20.6250	0.6416	****	1.7785
HEIGHT	133.8333	125.4583	112.9167	168.0417	123.8917	134.0417	123.0250	131.5000	147.3750	165.3750	141.8542	127.8333	4.0487	****	14.7496
NCOL	5.0417	5.0000	4.9583	5.2500	5.3750	2.2958	5.1833	4.9167	9.7917	8.8958	4.8750	4.1000	0.3622	****	-
DFCOL	6.9583	6.3333	7.1250	8.1667	8.9250	7.4000	6.7000	6.8750	13.3333	12.5625	5.9583	4.3833	0.4993	****	1.3840
AC	12.5613	14.8455	16.0166	16.5427	14.9317	15.4755	10.8941	13.0248	11.3518	16.1628	15.9628	21.6634	1.1454	****	3.1749
NEC	4.9667	7.2776	5.5833	6.0000	7.6167	7.8167	7.4499	6.2500	5.6250	6.9583	7.1042	8.9333	0.1054	**	1.7944
ARPOLAD	7.5417	9.8750	9.3333	10.0000	9.6667	9.7917	8.9333	9.9583	7.5833	9.4167	9.9167	9.6667	0.4529	***	-
NSTIG	7.3750	10.0000	9.5833	10.0000	9.4833	9.4375	9.5417	10.0000	8.1667	9.5833	9.9167	9.7917	0.4877	*	-
DEXT	8.0833	9.2083	7.5000	3.2917	9.0417	8.5708	8.5833	7.2500	7.0833	6.7083	9.1250	9.1083	0.3864	****	1.0710
PP	0.2083	0.0000	1.2083	1.4167	0.1917	0.6083	0.9250	0.2917	0.6667	0.7500	0.0000	0.0000	0.0216	****	-
ESTA	0.8750	0.2083	-0.2083	1.4583	0.2167	3.6250	1.3833	0.7083	1.1250	2.4583	0.8750	2.6667	1.1901	NS	-
SEC	5.1250	6.6667	7.1250	6.0000	4.5833	5.3750	4.9500	6.5417	6.4583	7.6875	6.6875	5.8250	0.4669	***	1.2941
TERT	6.5000	13.5417	9.8750	11.0833	7.6667	10.5417	9.1250	11.5417	15.2083	27.7000	15.1875	10.9917	2.0911	****	5.7962
QUART	0.2917	2.4583	0.8750	3.6250	2.4583	1.2917	1.6250	1.7500	13.9167	34.9417	4.6042	1.6167	2.0509	****	5.6847
QUIN	0.0000	0.5000	0.0000	0.1250	0.0000	0.0000	0.0000	0.0000	1.1667	4.6583	0.0000	0.0000	0.0872	****	

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$
(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

APPENDIX 6.7.1 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 1. Statistics were derived from adaptation analysis. F-test significance of genotype-environment interaction is also given.

Character	$\hat{\beta}$	se of β	Sig(0)	Sig(1)	Ratio to least ecovalence	R^2	Signif
DP%	0.554	0.387	NS	NS	1.99	0.507	NS
FREQST	‡	‡	‡	‡	‡	‡	****
PPTEXT	0.995	0.309	(NS)	NS	1.57	0.839	****
RSEXPO	0.393	1.253	NS	NS	2.93	0.047	****
PT	0.074	0.736	NS	NS	6.87	0.005	NS
ROSETTE	1.147	0.218	*	NS	1.16	0.933	****
HEIGHT	0.628	0.174	(NS)	NS	4.24	0.866	****
NCOL	‡	‡	‡	‡	‡	‡	****
DFCOL	-0.334	1.794	NS	NS	12.80	0.017	****
AC	1.565	1.135	NS	NS	15.17	0.487	****
NEC	2.490	1.523	NS	NS	10.18	0.572	****
ARPOLAD	‡	‡	‡	‡	‡	‡	****
NSTIG	‡	‡	‡	‡	‡	‡	****
DEXT	-0.048	1.041	NS	NS	6.31	0.001	****
PP	‡	‡	‡	‡	‡	‡	****
ESTA	0.554	0.413	NS	NS	9.04	0.473	****
SEC	0.736	0.481	NS	NS	2.62	0.539	***
TERT	0.238	0.368	NS	NS	2.94	0.172	****
QUART	0.193	0.164	NS	*	1.82	0.409	****
QUIN	‡	‡	‡	‡	‡	‡	NS

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$
(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

‡ divide by zero was encountered during adaptation analysis. Statistics could not be estimated.

APPENDIX 6.7.2 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 2. Statistics were derived from adaptation analysis. F-test significance of genotype-environment interaction is also given.

Character	$\hat{\beta}$	se of β	Sig(0)	Sig(1)	Ratio to least ecovalence	R^2	Signif
DP%	1.171	1.261	NS	NS	12.81	0.301	NS
FREQST	‡	‡	‡	‡	‡	‡	****
PPTEXT	0.309	0.179	NS	(NS)	4.46	0.600	****
RSEXPO	-0.700	1.462	NS	NS	5.99	0.103	****
PT	0.483	0.942	NS	NS	7.23	0.116	NS
ROSETTE	0.584	0.283	NS	NS	3.31	0.680	****
HEIGHT	0.411	0.240	NS	NS	9.84	0.594	****
NCOL	‡	‡	‡	‡	‡	‡	****
DFCOL	2.058	0.524	(NS)	NS	2.60	0.885	****
AC	0.569	1.189	NS	NS	16.34	0.103	****
NEC	-0.166	1.292	NS	NS	6.97	0.008	****
ARPOLAD	‡	‡	‡	‡	‡	‡	****
NSTIG	‡	‡	‡	‡	‡	‡	****
DEXT	1.240	0.951	NS	NS	3.60	0.460	****
PP	‡	‡	‡	‡	‡	‡	****
ESTA	-0.313	0.206	NS	*	30.30	0.536	****
SEC	1.057	1.062	NS	NS	11.10	0.331	***
TERT	0.739	0.352	NS	NS	1.09	0.688	****
QUART	-0.027	1.117	NS	NS	9.14	0.000	****
QUIN	‡	‡	‡	‡	‡	‡	NS

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$
(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

‡ divide by zero was encountered during adaptation analysis. Statistics could not be estimated.

APPENDIX 6.7.3 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 3. Statistics were derived from adaptation analysis. F-test significance of genotype-environment interaction is also given

Character	$\hat{\beta}$	se of β	Sig(0)	Sig(1)	Ratio to least ecovalence	R^2	Signif
DP%	1.432	0.179	*	NS	1.00	0.970	NS
FREQST	‡	‡	‡	‡	‡	‡	****
PPTEXT	1.188	0.468	NS	NS	3.91	0.763	****
RSEXPO	1.074	2.068	NS	NS	7.16	0.119	****
PT	-0.168	0.551	NS	NS	6.99	0.045	NS
ROSETTE	0.856	0.200	*	NS	1.00	0.902	****
HEIGHT	1.467	0.101	***	*	5.08	0.991	****
NCOL	‡	‡	‡	‡	‡	‡	****
DFCOL	2.928	0.398	*	*	6.28	0.954	****
AC	0.639	0.545	NS	NS	3.93	0.407	****
NEC	0.001	1.731	NS	NS	10.37	0.000	****
ARPOLAD	‡	‡	‡	‡	‡	‡	****
NSTIG	‡	‡	‡	‡	‡	‡	****
DEXT	2.552	1.352	NS	NS	11.72	0.641	****
PP	‡	‡	‡	‡	‡	‡	****
ESTA	-0.280	0.523	NS	NS	36.62	0.126	****
SEC	1.426	0.701	NS	NS	5.72	0.675	***
TERT	1.419	0.390	(NS)	NS	1.66	0.869	****
QUART	0.390	0.406	NS	NS	1.81	0.316	****
QUIN	‡	‡	‡	‡	‡	‡	NS

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$
(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

‡ divide by zero was encountered during adaptation analysis. Statistics could not be estimated.

APPENDIX 6.7.4 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 4. Statistics were derived from adaptation analysis. F-test significance of genotype-environment interaction is also given.

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least covalence	R^2	Signif
DP%	1.500	0.231	*	NS	1.42	0.955	NS
FREQST	‡	‡	‡	‡	‡	‡	****
PPTEXT	1.824	0.404	*	NS	8.30	0.911	****
RSEXPO	0.162	0.497	NS	NS	1.00	0.050	****
PT	1.991	0.801	NS	NS	8.03	0.755	NS
ROSETTE	1.225	0.467	NS	NS	4.83	0.775	****
HEIGHT	0.926	0.177	*	NS	1.45	0.932	****
NCOL	‡	‡	‡	‡	‡	‡	****
DFCOL	1.604	0.373	*	NS	1.00	0.902	****
AC	0.723	0.232	(NS)	NS	1.00	0.829	****
NEC	1.579	0.411	(NS)	NS	1.00	0.881	****
ARPOLAD	‡	‡	‡	‡	‡	‡	****
NSTIG	‡	‡	‡	‡	‡	‡	****
DEXT	1.615	0.264	*	NS	1.00	0.949	****
PP	‡	‡	‡	‡	‡	‡	****
ESTA	0.684	1.792	NS	NS	109.20	0.068	****
SEC	0.882	0.308	NS	NS	1.00	0.804	***
TERT	0.358	0.136	NS	*	1.55	0.777	****
QUART	0.635	0.357	NS	NS	1.00	0.613	****
QUIN	‡	‡	‡	‡	‡	‡	NS

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$
(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

‡ divide by zero was encountered during adaptation analysis. Statistics could not be estimated.

APPENDIX 6.7.5 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 5. Statistics were derived from adaptation analysis. F-test significance of genotype-environment interaction is also given.

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
DP%	0.658	0.476	NS	NS	2.28	0.488	NS
FREQST	‡	‡	‡	‡	‡	‡	****
PPTEXT	0.904	0.237	(NS)	NS	1.00	0.879	****
RSEXPO	1.844	1.716	NS	NS	5.52	0.366	****
PT	1.849	1.109	NS	NS	11.27	0.581	NS
ROSETTE	1.630	0.150	**	*	4.39	0.983	****
HEIGHT	1.407	0.227	*	NS	5.71	0.951	****
NCOL	‡	‡	‡	‡	‡	‡	****
DFCOL	1.369	1.885	NS	NS	11.28	0.209	****
AC	1.226	0.348	(NS)	NS	1.59	0.861	****
NEC	0.558	1.265	NS	NS	5.04	0.089	****
ARPOLAD	‡	‡	‡	‡	‡	‡	****
NSTIG	‡	‡	‡	‡	‡	‡	****
DEXT	1.552	0.648	NS	NS	2.21	0.741	****
PP	‡	‡	‡	‡	‡	‡	****
ESTA	0.306	0.510	NS	NS	16.78	0.152	****
SEC	0.542	0.438	NS	NS	2.92	0.434	***
TERT	1.391	0.334	(NS)	NS	1.30	0.896	****
QUART	1.236	0.621	NS	NS	2.13	0.665	****
QUIN	‡	‡	‡	‡	‡	‡	NS

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$
(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

‡ divide by zero was encountered during adaptation analysis. Statistics could not be estimated.

APPENDIX 6.7.6 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 6. Statistics were derived from adaptation analysis. F-test significance of genotype-environment interaction is also given

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
DP%	0.488	0.287	NS	NS	1.70	0.590	NS
FREQST	‡	‡	‡	‡	‡	‡	****
PPTEXT	0.782	0.333	NS	NS	2.22	0.734	****
RSEXPO	2.247	0.176	***	*	1.35	0.988	****
PT	0.998	1.522	NS	NS	16.41	0.177	NS
ROSETTE	0.429	0.203	*	NS	2.65	0.961	****
HEIGHT	1.526	0.197	*	NS	7.54	0.968	****
NCOL	‡	‡	‡	‡	‡	‡	****
DFCOL	0.333	0.937	NS	NS	3.43	0.059	****
AC	0.858	0.632	NS	NS	4.44	0.480	****
NEC	-0.658	2.041	NS	NS	16.44	0.049	****
ARPOLAD	‡	‡	‡	‡	‡	‡	****
NSTIG	‡	‡	‡	‡	‡	‡	****
DEXT	1.785	0.310	*	NS	1.56	0.943	****
PP	‡	‡	‡	‡	‡	‡	****
ESTA	3.779	0.355	**	*	133.57	0.983	****
SEC	1.688	0.448	(NS)	NS	4.30	0.876	***
TERT	1.607	0.214	*	NS	1.59	0.986	****
QUART	0.491	0.266	NS	NS	1.03	0.631	****
QUIN	‡	‡	‡	‡	‡	‡	NS

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$
(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

‡ divide by zero was encountered during adaptation analysis. Statistics could not be estimated.

APPENDIX 6.7.7 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 7. Statistics were derived from adaptation analysis. F-test significance of genotype-environment interaction is also given.

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
DP%	-0.192	0.416	NS	NS	7.05	0.096	NS
FREQST	‡	‡	‡	‡	‡	‡	****
PPTEXT	0.324	0.451	NS	NS	7.12	0.205	****
RSEXPO	2.969	2.961	NS	NS	17.90	0.335	****
PT	1.487	0.618	NS	NS	3.54	0.743	NS
ROSETTE	0.239	0.111	NS	*	6.00	0.698	****
HEIGHT	0.548	0.272	NS	NS	7.47	0.671	****
NCOL	‡	‡	‡	‡	‡	‡	****
DFCOL	1.864	1.584	NS	NS	8.97	0.409	****
AC	0.478	0.785	NS	NS	8.16	0.157	****
NEC	1.176	0.833	NS	NS	2.10	0.499	****
ARPOLAD	‡	‡	‡	‡	‡	‡	****
NSTIG	‡	‡	‡	‡	‡	‡	****
DEXT	1.847	0.759	NS	NS	3.61	0.748	****
PP	‡	‡	‡	‡	‡	‡	****
ESTA	0.750	0.666	NS	NS	15.93	0.387	****
SEC	1.735	1.065	NS	NS	13.81	0.570	***
TERT	1.462	1.148	NS	NS	9.82	0.448	****
QUART	0.785	0.515	NS	NS	1.49	0.537	****
QUIN	‡	‡	‡	‡	‡	‡	NS

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$
(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

‡ divide by zero was encountered during adaptation analysis. Statistics could not be estimated.

APPENDIX 6.7.8 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 8. Statistics were derived from adaptation analysis. F-test significance of genotype-environment interaction is also given.

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
DP%	0.849	0.379	NS	NS	1.24	0.715	NS
FREQST	‡	‡	‡	‡	‡	‡	****
PPTEXT	0.859	0.343	NS	NS	2.10	0.759	****
RSEXPO	0.721	0.831	NS	NS	1.22	0.273	****
PT	2.267	0.457	*	NS	7.17	0.925	NS
ROSETTE	1.210	0.379	(NS)	NS	3.29	0.836	****
HEIGHT	0.975	0.552	NS	NS	12.99	0.609	****
NCOL	‡	‡	‡	‡	‡	‡	****
DFCOL	2.224	2.113	NS	NS	16.24	0.356	****
AC	0.862	0.359	NS	NS	1.50	0.742	****
NEC	-0.037	1.910	NS	NS	12.43	0.000	****
ARPOLAD	‡	‡	‡	‡	‡	‡	****
NSTIG	‡	‡	‡	‡	‡	‡	****
DEXT	-2.091	2.949	NS	NS	52.07	0.201	****
PP	‡	‡	‡	‡	‡	‡	****
ESTA	-0.784	0.476	NS	(NS)	60.92	0.575	****
SEC	1.062	0.446	NS	NS	1.98	0.739	***
TERT	0.530	0.186	NS	NS	1.00	0.802	****
QUART	0.724	0.498	NS	NS	1.47	0.514	****
QUIN	‡	‡	‡	‡	‡	‡	NS

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$
(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

‡ divide by zero was encountered during adaptation analysis. Statistics could not be estimated.

APPENDIX 6.7.9 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 9. Statistics were derived from adaptation analysis. F-test significance of genotype-environment interaction is also given.

Character	$\hat{\beta}$	se of β	Sig (0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
DP%	4.329	0.437	**	*	45.72	0.980	NS
FREQST	‡	‡	‡	‡	‡	‡	****
PPTEXT	1.595	0.116	***	*	3.14	0.990	****
RSEXPO	-0.168	0.553	NS	NS	1.65	0.044	****
PT	1.026	0.375	NS	NS	1.00	0.789	NS
ROSETTE	0.555	0.390	NS	NS	4.98	0.504	****
HEIGHT	0.812	0.236	(NS)	NS	3.11	0.856	****
NCOL	‡	‡	‡	‡	‡	‡	****
DFCOL	0.755	1.043	NS	NS	3.48	0.208	****
AC	0.426	0.868	NS	NS	9.96	0.107	****
NEC	3.776	2.736	NS	NS	33.65	0.488	****
ARPOLAD	‡	‡	‡	‡	‡	‡	****
NSTIG	‡	‡	‡	‡	‡	‡	****
DEXT	0.177	0.414	NS	NS	1.97	0.084	****
PP	‡	‡	‡	‡	‡	‡	****
ESTA	0.783	0.080	**	NS	1.00	0.980	****
SEC	0.606	0.417	NS	NS	2.48	0.513	***
TERT	0.366	0.580	NS	NS	3.70	0.166	****
QUART	-0.463	1.511	NS	NS	17.28	0.045	****
QUIN	‡	‡	‡	‡	‡	‡	NS

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$
(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

‡ divide by zero was encountered during adaptation analysis. Statistics could not be estimated.

APPENDIX 6.7.10 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 10. Statistics were derived from adaptation analysis. F-test significance of genotype-environment interaction is also given.

Character	$\hat{\beta}$	se of β	Sig(0)	Sig(1)	Ratio to least ecovalence	R^2	Signif
DP%	0.107	0.345	NS	NS	4.13	0.046	NS
FREQST	‡	‡	‡	‡	‡	‡	****
PPTEXT	1.015	0.389	NS	NS	11.60	0.423	****
RSEXPO	-0.559	1.615	NS	NS	6.40	0.057	****
PT	0.323	0.174	NS	(NS)	1.84	0.633	NS
ROSETTE	1.002	0.371	NS	NS	2.74	0.785	****
HEIGHT	1.526	0.081	***	*	6.16	0.994	****
NCOL	‡	‡	‡	‡	‡	‡	****
DFCOL	-0.894	2.011	NS	NS	18.18	0.090	****
AC	2.061	0.554	(NS)	NS	9.43	0.874	****
NEC	0.301	0.509	NS	NS	1.49	0.149	****
ARPOLAD	‡	‡	‡	‡	‡	‡	****
NSTIG	‡	‡	‡	‡	‡	‡	****
DEXT	-0.354	1.269	NS	NS	9.77	0.037	****
PP	‡	‡	‡	‡	‡	‡	****
ESTA	2.261	0.532	*	NS	36.10	0.900	****
SEC	1.951	0.572	(NS)	NS	7.66	0.853	***
TERT	3.615	0.546	*	*	25.64	0.956	****
QUART	6.495	0.964	*	*	82.56	0.958	****
QUIN	‡	‡	‡	‡	‡	‡	NS

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$
(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

‡ divide by zero was encountered during adaptation analysis. Statistics could not be estimated.

APPENDIX 6.7.11 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 11. Statistics were dervied from adaptation analysis. F-test significance of genotype-environment interaction is also given.

Character	$\hat{\beta}_k$	se of β	Sig(0)	Sig (1)	Ratio to least ecovalence	R^2	Signif
DP%	0.592	0.264	NS	NS	1.22	0.715	NS
FREQST	‡	‡	‡	‡	‡	‡	****
PPTEXT	0.509	0.236	NS	NS	2.90	0.700	****
RSEXPO	1.916	1.618	NS	NS	5.08	0.412	****
PT	0.736	0.386	NS	NS	1.30	0.645	NS
ROSETTE	1.507	0.646	NS	NS	10.84	0.731	****
HEIGHT	0.807	0.171	*	NS	2.03	0.918	****
NCOL	‡	‡	‡	‡	‡	‡	****
DFCOL	1.090	0.835	NS	NS	2.18	0.460	****
AC	0.273	0.312	NS	NS	3.92	0.277	****
NEC	0.907	1.327	NS	NS	5.24	0.189	****
ARPOLAD	‡	‡	‡	‡	‡	‡	****
NSTIG	‡	‡	‡	‡	‡	‡	****
DEXT	2.438	0.703	(NS)	NS	5.91	0.857	****
PP	‡	‡	‡	‡	‡	‡	****
ESTA	1.041	0.474	NS	NS	7.56	0.707	****
SEC	-0.088	0.735	NS	NS	11.13	0.007	***
TERT	-0.298	0.983	NS	NS	12.47	0.044	****
QUART	1.127	1.107	NS	NS	6.35	0.342	****
QUIN	‡	‡	‡	‡	‡	‡	NS

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$
(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

‡ divide by zero was encountered during adaptation analysis. Statistics could not be estimated.

APPENDIX 6.7.12 Regression coefficients, their standard errors; significance from 0 and 1; ratio to least ecovalence; and coefficient of determination for genotype 12. Statistics were derived from adaptation analysis. F-test significance of genotype-environment interaction is also given.

Character	$\hat{\beta}$	se of β	Sig(0)	Sig(1)	Ratio to least ecovalence	R^2	Signif
DP%	0.512	0.437	NS	NS	2.48	0.406	NS
FREQST	‡	‡	‡	‡	‡	‡	****
PPTEXT	1.694	0.308	*	NS	5.54	0.938	****
RSEXPO	2.100	0.145	***	*	1.05	0.991	****
PT	0.935	0.996	NS	NS	7.04	0.306	NS
ROSETTE	0.615	0.039	***	**	1.50	0.992	****
HEIGHT	0.967	0.152	*	NS	1.00	0.953	****
NCOL	‡	‡	‡	‡	‡	‡	****
DFCOL	-0.997	0.621	NS	(NS)	7.41	0.563	****
AC	2.320	0.403	*	(NS)	11.21	0.943	****
NEC	2.073	0.483	*	NS	2.40	0.902	****
ARPOLAD	‡	‡	‡	‡	‡	‡	****
NSTIG	‡	‡	‡	‡	‡	‡	****
DEXT	1.285	0.824	NS	NS	2.78	0.549	****
PP	‡	‡	‡	‡	‡	‡	****
ESTA	3.221	1.276	NS	NS	137.18	0.761	****
SEC	0.404	0.101	(NS)	NS	1.85	0.889	***
TERT	0.573	0.606	NS	NS	3.16	0.309	****
QUART	0.413	0.170	NS	(NS)	1.04	0.747	****
QUIN	‡	‡	‡	‡	‡	‡	NS

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$
(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

‡ divide by zero was encountered during adaptation analysis. Statistics could not be estimated.

APPENDIX 7

Estimates of block and genotypic variance components with their standard error (in brackets) and significance in the F-test for each single environment. (Estimates of error variance within single environments are provided in Appendix 8, together with their standard errors).

Significance	NS	not significant
	(NS)	$0.001 \geq P > 0.050$
	*	$0.050 \geq P > 0.010$
	**	$0.010 \geq P > 0.005$
	***	$0.005 \quad P \geq 0.001$
	****	$P \leq 0.001$

	Environment 1				Environment 2			
Character	$\hat{\sigma}^2_B$		$\hat{\sigma}^2_G$		$\hat{\sigma}^2_B$		$\hat{\sigma}^2_G$	
VP%1	24.1909 (23.5039)	(NS)	139.8490 (70.3330)	****	-29.9977 (9.9696)	NS	28.8505 (46.6502)	NS
DP%	0.6546 (0.7399)	NS	0.1769 (0.6780)	NS	-0.0033 (0.0302)	NS	-0.0126 (0.0445)	NS
VP%2	5.2424 (11.2191)	NS	188.1825 (85.8200)	****	-0.4028 (16.6244)	NS	109.1135 (67.0346)	****
VP%3	11.0117 (12.0342)	(NS)	34.3886 (22.6324)	*	-20.1537 (9.9206)	NS	142.6778 (83.8572)	***
AP1	-0.4779 (0.1859)	NS	10.4215 (4.6588)	****	0.0863 (0.1824)	NS	2.2880 (1.0927)	****
AP2	-0.0490 (0.3164)	NS	5.6068 (2.6810)	****	-0.0247 (0.0954)	NS	1.7466 (0.8374)	****
AP3	-0.5789 (0.2633)	NS	4.6595 (2.5923)	***	0.2617 (0.2558)	(NS)	2.2315 (1.0439)	****
AVP1	0.2195 (0.3779)	NS	2.6163 (1.4045)	****	-0.2194 (0.0519)	NS	0.5626 (0.4324)	*
AVP2	0.2647 (0.3063)	NS	3.4143 (1.5775)	****	-0.9240 (0.0760)	NS	0.8452 (0.5053)	***
AVP3	0.2325 (0.2505)	(NS)	0.5922 (0.4210)	*	-0.1669 (0.0542)	NS	1.2606 (0.6792)	****
TAVP	2.0496 (1.9330)	(NS)	11.9711 (5.9209)	****	-1.0643 (0.2237)	NS	5.1591 (2.9668)	***
LCT1	-0.1309 (0.1441)	NS	4.7089 (2.1398)	****	-0.8230 (0.1673)	NS	4.0740 (1.8912)	****
LP1	-0.0029 (0.0052)	NS	0.0642 (0.0346)	****	-0.0014 (0.0034)	NS	0.1607 (0.0687)	****
LS2	-0.0394 (0.0203)	NS	1.5462 (0.6609)	****	0.0176 (0.0354)	NS	1.4688 (0.6129)	****
LCT2	0.0929 (0.1837)	NS	1.5727 (0.8104)	****	0.1780 (0.2854)	NS	2.1659 (1.1253)	****
LP2	0.0047 (0.0070)	NS	0.0794 (0.0376)	****	0.0020 (0.0052)	NS	0.1835 (0.0779)	****
FREQST	0.1601 (0.1982)	NS	1.3071 (0.6769)	****	-0.0385 (0.0886)	NS	0.9326 (0.5200)	***
LS2	0.4125 (0.2735)	****	1.7804 (0.7760)	****	0.1088 (0.1199)	(NS)	1.3547 (0.6208)	****
RSEXPA	0.0394 (0.0437)	(NS)	0.2229 (0.1206)	****	-0.0029 (0.0086)	NS	0.0631 (0.0392)	**
RCTEXPA	0.0329 (0.0300)	*	0.1123 (0.0624)	***	-0.0017 (0.0029)	NS	0.0204 (0.0134)	*
RPEXPA	-0.0002 (0.0002)	NS	0.0013 (0.0009)	*	0.0001 (0.0001)	NS	0.0002 (0.0002)	NS
PPTEXT	-0.0116 (0.0104)	NS	0.0924 (0.0594)	**	-0.0312 (0.0096)	NS	0.5198 (0.2371)	****
RSEXPO	0.0883 (0.0616)	***	0.1424 (0.0773)	****	-0.0124 (0.0139)	NS	0.3701 (0.1734)	****
PT	0.4905 (0.3233)	****	0.8484 (0.4172)	****	0.3806 (0.2770)	***	0.8207 (0.4260)	****
ROSETTE	0.0960 (0.2317)	NS	4.1217 (1.8736)	****	0.0773 (0.1116)	****	2.2187 (0.9708)	****
FLOW	0.0960 (0.7175)	NS	19.7586 (8.6876)	****	-0.5919 (0.2358)	NS	18.9773 (8.1567)	****
FLMED	-0.5505 (0.2092)	NS	22.8606 (9.6126)	****	-0.5188 (0.1643)	NS	27.4771 (11.3318)	****

	Environment 3				Environment 4			
Character	$\hat{\sigma}^2_B$		$\hat{\sigma}^2_G$		$\hat{\sigma}^2_B$		$\hat{\sigma}^2_G$	
VP%1	-5.8244 (7.1238)	NS	129.8679 (65.1066)	****	2.7079 (15.3986)	NS	168.2263 (85.9113)	****
DP%	-0.0077 (0.0208)	NS	0.3704 (0.1802)	****	0.0149 (0.0420)	NS	0.0546 (0.0727)	NS
VP%2	-5.8719 (4.2618)	NS	295.6659 (125.8846)	****	-2.9724 (11.6614)	NS	131.2766 (70.2429)	****
VP%3	-0.7038 (4.4803)	NS	115.0389 (51.9152)	****	21.1262 (25.5025)	NS	67.2210 (47.5339)	*
AP1	0.1256 (0.2632)	NS	2.6501 (1.3215)	****	0.0776 (0.1390)	NS	1.4299 (0.7013)	****
AP2	0.1611 (0.2772)	NS	0.9274 (0.6461)	*	-0.1672 (0.0582)	NS	1.6837 (0.8513)	****
AP3	-0.1196 (0.2461)	NS	1.0736 (0.8681)	*	-0.2420 (0.0799)	NS	1.4694 (0.8482)	***
AVP1	0.1370 (0.2299)	NS	2.2622 (1.1122)	****	0.2171 (0.2203)	(NS)	1.6469 (0.7979)	****
AVP2	-0.0147 (0.0780)	NS	3.1784 (1.3660)	****	-0.9140 (0.0833)	NS	1.6413 (0.8252)	****
AVP3	0.0094 (0.0614)	NS	0.9484 (0.4520)	****	0.2204 (0.2177)	(NS)	0.6128 (0.3890)	**
TAVP	0.4302 (0.5981)	NS	11.6388 (5.0923)	****	1.2348 (1.1290)	*	4.9118 (2.6177)	****
LCT1	0.2451 (0.3143)	NS	3.5953 (1.6747)	****	0.1376 (0.3565)	NS	3.5861 (1.8130)	****
LP1	-0.0059 (0.0034)	NS	0.0839 (0.0417)	****	-0.0051 (0.0027)	NS	0.3341 (0.1382)	****
LS1	-0.0380 (0.0128)	NS	1.9176 (0.7941)	****	0.0145 (0.0322)	NS	0.8181 (0.3556)	****
LCT2	-0.0640 (0.1563)	NS	0.8873 (0.6313)	*	-0.0855 (0.1265)	NS	3.1208 (1.4617)	****
LP2	-0.0070 (0.0023)	NS	0.0812 (0.0395)	****	-0.0047 (0.0018)	NS	0.2965 (0.1219)	****
FREQST	0.0177 (0.0930)	NS	2.2949 (1.0180)	****	0.0380 (0.0871)	NS	1.4590 (0.6675)	****
LS2	0.0423 (0.0738)	NS	3.0337 (1.2625)	****	0.0829 (0.0937)	NS	1.9544 (0.8375)	****
RSEXPA	-0.0042 (0.0118)	NS	0.1667 (0.0851)	****	0.0015 (0.0129)	NS	0.1184 (0.0637)	****
RCTEXPA	-0.0041 (0.0051)	NS	0.0837 (0.0429)	****	0.0006 (0.0061)	NS	0.0304 (0.0204)	*
RPEXPA	-0.0002 (0.0000)	NS	-0.0002 (0.0001)	NS	0.0001 (0.0001)	NS	-0.0000 (0.0001)	NS
PPTEXT	-0.0008 (0.0312)	NS	0.6644 (0.3050)	****	0.0558 (0.0513)	*	0.9640 (0.4091)	****
RSEXPO	-0.0014 (0.0076)	NS	0.2212 (0.0984)	****	-0.0177 (0.0089)	NS	0.4505 (0.2010)	****
PT	0.0355 (0.0899)	NS	1.4479 (0.6691)	****	0.0156 (0.0577)	NS	0.9394 (0.4613)	****
ROSETTE	0.2833 (0.2982)	(NS)	5.6939 (2.4446)	****	0.5207 (0.4151)	*	4.2414 (1.8628)	****
FLOW	0.5485 (0.6603)	NS	19.7066 (8.2547)	****	-0.3121 (0.2263)	NS	23.5742 (9.7717)	****
FLMED	0.2561 (0.4445)	NS	36.3615 (14.6972)	****	-0.3976 (0.1828)	NS	43.0731 (17.4079)	****

	Environment 1				Environment 2			
Character	$\hat{\sigma}^2_B$		$\hat{\sigma}^2_G$		$\hat{\sigma}^2_B$		$\hat{\sigma}^2_G$	
FS	0.3783 (0.4126)	(NS)	1.5333 (0.9123)	***	-0.0392 (0.1927)	NS	7.5693 (3.2660)	****
FL	0.0250 (0.0332)	NS	0.2533 (0.1281)	****	0.0093 (0.0172)	NS	0.0586 (0.0411)	*
HEIGHT	-3.1449 (3.1915)	NS	267.6460 (111.5732)	****	-8.4308 (2.4914)	NS	337.1161 (140.9439)	****
SEC	-0.0434 (0.0640)	NS	0.6470 (0.3764)	***	-0.0020 (0.1131)	NS	0.3203 (0.2936)	(NS)
TERT	0.1217 (0.8000)	NS	40.0223 (16.7277)	****	0.3434 (0.9223)	NS	11.1662 (5.9385)	****
QUART	0.0673 (1.4846)	NS	143.4833 (58.2948)	****	0.0071 (1.1598)	NS	42.0965 (18.1291)	****
QUIN	0.0000 (0.0101)	NS	1.1678 (0.4720)	****	-0.1571 (0.0676)	NS	1.8409 (0.9219)	****
TNH	2.3896 (5.0264)	NS	285.7953 (156.6090)	****	-4.2182 (3.0445)	NS	123.1173 (55.4279)	****
FCOL	-0.0101 (0.0328)	NS	2.3030 (0.9561)	****	0.0013 (0.0051)	NS	2.9103 (1.1477)	****
NCOL	-0.0130 (0.0170)	NS	1.5447 (0.6385)	****	-0.0130 (0.0170)	NS	1.5447 (0.6385)	****
DFCOL	0.1747 (0.0394)	NS	5.1646 (2.1830)	****	0.0385 (0.0602)	NS	5.5035 (2.2148)	****
FLWID	-0.2873 (0.6132)	NS	10.7303 (5.2796)	****	0.7657 (0.6754)	*	5.8059 (2.6649)	****
AC	0.0150 (0.6954)	(NS)	9.7660 (4.8048)	****	0.6410 (0.5454)	*	4.4066 (2.0242)	****
NEC	0.0924 (0.2033)	NS	0.6215 (0.4713)	*	0.4751 (0.3744)	*	2.5896 (1.1921)	****
FDENS	-0.0404 (0.0731)	NS	2.0540 (0.9367)	****	0.2034 (0.1542)	**	3.5075 (1.4417)	****
FE	0.0283 (0.0312)	(NS)	9.7566 (3.8497)	****	-0.0366 (0.0216)	NS	7.9606 (3.1766)	****
AMTPOL	0.0949 (0.2408)	NS	6.1364 (2.6763)	****	0.2551 (0.3586)	NS	4.2862 (2.0014)	****
ARPOLAD	-0.1086 (0.0341)	NS	0.9308 (0.4832)	****	0.0126 (0.2502)	NS	1.8468 (1.0742)	***
NSTIG	-0.0131 (0.0365)	NS	0.2510 (0.1607)	**	-0.0056 (0.3007)	NS	2.0221 (1.2299)	***
DEXT	0.2662 (0.2564)	(NS)	2.4773 (1.1374)	****	0.1434 (0.1613)	NS	2.8062 (1.2224)	****
PP	0.0071 (0.0086)	NS	0.1005 (0.0463)	****	-0.0026 (0.0052)	NS	0.2949 (0.1248)	****
TEXT	-0.0202 (0.0079)	NS	0.2717 (0.1309)	****	-0.0224 (0.0081)	NS	1.2034 (0.4977)	****
ESTA	0.0667 (0.1662)	NS	0.4727 (0.3787)	*	-0.1730 (0.0848)	NS	-0.0977 (0.2214)	NS
CROSS	2.4987 (4.4432)	NS	7.6064 (11.4848)	NS	11.3982 (9.8270)	*	37.7369 (20.3212)	****
SELF1	0.4200 (0.9408)	NS	6.6894 (3.6609)	****	0.0039 (0.1837)	NS	2.7230 (1.3252)	****
SELF2	-5.1118 (1.2096)	NS	3.9597 (6.6273)	NS	2.8075 (2.7086)	(NS)	19.5791 (9.4421)	****
SELF1%	6.1645 (9.7250)	NS	67.4620 (35.8017)	****	-0.0936 (2.7531)	NS	39.1297 (19.3154)	****

	Environment 3				Environment 4			
Character	$\hat{\sigma}^2_B$		$\hat{\sigma}^2_G$		$\hat{\sigma}^2_B$		$\hat{\sigma}^2_G$	
FS	-0.1652 (0.1214)	NS	8.3519 (3.5570)	****	-0.0748 (0.2609)	NS	8.8666 (3.9088)	****
FL	0.0803 (0.0621)	*	0.1372 (0.0824)	***	-0.0185 (0.0176)	NS	0.0476 (0.0583)	NS
HEIGHT	6.1028 (8.3827)	NS	288.9201 (120.6163)	****	2.7647 (7.7419)	NS	353.1813 (147.3583)	****
SEC	-0.0730 (0.1049)	NS	0.8894 (0.5519)	**	-0.0649 (0.1410)	NS	2.4878 (1.2211)	****
TERT	-0.2768 (1.4180)	NS	67.4713 (28.6392)	****	-0.4123 (0.96[illegible]9)	NS	38.9181 (16.8976)	****
QUART	0.8155 (0.9379)	NS	168.0863 (66.6438)	****	-0.9346 (1.9532)	NS	66.2855 (29.3914)	****
QUIN	-0.0091 (0.0614)	NS	1.0894 (0.5205)	****	0.2409 (0.3205)	NS	2.9277 (1.4259)	****
TNH	2.2063 (4.1977)	NS	513.4408 (205.6453)	****	-3.9378 (4.6235)	NS	272.3975 (116.0060)	****
FCOL	-0.0263 (0.0346)	NS	3.6813 (1.5101)	****	0.0130 (0.0429)	NS	3.4646 (1.4095)	****
NCOL	0.0071 (0.0248)	NS	3.5414 (1.4184)	****	-0.0246 (0.0335)	NS	6.4337 (2.5869)	****
DFCOL	0.1717 (0.1841)	(NS)	10.1418 (4.1099)	****	0.0798 (0.1009)	NS	8.4410 (3.3936)	****
FLWID	0.7663 (0.9291)	NS	12.6601 (5.7143)	****	0.5323 (0.5698)	(NS)	15.7224 (6.5161)	****
AC	0.7772 (0.9277)	NS	13.7290 (6.1225)	****	0.4933 (0.5242)	(NS)	14.7196 (6.1474)	****
NEC	-0.2053 (0.0630)	NS	2.1225 (1.0522)	****	-0.0378 (0.1494)	NS	2.7183 (1.3041)	****
FDENS	-0.0414 (0.0331)	NS	3.2203 (1.3373)	****	-0.0106 (0.0376)	NS	3.5055 (1.4346)	****
FE	0.0556 (0.0578)	(NS)	9.9145 (3.9290)	****	-0.0633 (0.0507)	NS	9.5917 (3.8752)	****
AMTPOL	-0.0371 (0.0763)	NS	5.4471 (2.2686)	****	-0.0414 (0.2551)	NS	3.5307 (1.7763)	****
ARPOLAD	0.0101 (0.0315)	NS	0.2374 (0.1308)	***	-0.0251 (0.0673)	NS	0.9471 (0.4848)	****
NSTIG	0.0111 (0.0096)	*	0.0040 (0.0073)	NS	-0.0019 (0.1456)	NS	1.4470 (0.7766)	****
DEXT	-0.0091 (0.0402)	NS	3.5564 (1.4572)	****	0.0532 (0.0754)	NS	3.0662 (1.2695)	****
PP	-0.0051 (0.0062)	NS	0.2576 (0.1133)	****	0.0093 (0.0099)	(NS)	0.4162 (0.1704)	****
TEXT	-0.0111 (0.0209)	NS	1.2013 (0.5116)	****	0.0155 (0.0253)	NS	1.9226 (0.7781)	****
ESTA	-0.1732 (0.4502)	NS	4.7965 (2.6483)	***	-0.6154 (0.1871)	NS	12.3417 (5.4900)	****
CROSS	1.9043 (6.1400)	NS	171.3094 (74.4324)	****	4.9184 (6.7757)	NS	65.8307 (31.8153)	****
SELF1	4.9766 (4.6134)	*	56.4563 (24.9752)	****	-0.5302 (0.4170)	NS	9.2046 (4.5654)	****
SELF2	6.6969 (7.4888)	NS	58.8515 (28.7691)	****	11.1173 (9.3553)	*	80.6551 (36.6112)	****
SELF1%	25.5017 (38.5329)	NS	394.2303 (190.5571)	****	-2.1122 (2.5624)	NS	68.4219 (31.9130)	****

APPENDIX 8

Estimates of error variance with standard errors (in brackets) for each single environment and the pool. Chi-square values and probabilities for tests of homogeneity of error variances.

	Environments							
Character	1	2	3	4	Pool	χ^2	Probability	
VP%1	231.1174 (43.2923)	499.4638 (93.5581)	211.5926 (39.6349)	297.6349 (55.6609)	309.8304 (29.4078)	13.131	0.005	HET
DP%	8.4862 (1.5896)	0.6747 (0.1264)	0.5223 (0.0978)	0.7280 (0.1364)	2.6028 (0.2470)	167.663	0.000	HET
VP%2	180.8538 (33.8770)	356.5172 (66.7818)	150.3303 (28.1594)	278.5819 (52.1832	241.5708 (22.9289)	12.762	0.006	HET
VP%3	133.9197 (25.0877)	411.5550 (77.0913)	102.4083 (19.1828)	308.7010 (57.8250)	239.1460 (22.6987)	34.638	0.000	HET
AP1	8.6171 (1.6141)	2.9287 (0.5486)	4.2146 (0.7895)	2.1008 (0.3935)	4.4653 (0.4238)	31.689	0.000	HET
AP2	7.2246 (1.3533)	2.2855 (0.4277)	4.1205 (0.7718)	2.8409 (0.5337)	4.1194 (0.3910)	21.818	0.000	HET
AP3	11.3276 (2.1219)	2.5341 (0.4747)	6.4733 (1.2126)	4.0159 (0.7523)	6.0878 (0.5778)	33.554	0.000	HET
AVP1	5.1689 (1.0525)	3.0742 (0.5758)	3.3793 (0.6330)	2.2760 (0.4263)	3.5871 (0.3405)	12.105	0.008	HET
AVP2	3.5842 (0.6714)	2.5610 (0.4797)	1.8080 (0.3387)	2.7083 (0.5073)	2.6654 (0.2530)	6.375	0.094	HOMO
AVP3	2.7516 (0.5154)	2.7481 (0.5148)	1.2004 (0.2249)	2.1818 (0.4087)	2.2205 (0.2108)	11.275	0.011	HET
TAVP	18.3221 (3.4321)	13.9385 (2.6109)	7.9706 (1.4930)	10.2709 (1.9239)	12.6255 (1.1984)	10.727	0.014	HET
LCT1	4.4115 (0.8263)	4.4096 (0.8260)	3.9761 (0.7448)	6.0650 (1.1361)	4.7156 (0.4476)	2.895	0.590	HOMO
LP1	0.1397 (0.0262)	0.0856 (0.0160)	0.1321 (0.0246)	0.1087 (0.0204)	0.1163 (0.0110)	3.864	0.276	HOMO
LS1	0.8257 (1.5470)	0.5584 (0.1046)	0.6378 (0.1195)	0.5256 (0.0985)	0.6368 (0.0604)	3.433	0.330	HOMO
LCT2	2.8846 (0.5403)	4.1063 (0.7692)	3.9867 (0.7468)	3.5706 (0.6688)	3.6371 (0.3452)	2.040	0.560	HOMO
LP2	0.0976 (0.0183)	0.0892 (0.0167)	0.1153 (0.0216)	0.0848 (0.0159)	0.0967 (0.0092)	1.526	0.681	HOMO
FREQST	2.4455 (0.4581)	2.2838 (0.4278)	1.7795 (0.3333)	1.4345 (0.2685)	1.9858 (0.1885)	4.779	0.188	HOMO
LS2	1.1751 (0.2201)	1.3457 (0.2521)	1.1040 (0.2068)	1.0741 (0.2012)	1.1747 (0.1115)	0.849	0.839	HOMO
RSEXPA	0.4925 (0.0923)	0.2125 (0.0398)	0.2935 (0.0550)	0.2570 (0.0481)	0.3139 (0.0298)	11.314	0.010	HET

Appendix 8 continued

	Environments							
Character	1	2	3	4	Pool	χ^2	Probability	
PPTEXT	0.3394 (0.0636)	0.4998 (0.0936)	0.6688 (0.1253)	0.4698 (0.0880)	0.4944 (0.0469)	6.304	0.097	HOMO
RSEXPO	0.3190 (0.0597)	0.4242 (0.1734)	0.1753 (0.0328)	0.3664 (0.0686)	0.3212 (0.3050)	11.163	0.011	HET
PT	1.2635 (0.2367)	1.5505 (0.2904)	1.5213 (0.2850)	1.3892 (0.2602)	1.4311 (0.1358)	0.720	0.869	HOMO
ROSETTE	3.8707 (0.7250)	1.5199 (0.2847)	3.2000 (0.5994)	3.0098 (0.5638)	2.9001 (0.2753)	12.202	0.007	HET
FLOW	14.1707 (2.6544)	10.8030 (2.0236)	7.9765 (1.4941)	7.9843 (1.4956)	10.2336 (0.9713)	6.476	0.090	HOMO
FLMED	9.8061 (1.8368)	8.4335 (1.5797)	6.6328 (1.2424)	7.8240 (1.4656)	8.1741 (0.7759)	2.169	0.542	HOMO
FS	4.5828 (0.8584)	4.4984 (0.8426)	4.2624 (0.7984)	6.3200 (1.1839)	4.9159 (0.4666)	2.768	0.569	HOMO
FL	0.4294 (0.0804)	0.1770 (0.1820)	0.4220 (0.0790)	0.5644 (0.1057)	0.4198 (0.0398)	7.816	0.050	HET
HEIGHT	100.1649 (18.7682)	132.4036 (24.8015)	110.9014 (20.7737)	134.1497 (25.1285)	119.4124 (11.3341)	1.637	0.656	HOMO
SEC	1.8101 (0.3391)	2.4181 (0.4530)	2.9855 (0.5592)	3.6702 (0.6875)	0.4184 (0.2128)	7.347	0.061	HOMO
TERT	15.6416 (2.9299)	23.1684 (4.3398)	32.9237 (6.1784)	24.7062 (4.6279)	24.1250 (2.2898)	7.546	0.056	HOMO
QUART	30.7333 (5.7569)	24.4957 (4.5885)	10.9223 (2.0459)	51.2230 (9.5949)	29.3436 (2.7852)	31.100	0.000	HET
QUIN	0.2133 (0.0400)	2.9848 (0.5591)	1.3980 (0.2619)	4.1563 (0.7785)	2.1881 (0.2077)	100.312	0.000	HET
TNH	80.5765 (15.0934)	107.6204 (20.1591)	64.9701 (12.1700)	138.9253 (26.0231)	98.0231 (9.3039)	9.082	0.028	HET
FCOL	0.8018 (0.1502)	0.0946 (0.0177)	1.0068 (0.1183)	0.7695 (0.1441)	0.6682 (0.0634)	67.193	0.000	HET
NCOL	0.4616 (0.0865)	0.4955 (0.0928)	0.4485 (0.0840)	0.9671 (0.1812)	0.4260 (0.1258)	12.182	0.007	HET
DFCOL	2.3859 (0.4469)	0.8565 (0.1604)	2.0116 (0.3768)	1.2632 (0.2366)	1.6293 (0.1546)	16.793	0.001	HET
FLWID	16.0169 (3.0002)	5.8349 (1.0930)	11.2845 (2.1138)	6.2172 (1.1646)	9.8384 (0.9338)	19.630	0.000	HET
AC	14.5727 (2.7297)	4.4525 (0.8340)	11.1308 (2.0850)	5.6798 (1.0639)	8.9589 (0.8503)	24.825	0.000	HET

	Environments							
Character	1	2	3	4	Pool	χ^2	Probability	
NEC	3.3048 (0.6198)	2.6533 (0.4970)	3.2839 (0.6151)	3.5667 (0.6681)	3.2022 (0.3039)	1.291	0.735	HOMO
FDENS	1.9737 (0.3697)	1.0030 (0.1879)	1.1275 (0.2712)	0.9081 (0.1701)	1.2531 (0.1189)	10.775	0.013	HET
FE	0.3495 (0.0655)	0.8274 (0.1550)	0.6139 (0.1150)	1.7235 (0.3228)	0.8786 (0.0834)	36.658	0.000	HET
AMTPOL	4.0745 (0.7682)	4.8116 (0.9013)	2.0080 (0.3761)	5.8444 (1.0948)	4.1846 (0.3972)	15.801	0.002	HET
ARPOLAD	1.7586 (0.3294)	5.1652 (0.9675)	0.5593 (0.1048)	1.6895 (0.3165)	0.2931 (0.2177)	64.340	0.000	HET
NSTIG	0.9131 (0.1710)	6.4292 (1.2042)	0.0806 (0.0151)	3.1053 (0.5817)	2.6320 (0.2498)	191.772	0.000	HET
DEXT	2.4949 (0.4673)	1.8418 (0.3450)	0.9480 (0.1776)	1.0168 (0.1905)	1.5754 (0.1495)	18.137	0.001	HET
PP	0.1040 (0.0195)	0.1382 (0.0259)	0.1856 (0.0348)	0.1079 (0.0202)	0.1339 (0.0127)	6.108	0.106	HOMO
TEXT	0.3646 (0.0683)	0.3899 (0.0730)	0.5597 (0.1048)	0.3661 (0.0686)	0.4201 (0.0399)	3.669	0.299	HOMO
ESTA	2.8000 (0.5245)	3.5253 (0.6603)	11.3677 (2.1294)	9.8009 (1.8359)	6.8735 (0.6524)	38.932	0.000	HET
CROSS	120.3739 (22.5481)	81.9596 (15.3524)	109.5382 (20.5184)	89.8036 (16.8216)	100.4188 (9.5313)	2.567	0.534	HOMO
SELF1	15.3810 (2.8811)	3.8503 (0.7212)	42.7627 (8.0102)	14.2756 (2.6741)	19.0674 (1.8098)	71.304	0.000	HET
SELF2	71.6686 (13.4248)	26.4100 (4.9470)	85.0941 (15.9396)	74.9680 (14.0428)	64.5352 (6.1254)	19.923	0.000	HET
SELF1%	138.8596 (26.0108)	59.3289 (11.1133)	538.2271 (100.8192)	76.2828 (14.2891)	203.1746 (19.2845)	88.934	0.000	HET

HOMO = error variances homogeneous
HET = error variances heterogeneous

APPENDIX 9

Genotype means within single environments for all characters studied.

APPENDIX 9.1 Genotype means in environment 1 with standard errors, F-test significance for genotypes and least significant differences at the 5% level

Character	1	2	3	4	5	6	7	8	9	10	11	12	se	Sig	$LSD_{0.05}$
VP%1	38.7897	23.6022	49.6660	38.6293	55.2620	54.9508	67.6813	47.4280	43.6252	58.0917	37.0287	23.9797	6.2064	****	17.5939
DP%	0.8783	2.0742	1.8060	1.7200	0.9002	0.8967	1.0762	1.3385	5.1990	0.9027	0.9027	0.0947	1.1893	NS	-
VP%2	18.6048	9.0487	42.1000	31.9310	11.7782	34.9363	17.3522	13.5668	48.8452	20.0073	2.8685	5.5992	5.4902	****	15.5636
VP%3	17.0792	7.8200	21.0335	10.4195	6.3803	19.1662	13.0687	0.9100	20.8217	11.1923	1.7703	0.9968	4.7244	*	13.3927
AP1	6.8667	18.3775	9.3037	16.7185	15.0517	13.6295	13.0520	14.6222	12.8518	8.2368	11.2593	14.8815	1.1984	****	3.3972
AP2	6.3703	12.4815	10.5630	12.9925	13.7408	12.7850	13.9853	15.0148	13.8815	7.8518	12.6815	13.5333	1.0973	****	3.1107
AP3	6.9407	10.8742	11.4002	10.6892	11.2887	13.0073	12.0888	16.3038	13.8372	8.8890	12.0518	15.1852	1.3740	***	3.8951
AVP1	2.7407	4.2518	4.9112	6.5260	8.1925	7.2517	8.8740	6.9628	5.6370	4.7852	4.5110	3.6073	0.9677	****	2.7433
AVP2	1.1258	1.1262	4.7850	4.1480	1.5555	4.2445	2.4297	2.0965	7.0000	1.5407	0.4370	0.7630	0.7729	****	2.1910
AVP3	1.2593	0.6888	2.6297	1.1923	0.6962	2.7553	1.4815	0.1482	3.0297	0.9185	0.2222	0.1703	0.6772	*	1.9197
TAVP	5.1260	6.0667	12.3258	11.8667	10.4443	14.2518	12.7852	9.2075	15.6667	7.2443	5.1703	4.5407	1.7475	****	4.9537
LCT1	16.0112	21.9000	17.6667	17.3000	21.3667	19.8000	19.9333	22.2000	16.3333	18.9000	21.3000	22.5333	0.8575	****	2.4307
LP1	6.9500	7.1000	7.4167	7.5500	7.4000	7.9500	7.5667	7.3000	7.8000	7.5167	7.3000	7.8333	0.1526	****	0.4325
LS1	7.8222	10.1667	7.5000	7.6167	10.0000	9.7167	9.5833	9.8000	9.0333	8.3333	10.9167	11.5167	0.3710	****	1.0516
LCT2	21.2000	22.8000	21.6333	20.2333	24.0333	22.2000	21.3667	22.4667	18.4000	22.0333	22.0667	22.9333	0.6934	****	1.9656
LP2	6.9333	7.1667	7.5167	7.7667	7.5000	8.0000	7.5667	7.7833	7.8833	7.4676	7.6500	7.8833	0.1275	****	0.3615
FREQST	3.6667	0.5000	3.6667	5.0000	1.6667	3.8333	2.5000	4.1667	5.0000	4.0000	3.1667	3.8333	0.6384	****	1.8098
LS2	10.7833	13.0667	11.8000	9.0167	13.9167	13.4167	13.3833	11.9333	11.2833	12.4000	12.7667	13.4833	0.4425	****	1.2545

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

APPENDIX 9.1 ctd. Genotype means in environment 1 with standard errors, F-test significance for genotypes and least significant difference at the 5% level

Character	1	2	3	4	5	6	7	8	9	10	11	12	S.e	Sig	$LSD_{0.05}$
RSEXPA	2.2500	0.9195	1.9497	1.0833	1.9167	1.6803	1.3763	0.8000	0.8483	1.7350	0.6542	0.7888	0.2865	****	0.8122
RCTEXPA	1.4055	0.2162	0.9655	0.7333	0.8140	0.6643	0.3805	0.0890	0.4077	0.7517	0.1917	0.1332	0.2130	***	0.6037
RPEXPA	-0.0013	0.0145	0.0178	0.0542	0.0305	0.0158	0.0013	0.1612	0.0220	-0.0125	0.0875	0.0167	0.0322	*	0.0912
PPTEXT	2.3333	2.8333	2.5000	2.3333	2.6667	2.6667	2.6667	2.0000	3.3333	2.6667	3.0000	2.0000	0.2378	**	0.6742
RSEXPO	1.3640	0.9167	1.7570	0.5445	1.5083	1.4042	1.5000	0.8250	0.6375	1.5748	0.5000	0.9583	0.2306	****	0.6536
PT	5.7380	3.3423	3.6270	5.0032	4.3812	4.6428	3.5697	4.3392	6.5000	6.3097	4.7618	5.1667	0.4589	****	1.3009
ROSETTE	19.5000	19.0000	24.0000	17.5000	19.3333	16.6667	19.0000	19.3333	16.0000	22.1667	20.1667	19.6667	0.8032	****	2.2769
FLOW	60.6667	52.3333	60.3333	64.1667	58.6667	61.3333	57.8333	52.3333	56.3333	68.3333	61.1667	54.8333	1.5368	****	4.3565
FLMED	66.3333	59.0000	67.0000	72.8333	63.0000	66.1667	64.5000	61.0000	65.3333	76.3333	67.6667	60.8333	1.2784	****	3.6240
FS	5.6667	6.6667	6.6667	8.6667	4.3333	4.8333	6.6667	8.6667	9.0000	8.0000	6.5000	6.0000	0.8740	***	2.4775
FL	3.1112	3.8333	3.8333	4.4167	4.3333	4.3612	4.5278	4.2500	4.8612	3.2500	3.4167	3.4167	0.2675	****	0.7583
HEIGHT	130.1667	122.3333	111.8333	166.5000	124.6666	136.0000	129.3333	111.1667	137.6667	160.5000	141.8333	129.3333	4.0865	****	11.5843
SEC	5.3333	7.0000	7.5000	5.5000	5.1667	4.6667	5.8333	6.3333	6.0000	8.0000	6.3333	6.0000	0.5493	***	1.5570
TERT	7.0000	14.5000	8.1667	11.8333	9.1667	10.3333	13.1667	10.6667	11.6667	31.8000	17.3333	10.8333	1.6146	****	4.5771
QUART	0.0000	1.3333	2.8333	3.0000	5.8333	0.8333	4.3333	1.0000	7.6667	44.6000	8.8333	2.5000	2.2632	****	6.4158
QUIN	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	3.8000	0.0000	0.0000	0.1886	****	0.5345
TNH	13.0000	23.5000	19.5000	21.1667	20.3333	16.0000	23.6667	18.3333	25.3333	88.3667	33.1667	20.3333	3.6646	****	10.3884
FCOL	5.1667	5.0000	4.8333	5.0000	6.0000	5.3333	5.3333	5.0000	9.8333	7.5000	4.8333	4.0000	0.3656	****	1.0363

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

Appendix 9.1 ctd.

Genotype means in environment 1 with standard errors, F-test significance for genotypes and least-significant difference at the 5% level

Character	1	2	3	4	5	6	7	8	9	10	11	12	se	Sig	$LSD_{0.05}$
NCOL	5.1667	5.0000	4.8333	5.0000	5.5000	5.3333	5.3333	5.0000	5.8333	7.5000	4.8333	4.0000	0.2774	****	0.7863
DFCOL	6.3333	7.6667	8.8333	9.1667	8.8333	7.5000	8.3333	8.5000	13.5000	11.3333	6.8333	4.0000	0.6306	****	1.7876
FLWID	26.6945	35.2220	33.7777	32.6110	30.0557	33.5002	28.3310	30.0000	23.7223	30.7222	30.4445	36.6668	1.6339	****	4.6316
AC	11.4823	19.6638	18.0453	16.7500	14.2772	17.8843	12.6533	14.5827	8.9660	15.1072	14.9928	21.2793	1.5585	****	4.4179
NEC	5.8333	6.0000	5.8333	6.8333	8.3333	7.5000	8.3332	7.5000	7.1667	6.6667	6.3333	9.1667	0.7422	*	2.1039
FDENS	0.6667	6.5000	7.6667	4.8333	8.3333	6.1667	6.3333	8.0000	3.6667	6.5000	7.6667	9.3333	0.5735	****	1.6259
FE	8.5000	2.5000	9.3333	7.5000	2.5000	7.5000	2.1667	2.3333	9.6667	6.5000	2.8333	2.0000	0.2413	****	0.6842
AMTPOL	3.1667	9.0000	5.6667	12.0000	3.5000	7.8333	7.3333	8.1667	6.0000	8.6667	7.8333	10.6667	0.8241	****	2.3361
ARPOLAD	6.1667	10.0000	10.0000	10.0000	8.6667	10.0000	9.6667	9.8333	9.3333	9.6667	10.0000	10.0000	0.5414	****	1.5347
NSTIG	7.8333	10.0000	10.0000	10.0000	9.3333	10.0000	9.8333	10.0000	9.8333	9.1667	9.6667	10.0000	0.3901	**	1.1059
DEXT	8.1667	8.3333	6.8333	2.6667	8.1667	7.6667	7.5000	9.3333	6.8333	6.3333	7.8333	8.6667	0.6448	****	1.8280
PP	0.3333	0.0000	0.8333	0.6667	0.0000	0.0000	0.1667	0.0000	0.8333	0.5000	0.0000	0.0000	0.1317	****	0.3733
TEXT	2.6667	2.8333	3.3333	3.0000	2.6667	2.6667	2.8333	2.0000	4.1667	3.1667	3.0000	2.0000	0.2465	****	0.6988
ESTA	-0.6667	0.0000	0.8333	-0.5000	0.0000	-0.8333	2.1667	2.1667	0.3333	0.1667	0.1667	0.1667	0.6831	*	1.9365
CROSS	30.2500	21.9167	28.1667	36.2777	20.8333	30.0277	30.0278	24.5278	25.9167	34.5833	35.0000	22.8055	4.4791	NS	-
SELF 1	9.6112	4.5555	5.1250	5.5555	2.1667	1.2777	1.0833	3.2222	0.2778	9.5000	2.8055	3.0555	1.6011	****	4.5388
SELF 2	25.6667	19.4445	15.4345	17.6667	16.2223	8.5833	18.5555	19.6667	17.3310	20.2222	19.3890	20.3890	3.4561	NS	_
SELF 1%	32.2235	17.1390	19.5843	15.8095	10.7762	4.5588	3.8453	14.5425	0.9855	27.7992	7.5052	9.9730	4.8107	****	13.6375

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

APPENDIX 9.2 Genotype means in environment 2 with standard errors, F-test signififance for genotypes and least significant difference at the 5% level

Character	1	2	3	4	5	6	7	8	9	10	11	12	se	Sig	$LSD_{0.05}$
VP%1	28.8595	45.6395	29.8147	34.2965	57.2680	37.3168	42.8353	61.9470	38.6220	30.2138	44.4287	34.4188	9.1238	NS	-
DP%	0.0000	0.8280	0.3703	0.4462	0.8770	0.3967	1.0452	0.3310	0.8607	0.6927	0.7137	0.9755	0.3353	NS	-
VP%2	41.6678	21.1148	31.6785	47.8362	36.8293	60.6303	49.5020	46.0160	55.7398	45.8168	22.2918	25.5670	7.7084	**	21.8517
VP%3	26.1902	20.0623	31.5552	47.5967	38.8818	53.6497	54.7515	23.8965	58.6573	43.8543	21.0712	21.4613	8.2821	***	23.4779
AP1	2.9557	7.2593	5.9112	9.2740	7.0043	6.9557	6.0000	7.2445	8.5333	5.2075	8.1185	7.4815	0.6987	****	1.9805
AP2	3.2150	7.8150	6.0370	8.7333	5.7957	6.1220	6.9110	8.1852	7.4668	5.5852	6.9777	7.0815	0.6169	****	1.7488
AP3	3.2667	7.3408	7.4518	9.1258	4.7112	8.2000	6.6220	6.7923	7.0592	5.0223	7.6518	7.3925	0.6499	****	1.8423
AVP1	0.9778	3.2667	1.7555	3.3038	3.9558	2.5220	2.6887	4.4740	3.2740	1.5335	3.7333	2.6148	0.7158	*	2.0291
AVP2	1.3927	1.5037	1.9408	4.3482	2.1510	3.7442	3.3998	3.9777	3.9925	2.5632	1.3702	1.9332	0.6533	***	1.8520
AVP3	1.0592	1.4223	2.2148	4.8223	1.9022	4.3443	3.3482	1.6148	4.3335	2.2220	1.6075	1.6517	0.6768	****	1.9185
TAVP	3.4297	6.1925	5.9108	12.4742	8.0090	10.6112	9.4372	10.0667	11.6000	6.3185	6.7112	6.2000	1.5242	***	5.7530
LCT1	15.2333	20.4000	16.5667	16.1333	18.2400	18.1500	17.0000	18.6667	17.5000	15.0333	21.5333	21.3000	0.8573	****	2.4302
LP1	6.3833	7.2500	7.4667	7.7000	6.7561	7.5250	7.1667	7.1667	7.9167	6.9333	7.4500	7.3333	0.1193	****	0.3385
LS1	7.0500	9.1500	7.5833	7.7167	7.9600	8.0250	7.2667	9.6600	8.9833	7.7000	10.1833	11.0000	0.3051	****	0.8648
LCT2	17.6333	21.4000	20.3333	18.4000	19.6800	20.4000	17.7667	19.5667	20.8667	19.0000	22.9667	22.2667	0.8273	****	2.3452
LP2	6.2833	7.2500	7.3000	7.7333	6.8000	7.5000	7.1667	7.2000	7.9833	7.0000	7.6167	7.3167	0.1220	****	0.3457
FREQST	2.3333	3.0000	5.0000	5.0000	3.2000	3.2500	3.0000	4.5000	4.6667	3.3333	3.1667	1.1667	0.6170	***	1.7489
LS2	10.6667	12.1500	11.6167	9.3500	12.1800	13.2250	12.9500	11.6833	12.0333	12.2833	13.5000	13.9333	0.4736	****	1.3425

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

APPENDIX 9.2 contd.

Genotype means in environment 2 with standard errors, F-test significance for genotypes and least significant difference at the 5% level

Character	1	2	3	4	5	6	7	8	9	10	11	12	se	Sig	$LSD_{0.05}$
RSEXPA	1.5208	1.1070	1.5057	0.6027	1.5145	1.5960	1.4350	0.7317	1.1612	1.3168	1.2728	1.2553	0.1882	**	0.5335
RCTEXPA	9.6067	0.2833	0.7445	0.3507	0.3760	0.4880	0.1583	0.2183	0.6132	0.6095	0.3405	0.3165	0.1148	*	0.3255
RPEXPA	-0.0275	0.0000	-0.0343	0.0047	0.0120	-0.0050	0.0017	0.0083	0.0128	0.0105	0.0490	-0.0028	0.0166	NS	-
PPTEXT	3.0000	2.6667	3.1667	4.1667	2.6000	2.7500	2.1667	3.0000	3.8333	4.6667	2.6667	2.1667	0.2886	****	0.8181
RSEXPO	1.3305	1.1472	1.4542	0.4092	1.7875	1.9612	2.9445	0.7515	0.8013	0.9845	1.2513	1.3917	0.2659	****	0.7537
PT	4.9287	4.6903	4.1428	5.2618	4.4000	6.6262	5.1695	5.4050	7.5952	6.7143	5.1457	4.7857	0.5083	****	1.4411
ROSETTE	17.8333	18.5000	22.8333	20.1667	19.6667	17.5000	19.5000	17.8333	17.1667	19.5000	17.8333	19.5000	0.5033	****	1.4268
FLOW	58.1667	52.8333	58.6667	65.1667	60.0000	64.0000	60.0000	55.0000	53.3333	65.6667	53.3333	57.8333	1.3418	****	3.8028
FLMED	64.5000	59.5000	63.6667	70.8333	65.2000	68.2500	62.6667	61.6667	65.0000	78.0000	58.0000	62.5000	1.1856	****	3.3609
FS	6.3333	6.6667	5.0000	5.6667	5.2000	4.2500	2.6667	6.6667	11.6667	12.3333	4.6667	4.6667	0.8659	****	2.4546
FL	4.0000	4.1667	4.0833	3.9722	4.4000	4.6250	4.0833	4.8333	4.3333	4.0000	3.8333	3.7500	0.2096	*	0.5941
HEIGHT	122.1667	117.6667	81.6667	148.5000	93.4000	100.1667	108.5000	119.6667	134.1667	134.5000	124.6667	106.1667	4.6976	****	13.3167
SEC	4.8333	4.5000	6.3333	5.3333	4.2000	4.0000	4.0000	5.1667	6.3333	5.1667	6.1667	5.3333	0.6348	(NS)	-
TERT	6.6667	9.3333	4.6667	9.1667	3.0000	4.0000	6.0000	9.8333	14.1667	14.3333	12.8333	6.8333	1.9650	****	5.5705
QUART	0.0000	0.3333	0.0000	2.1667	0.0000	0.0000	0.0000	0.5000	15.1667	20.0000	0.1667	0.8333	2.0205	****	5.7278
QUIN	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	3.5000	4.3333	0.0000	0.0000	0.7053	****	1.9994
TNH	11.6667	14.1667	11.0000	16.8333	7.2000	8.0000	10.0000	15.8333	39.6667	43.8333	19.3333	13.0000	4.2352	****	12.0054
FCOL	5.0000	5.0000	5.0000	6.0000	5.0000	5.7500	5.0000	5.0000	9.6667	8.8333	4.8333	4.0000	0.1255	****	0.3559

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

APPENDIX 9.2 ctd.

Genotype means in environment 2 with standard errors, F-test significance for genotypes and least significant difference at the 5% level

Character	1	2	3	4	5	6	7	8	9	10	11	12	se	Sig	$LSD_{0.05}$
NCOL	5.0000	5.0000	5.0000	5.8333	4.4000	5.2500	5.0000	5.0000	8.6667	7.1667	5.0000	4.0000	0.2874	****	0.8146
DFCOL	5.6667	6.0000	6.0000	7.5000	8.6000	8.0000	7.0000	7.8333	12.3333	11.6667	6.1667	4.3333	0.3778	****	1.0711
FLWID	23.6668	28.0000	29.5275	30.5278	27.2000	28.0805	24.6110	25.6112	25.6110	26.0000	31.2222	31.3055	0.9861	****	2.7955
AC	8.9298	12.4028	13.8230	14.6485	11.6642	12.6027	9.6100	10.3473	10.3388	10.6948	15.4338	15.4422	0.8614	****	2.4420
NEC	6.8333	8.1667	4.0000	6.0000	8.4000	6.0000	8.0000	4.3333	8.6667	7.0000	7.3333	9.8333	0.6650	****	1.8851
FDENS	4.1667	7.5000	8.8333	4.6667	7.2000	5.7500	7.3333	7.3333	3.5000	7.0000	8.3333	9.8333	0.4089	****	1.1590
FE	5.8333	2.0000	9.5000	6.0000	2.6000	5.2500	2.1667	2.1667	8.6667	7.6667	2.0000	2.1667	0.3714	****	1.0527
AMTPOL	2.5000	9.1667	5.0000	10.8333	5.0000	5.5000	4.3333	8.0000	7.5000	5.8333	6.6667	5.8333	0.8955	****	2.5386
ARPOLAD	4.6667	9.5000	8.3333	10.0000	10.0000	9.5000	7.6667	10.0000	6.5000	8.0000	9.6667	8.6667	0.9278	***	2.6302
NSTIG	4.0000	10.0000	8.5000	10.0000	10.0000	7.7500	8.5000	10.0000	7.8333	9.1667	10.0000	10.0000	1.0351	***	2.9344
DEXT	7.3333	9.1667	6.8333	3.5000	9.6000	8.7500	9.1667	7.0000	7.1667	7.1667	9.1667	9.6667	0.5541	****	1.5706
PP	0.1667	0.0000	1.3333	1.3333	0.2000	1.0000	1.3333	0.1667	0.8333	0.8333	0.0000	0.0000	0.1518	****	0.4302
TEXT	3.1667	2.6667	4.5000	5.5000	2.8000	3.7500	3.5000	3.1667	4.6667	5.5000	2.6667	2.1667	0.2549	****	0.7227
ESTA	1.0000	1.0000	0.0000	-0.3333	-0.8000	0.0000	-0.3333	1.5000	0.1667	-0.6667	0.0000	0.0000	0.7665	NS	-
CROSS	33.1667	16.6667	8.9167	19.1667	9.5000	11.8750	7.1667	21.9000	15.0000	10.7500	19.1667	15.8333	3.6950	****	10.4772
SELF1	6.4167	0.0833	0.0000	0.2500	0.0000	0.0000	0.0000	0.0833	0.0000	0.0833	0.0833	0.1667	0.8011	****	2.2709
SELF2	17.2222	7.0278	3.6345	2.5555	0.8000	4.3750	1.8057	11.2220	6.2777	5.0000	12.6665	8.4722	2.0980	****	5.9474
SELF1%	24.5887	0.2732	0.0000	1.7833	0.0000	0.0000	0.0000	0.4630	0.0000	0.7575	0.3968	0.7575	3.1445	****	8.9141

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

APPENDIX 9.3 Genotype means in environment 3 with standard errors, F-test significance for genotypes and least significant difference at the 5% level

Character	1	2	3	4	5	6	7	8	9	10	11	12	s.e	Sig	$LSD_{0.05}$
VP%1	38.8815	51.4585	22.3653	52.9790	33.5212	38.1577	63.8500	51.8038	46.7042	61.7183	39.1418	28.4378	5.9385	****	16.8343
DP%	0.1190	2.3268	0.3063	0.0000	0.0000	0.1165	0.8568	0.8823	1.0898	0.1942	0.2460	0.1918	0.2950	****	0.8364
VP%2	23.2308	4.9192	35.1222	49.9217	5.8423	37.8417	19.8947	17.9935	44.7232	43.3540	1.1998	2.3263	5.0055	****	18 8934
VP%3	22.3795	2.3840	32.0217	31.1273	0.8713	14.0012	1.7273	5.2492	16.8100	10.4978	2.7997	2.1208	4.1313	****	11.7115
AP1	9.2592	13.8593	8.3927	12.9850	9.2742	10.9925	9.2592	11.1333	13.2518	9.6000	9.3443	11.2815	0.8381	****	2.3759
AP2	8.8963	12.9333	8.5483	11.0815	9.7258	10.2447	8.4147	10.6815	10.6297	9.4742	9.0778	10.1482	0.8287	*	2.3492
AP3	6.6668	12.3927	8.7630	11.1557	9.9702	9.1557	8.9555	9.5260	9.7482	9.9035	7.8558	10.1630	1.0387	*	2.9445
AVP1	3.6443	7.1257	1.9555	6.7112	3.1555	4.3037	6.0145	5.8517	6.1852	5.8742	3.6772	3.1482	0.7505	****	2.1274
AVP2	2.0963	0.6593	2.9998	5.6223	0.6075	3.8740	1.6447	1.9703	4.6443	4.6443	4.2073	0.1000	0.2368	****	0.5489
AVP3	1.4667	0.3035	2.8742	3.1928	0.0888	1.4370	0.1630	0.4667	1.6962	1.1777	0.2110	0.2220	0.4473	****	1.2680
TAVP	7.2073	8.0888	7.8293	15.5258	3.8517	9.6147	7.8222	8.2890	12.5260	11.2593	3.9888	3.6075	1.1526	****	3.2673
LCT1	20.2667	22.8333	18.9667	17.9333	22.8000	22.3333	21.1000	22.4333	20.2000	18.4667	23.3000	24.2667	0.8140	****	2.3077
LP1	7.9667	7.8833	8.0500	7.9167	7.3833	8.5333	7.9500	7.7167	8.6167	7.9000	7.9500	8.0167	0.1479	****	0.4192
LS1	9.9000	11.8500	8.5500	7.9500	10.1500	9.6167	8.4167	10.4167	9.9167	8.3833	11.4750	12.2333	0.3260	****	0.9242
LCT2	26.5333	25.3667	26.6000	23.0667	24.7333	25.8000	24.4333	24.6000	24.7333	25.8333	25.5000	27.8667	0.8151	*	2.3108
LP2	8.0667	7.9667	8.0333	7.9500	7.4500	8.7333	8.0000	7.9667	8.5333	7.9833	7.9500	8.1167	0.1386	****	0.3929
FREQST	2.1667	0.0000	3.8333	5.0000	1.1667	3.1667	0.6667	4.5000	2.6667	4.5000	2.0000	1.8333	0.5446	****	1.5438
LS2	14.0667	16.4500	12.0833	9.9667	13.8667	14.5667	15.5000	12.5500	15.0667	12.7833	14.3500	15.4667	0.4289	****	1.2160

Significance NS not significant * $0.05 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

APPENDIX 9.3 ctd.

Genotype means in environment 3 with standard errors, F-test significance for genotypes and least-significant difference at the 5% level

Character	1	2	3	4	5	6	7	8	9	10	11	12	se	Sig	LSD $_{0.05}$
RSEXPA	2.1492	1.7767	1.7877	0.8312	1.0943	1.4123	1.9758	0.8267	1.3657	1.9560	1.0548	1.1917	0.2212	****	0.6270
RCTEXPA	1.2977	0.6183	1.2300	0.5955	0.3660	0.5855	0.6267	0.4100	0.6440	1.2212	0.4648	0.6335	0.1587	****	0.4498
RPEXPA	0.0238	0.0167	-0.0028	0.0048	0.0068	0.0310	0.0095	0.0467	-0.0123	0.0152	0.0000	0.0183	0.0205	NS	-
PPTEXT	3.8333	3.1667	4.1667	5.8333	4.1667	4.1667	3.3333	3.8333	6.0000	4.3333	3.7500	4.8333	0.3339	****	0.9465
RSEXPO	1.0758	1.5513	0.8533	0.3367	0.9850	1.1917	2.2227	0.4958	0.8843	1.0057	0.7478	0.6533	0.1709	****	0.4845
PT	5.9763	3.6192	3.4523	7.2143	6.6190	5.2380	5.1428	6.6430	7.5475	6.6430	5.4275	6.4285	0.5035	****	1.4274
ROSETTE	22.8333	21.6667	25.6667	23.3333	25.1667	21.8333	19.8333	21.3333	17.3333	23.5000	26.0000	21.5000	0.7303	****	2.0702
FLOW	70.3333	61.6667	68.6667	71.8333	69.1667	66.8333	67.6667	65.0000	66.6667	78.1667	75.0000	64.5000	1.1530	****	3.2685
FLMED	78.6667	70.0000	77.0000	80.1667	76.5000	74.8333	72.0000	71.3333	79.8333	92.8333	79.5000	72.1667	1.0514	****	2.9805
FS	8.3333	8.3333	8.3333	8.3333	7.3333	8.0000	4.3333	6.3333	13.1667	14.6667	4.5000	7.6667	0.8428	****	2.3893
FL	5.0833	5.8333	5.0833	6.1388	5.5000	5.8055	6.0000	6.0555	6.1667	5.2500	5.0000	6.0833	0.2652	***	0.7518
HEIGHT	146.3333	125.1667	129.5000	174.8333	144.5000	150.8333	130.6667	149.5000	158.5000	182.5000	155.2500	136.8333	4.2993	****	12.1875
SEC	6.1667	7.0000	9.0000	7.1667	5.1667	7.5000	7.1667	7.5000	7.5000	9.3333	6.2500	6.1667	0.7054	**	1.9996
TERT	8.3333	15.0000	16.1667	11.8333	13.5000	16.6667	16.3333	14.1667	17.8333	41.6667	10.2500	11.5000	2.3446	****	6.6465
QUART	1.1667	1.1667	0.6667	5.8333	4.0000	2.8333	2.1667	4.6667	17.0000	46.6667	3.2500	2.3333	1.3492	****	3.8248
QUIN	0.0000	0.0000	0.0000	0.3333	0.0000	0.0000	0.0000	0.0000	0.0000	4.0000	0.0000	0.0000	0.4827	****	1.3683
TNH	16.5000	24.1667	26.8333	26.1667	22.8333	28.0000	26.5000	27.3333	43.3333	101.8333	20.7500	21.0000	3.2906	****	9.3283
FCOL	5.0000	5.1667	5.1667	5.0000	8.1667	5.0000	5.3333	5.3333	10.1667	9.1667	5.0000	4.0000	0.4096	****	1.1612

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

APPENDIX 9.3 ctd. Genotype means in environment 3 with standard errors, F-test significance for genotypes and least significant difference at the 5% level

Character	1	2	3	4	5	6	7	8	9	10	11	12	se	Sig	$LSD_{0.05}$
NCOL	5.0000	5.0000	5.0000	4.8333	5.0000	5.0000	5.0000	5.0000	4.8333	10.1667	9.1667	5.0000	4.0000	****	0.7750
DFCOL	7.0000	6.1667	7.3333	8.1667	10.6667	7.5000	5.6667	6.1667	14.0000	14.0000	5.5000	4.0000	0.5790	****	1.6414
FLWID	34.3333	28.3888	30.7778	34.0555	32.0555	30.1665	28.5551	28.5555	26.7223	35.1665	33.0805	40.3332	1.3714	****	3.8876
AC	18.7042	12.6727	15.1378	18.3163	16.8402	14.6162	12.9882	13.0532	11.3660	19.5733	17.2428	25.6010	1.3620	****	3.8611
NEC	3.2000	7.2770	5.5000	4.8333	7.3333	8.1667	6.6663	6.3333	3.0000	6.6667	6.2500	7.3333	0.7398	****	2.0972
FDENS	8.8333	6.8333	8.5000	4.6667	8.3333	4.6667	5.8333	7.0000	4.6667	7.3333	9.5000	9.5000	0.4335	****	1.2289
FE	6.6667	2.1667	9.8333	8.3333	3.3333	4.3333	2.0000	2.0000	9.1667	8.3333	2.5000	2.0000	0.3199	****	0.9068
AMTPOL	6.5000	7.3333	5.5000	11.6667	7.0000	7.1667	4.5000	12.0000	5.1667	9.3333	7.2500	9.3333	0.5785	****	1.6399
ARPOLAD	10.0000	10.0000	9.0000	10.0000	10.0000	9.6667	10.0000	10.0000	8.1667	10.0000	10.0000	10.0000	0.3053	***	0.8655
NSTIG	9.6667	10.0000	10.0000	10.0000	10.0000	10.0000	9.8333	10.0000	9.6667	10.0000	10.0000	10.0000	0.1159	NS	-
DEXT	8.5000	9.8333	7.1667	3.0000	9.0000	8.6667	8.6667	5.3333	7.3333	7.3333	9.5000	8.5000	0.3975	****	1.1268
PP	0.3333	0.0000	1.1667	1.6667	0.1667	0.8333	1.0000	0.5000	0.1667	0.6667	0.0000	0.0000	0.1759	****	0.4986
TEXT	4.1667	3.1667	5.3333	7.5000	4.3333	5.0000	4.3333	4.3333	6.1667	5.0000	3.7500	4.8333	0.3054	****	0.8658
ESTA	1.5000	0.1667	-1.6667	6.6667	1.6667	0.3333	0.5000	-0.8333	1.6667	4.8333	0.0000	0.5000	1.3764	***	3.9019
CROSS	41.4167	12.5833	20.3333	64.2500	34.5000	42.2778	21.0000	32.1667	41.2500	43.2500	41.3750	44.8333	4.2727	****	12.1123
SELF 1	20.7500	4.1390	6.3333	7.3333	9.5833	4.4167	0.8333	15.0000	1.3333	27.5000	8.8333	8.3333	2.6697	****	7.5679
SELF 2	32.7778	16.3888	24.2780	40.4998	27.2222	36.5555	17.0000	27.1112	26.0000	38.3332	38.6668	38.9443	3.7659	****	10.6757
SELF 1%	49.1263	63.9542	29.4562	11.5452	28.4648	11.4218	3.1412	48.3945	3.2690	64.0225	21.2550	19.4445	9.4712	****	26.8490

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

APPENDIX 9.4 Genotype means in environment 4 with standard errors, F-test significance for genotypes and least-significant difference at the 5% level

Character	1	2	3	4	5	6	7	8	9	10	11	12	se	Sig	$LSD_{0.05}$
VP%1	24.6827	66.6883	32.8248	50.6780	43.3325	23.4038	24.4612	45.0593	35.3028	36.2942	64.1965	51.7013	7.0374	****	19.9495
DP%	0.4985	0.0000	0.2873	0.1422	0.1185	0.5385	1.5948	0.2382	0.3637	0.1168	0.1650	0.2755	0.3483	NS	-
VP% 2	34.3547	23.1627	43.5920	49.1662	32.9100	45.0282	27.1432	12.1917	55.2288	37.7228	20.5022	18.8828	6.8140	****	19.3162
VP%3	24.5542	29.5427	19.3233	32.4692	9.5275	33.6335	40.6605	16.2003	37.4263	12.0270	14.5210	12.6368	7.1729	*	20.3336
AP1	6.2963	7.9850	7.9260	10.6742	8.1777	9.5645	5.5912	8.0445	7.6297	9.0667	8.1483	8.3378	0.5917	****	1.6774
AP2	6.6073	9.1555	7.6222	9.4520	8.3645	11.8222	6.2488	7.4295	8.1705	9.0443	8.1928	9.0843	0.6891	****	1.9534
AP3	6.2000	7.8665	8.1778	10.2815	7.4045	10.1215	5.5555	7.4000	8.8297	9.2778	6.7777	8.1600	0.8181	***	2.3192
AVP1	1.5038	5.2888	2.6668	5.5037	3.5202	2.3198	1.3332	3.7407	2.6817	3.2557	5.2517	4.2042	0.6159	****	1.7460
AVP2	2.0297	2.1482	3.2888	4.8445	2.9067	5.3333	1.7512	0.8370	4.5335	3.4332	1.5183	1.7067	0.6719	****	1.9046
AVP3	1.4222	2.3630	1.6667	3.5927	0.3888	3.1705	2.6223	1.1852	3.1852	1.1442	1.0148	1.0490	0.6030	**	1.7094
TAVP	4.9555	9.8000	7.6222	13.9407	7.3157	10.8237	5.7068	5.7628	10.4000	7.8333	7.7850	9.9602	1.3084	****	3.7089
LCT1	18.3333	22.4333	17.6000	17.3000	21.7200	22.5200	18.4000	21.8333	19.5000	21.6000	22.9667	22.3600	1.0054	****	2.8501
LP1	7.1167	7.4333	7.9667	7.8833	6.9000	8.7400	7.1400	7.6167	8.7167	7.6500	8.0667	8.1800	0.1346	****	0.3815
LS1	7.9500	9.3333	8.1667	7.9500	8.3400	9.2200	7.2200	9.0667	9.4667	9.0000	10.5000	10.0400	0.2960	****	0.8390
LCT2	22.0667	24.8667	25.4667	20.5000	24.2400	25.3600	21.3200	22.9000	25.9333	25.2000	25.9333	25.7200	0.7714	****	2.1668
LP2	7.2333	7.4667	8.0000	7.9667	7.0600	8.6800	7.2000	7.8000	8.8000	7.8750	8.1333	8.2200	0.1189	****	0.3371
FREQST	4.5000	2.1667	5.0000	5.0000	5.0000	5.0000	2.8000	4.1667	5.0000	3.7500	1.1667	3.2000	0.4890	****	1.3861
LS2	11.3667	14.4167	12.1500	10.3833	11.3200	13.9800	13.4000	12.0333	12.8000	13.4000	15.3333	13.9400	0.4231	****	1.1994

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

APPENDIX 9.4 ctd. Genotype means in environment 4 with standard errors, F-test significance for genotypes and least significant difference at the 5% level

Character	1	2	3	4	5	6	7	8	9	10	11	12	se	Sig	$LSD_{0:05}$
RSEXPA	1.3893	1.7893	1.6223	0.7278	1.1410	1.6778	2.0930	0.9483	1.4257	1.0765	1.8050	1.6097	0.2070	****	0.5867
RCTEXPA	0.7290	0.5867	1.0787	0.3987	0.5275	0.6462	0.6740	0.2367	0.9410	0.4873	0.6833	0.7300	0.1438	*	0.4077
RPEXPA	0.0250	0.0067	0.0048	0.0102	0.0338	-0.0147	0.0140	0.0400	0.0128	0.0283	0.0158	0.0098	0.0161	NS	-
PPTEXT	4.1667	3.3333	4.8333	4.6667	3.4000	3.0000	2.2000	2.8333	5.1667	5.5000	3.3333	3.6000	0.2798	****	0.7932
RSEXPO	0.7908	1.5723	0.8342	0.5528	0.8298	1.6553	3.1580	0.9807	0.6608	0.7680	1.4457	1.1273	0.2471	****	0.7006
PT	5.7178	3.4525	4.1192	5.4762	5.4357	4.2575	4.8268	4.6190	7.1905	6.5965	4.5238	5.9273	0.4812	****	1.3640
ROSETTE	22.1667	19.8333	26.8333	23.0000	25.0000	22.1667	20.3333	23.8333	19.6667	24.6667	22.1667	21.8333	0.7083	****	2.0078
FLOW	72.8333	61.1667	70.1667	75.3333	68.0000	67.4000	71.8000	66.3333	65.8333	78.5000	64.3333	65.0000	1.1536	****	3.2701
FLMED	76.8333	66.3333	77.8333	83.1667	73.6667	75.0000	75.6000	75.3333	78.5000	92.7500	71.3333	71.2000	1.1419	****	3.2371
FS	4.0000	5.1667	7.6667	7.8333	5.6667	7.6000	3.8000	8.0000	12.6667	14.2500	7.0000	6.2000	1.0263	****	2.9094
FL	5.5833	4.7500	4.6667	5.0000	4.9000	5.7000	5.1000	5.6667	5.0833	5.1250	4.9167	4.6000	0.3067	NS	_
HEIGHT	136.6667	136.6667	128.6667	182.3333	133.0000	149.1667	123.6000	145.6667	159.1667	184.0000	145.6667	139.0000	4.7285	****	13.4042
SEC	4.1667	8.1667	5.6667	6.0000	3.8000	5.3333	2.8000	7.1667	6.0000	8.2500	8.0000	5.8000	0.7821	****	2.2171
TERT	4.0000	15.3333	10.5000	11.5000	5.0000	11.1667	1.0000	11.5000	17.1667	23.0000	20.3333	14.8000	2.0292	****	5.7524
QUART	0.0000	7.0000	0.0000	3.5000	0.0000	1.5000	0.0000	0.8333	15.8333	28.5000	6.1667	0.8000	2.9218	****	8.2828
QUIN	0.0000	0.2000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	1.1667	6.5000	0.0000	0.0000	0.8323	****	2.3594
TNH	8.1667	32.8333	16.5000	21.1667	9.0000	18.3333	3.8000	20.1667	40.5000	60.2500	34.8332	21.6000	4.8119	****	13.6407
FCOL	5.0000	5.0000	5.0000	5.5000	6.2000	5.4000	5.0000	4.8333	10.3333	9.2500	4.6667	4.4000	0.3581	****	1.0152

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

APPENDIX 9.4 ctd. Genotype means in environment 4 with standard errors, F-test significance for genotypes and least significant difference at the 5% level

Character	1	2	3	4	5	6	7	8	9	10	11	12	s.e	Sig	$LSD_{0.05}$
NCOL	5.0000	5.0000	5.0000	5.3333	6.6000	5.6000	5.4000	4.8333	11.5000	11.7500	4.6667	4.4000	0.4015	****	1.1381
DFCOL	8.3333	5.5000	6.3333	7.8333	7.6000	6.6000	5.8000	5.0000	13.5000	13.2500	5.3333	5.2000	0.4588	****	1.3007
FLWID	26.4722	30.4443	32.8888	32.3333	32.8000	32.6555	22.8000	29.9445	30.3332	35.0000	32.0555	39.2690	1.0179	****	2.8856
AC	11.1288	14.6425	17.0603	16.4558	16.9453	16.7990	8.3248	14.1160	14.7362	19.2758	16.1818	24.3312	0.9729	****	2.7581
NEC	4.0000	7.6667	7.0000	6.3333	6.4000	9.6000	6.8000	6.8333	3.6667	7.5000	8.5000	9.4000	0.7710	****	2.1856
FDENS	7.3333	9.6667	9.6667	4.0000	9.2000	8.0000	8.8000	7.1667	4.6667	8.7500	9.6667	9.0000	0.3890	****	1.1028
FE	8.3333	2.6667	9.8333	7.8333	2.8000	4.4000	2.0000	2.0000	9.0000	9.2500	2.6667	6.6000	0.5360	****	1.5193
AMTPOL	4.5000	8.5000	6.6667	10.1667	6.0000	7.8000	5.2000	9.6667	4.6667	9.2500	10.0000	9.0000	0.9870	****	2.7978
ARPOLAD	9.3333	10.0000	10.0000	10.0000	10.0000	10.0000	8.4000	10.0000	6.3333	10.0000	10.0000	10.0000	0.5306	****	1.5043
NSTIG	8.0000	10.0000	9.8333	10.0000	8.6000	10.0000	10.0000	10.0000	5.3333	10.0000	10.0000	9.1667	0.7194	****	2.0394
DEXT	8.3333	9.5000	9.1667	4.0000	9.4000	9.2000	9.0000	7.3333	7.0000	6.0000	10.0000	9.6000	0.4117	****	1.1670
PP	0.0000	0.0000	1.5000	2.0000	0.4000	0.6000	1.2000	0.5000	0.8333	1.0000	0.0000	0.0000	0.1341	****	0.3802
TEXT	4.1667	3.3333	6.3333	6.6667	3.8000	3.6000	3.4000	3.3333	6.0000	6.5000	3.3333	3.6000	0.2510	****	0.7000
ESTA	1.6667	-0.3333	0.0000	0.0000	0.0000	10.0000	3.2000	0.0000	2.3333	5.5000	3.3333	10.0000	1.2781	****	3.6231
CROSS	35.4167	30.2500	27.2500	42.7500	24.5000	38.3000	9.5000	31.1667	28.1667	41.6250	37.3333	32.0000	3.8688	****	10.9671
SELF 1	10.0000	0.2500	0.5833	4.8333	0.2000	0.4000	0.0000	6.6667	0.7500	6.6250	2.4167	0.4000	1.5425	****	4.3726
SELF 2	13.6667	24.4998	17.1112	26.0000	7.2000	16.8557	0.0000	26.6110	11.6667	22.3750	32.6665	28.9345	3.5348	****	10.0204
SELF 1%	26.4995	1.0000	2.4470	11.5903	0.6055	0.9345	0.0000	20.1593	2.5837	16.0707	6.7792	1.0417	3.5656	****	19.1079

Significance NS not significant $*0.050 \geq P > 0.010$ $***$ $0.055 \geq P > 0.001$

(NS) $0.100 \geq P > 0.050$ $**$ $0.010 \geq P > 0.005$ $****$ $P \leq 0.001$

APPENDIX 10

Coefficients of variation estimates of variance components with standard errors in brackets, heritability estimates and genotype means for standardised data in the pooled environment.

APPENDIX 10.1 Coefficients of variation for the standardised data in the pooled environment

VP%1	0.3920
DP%	1.6431
VP%2	0.5214
VP%3	0.7598
AP1	0.2082
AP2	0.2122
AP3	0.2583
AVP1	0.4488
AVP3	0.8648
TAVP	0.4037
RSEXPA	0.3945
RCTEXPA	0.6368
RPEXPA	3.4853
RSEXPO	0.4743
ROSETTE	0.0786
FL	0.1347
QUART	0.8058
QUIN	2.2573
TNH	0.3720
FCOL	0.1059
NCOL	0.1303
DFCOL	0.1538
FLWID	0.0969
AC	0.1873
FDENS	0.1496
FE	0.1614
AMTPOL	0.2630
ARPOLAD	0.1282
NSTIG	0.0744
DEXT	0.1506
ESTA	2.3254
SELF1	1.1352
SELF2	0.4473
SELF1%	1.1097

APPENDIX 10.2 Estimates of block, environment, genotype and genotype-environment interaction variance components together with their standard errors (in brackets) and significance in the F-test for standardised data.

	$\hat{\sigma}^2_B$(within environment)		$\hat{\sigma}^2_{Environment}$		$\hat{\sigma}^2_{Genotype}$		$\hat{\sigma}^2_{GE}$	
VP%1	0.0066 (0.0282)	NS	0.2656 (0.2027)	**	-0.0098 (0.0699)	NS	0.4704 (0.1531)	****
DP%	0.0195 (0.0320)	NS	-0.0014 (0.0190)	NS	0.0588 (0.0560)	(NS)	0.1378 (0.0745)	**
VP%2	-0.0055 (0.0248)	NS	0.0272 (0.0375)	NS	0.7751 (0.3377)	****	0.1711 (0.0823)	***
VP%	0.0237 (0.0332)	NS	0.1019 (0.0871)	*	0.2786 (0.1477)	***	0.2075 (0.0908)	****
AP1	0.0102 (0.0293)	NS	0.5079 (0.3459)	****	0.5474 (0.2596)	****	0.2776 (0.1074)	****
AP2	-0.0093 (0.0237)	NS	0.0486 (0.0541)	NS	0.3101 (0.1675)	***	0.2791 (0.1071)	****
AP3	-0.0066 (0.0244)	NS	0.0594 (0.0578)	(NS)	0.2381 (0.1331)	***	0.2178 (0.0933)	****
AVP1	0.0259 (0.0339)	NS	0.1350 (0.1164)	*	0.1510 (0.1153)	*	0.3588 (0.1266)	****
AVP3	0.0332 (0.0360)	NS	0.0889 (0.0730)	*	0.3592 (0.1654)	****	0.0770 (0.0604)	(NS)
TAVP	0.0524 (0.0417)	*	0.0853 (0.0810)	(NS)	0.5112 (0.2405)	****	0.2293 (0.0960)	****
RSEXPA	0.0144 (0.0305)	NS	0.1541 (0.1167)	**	0.2805 (0.1428)	****	0.1639 (0.0806)	***
RCTEXPA	0.0191 (0.0319)	NS	0.1098 (0.0839)	**	0.3028 (0.1421)	****	0.0645 (0.0575)	(NS)
RPEXPA	-0.0014 (0.0260)	NS	0.0148 (0.0186)	NS	0.0561 (0.0392)	*	-0.0039 (0.0420)	NS
RSEXPO	0.0478 (0.0403)	(NS)	-0.0056 (0.0256)	NS	0.7055 (0.3183)	****	0.2470 (0.1001)	****
ROSETTE	0.0843 (0.0512)	**	5.1366 (3.2874)	****	1.0302 (0.4607)	****	0.3979 (0.1359)	****
FL	0.0628 (0.0448)	*	1.4601 (0.9450)	****	1.1902 (0.1036)	***	0.1153 (0.0692)	*
QUART	0.0147 (0.0306)	NS	0.4175 (0.3673)	*	4.0434 (1.7750)	****	1.7242 (0.4523)	****
QUIN	-0.0308 (0.0229)	NS	-0.0003 (0.0263)	NS	1.3563 (0.6025)	****	0.5371 (0.1690)	****
TNH	-0.0010 (0.0261)	NS	0.9600 (0.6644)	****	3.0342 (1.2978)	****	0.9147 (0.2590)	****
FCOL	-0.0021 (0.0257)	NS	38.0472 (24.2636)	****	6.8129 (3.0540)	****	3.6397 (0.9100)	****
NCOL	0.8061 (0.5393)	****	0.0209 (0.0324)	NS	4.9713 (2.0005)	****	0.3472 (0.1238)	****
DFCOL	0.0301 (0.0351)	NS	1.5040 (0.9965)	****	4.4490 (1.8237)	****	0.6295 (0.1910)	****
FLWID	0.0667 (0.0459)	*	4.5231 (2.9025)	****	0.8353 (0.3944)	****	0.4936 (0.1586)	****
AC	0.0754 (0.0485)	*	1.1755 (0.7862)	****	0.8804 (0.4117)	****	0.4908 (0.1580)	****
FDENS	0.0335 (0.0361)	NS	2.0175 (1.3281)	****	2.0616 (0.9004)	****	0.7519 (0.2201)	****
FE	3.8778 (2.6019)	****	0.0226 (0.0329)	NS	12.2023 (5.0612)	****	2.6107 (0.6641)	****

APPENDIX 10.2 continued

	$\hat{\sigma}^2_B$(within environment)		$\hat{\sigma}^2_{Environment}$		$\hat{\sigma}^2_{Genotype}$		$\hat{\sigma}^2_{GE}$	
AMTPOL	0.0127 (0.0300)	NS	1.2773 (0.8409)	****	0.9966 (0.4510)	****	0.4319 (0.1440)	****
ARPOLAD	-0.0140 (0.0223)	NS	14.7245 (9.3311)	****	0.2559 (0.1394)	***	0.2120 (0.0919)	****
NSTIG	0.0305 (0.0352)	NS	214.0209 (135.3726)	****	0.2398 (0.1146)	****	0.0367 (0.0511)	NS
DEXT	0.0568 (0.0430)	*	2.8040 (1.8097)	****	1.9142 (0.8078)	****	0.4071 (0.1381)	****
ESTA	-0.0258 (0.0191)	NS	0.1007 (0.0980)	(NS)	-0.0611 (0.0593)	NS	0.5167 (0.1641)	****
SELF1	0.2073 (0.1511)	***	0.0269 (0.0342)	NS	0.6225 (0.2763)	****	0.1543 (0.0783)	***
SELF2	0.0655 (0.0456)	*	0.5978 (0.4137)	****	0.2656 (0.1606)	**	0.3755 (0.1306)	****
SELF1%	0.0156 (0.0309)	NS	0.1525 (0.1168)	**	0.5123 (0.2360)	****	0.1814 (0.0847)	***

Significance NS not significant * $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$
(NS) $0.100 \geq P > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

APPENDIX 10.3 Full and restricted broadsense heritability estimates with standard errors (in brackets) and coefficients of variation, from the pooled analysis of standardised data.

	$\hat{h}^2$(full)		$\hat{h}^2$(restricted)	
VP%1	-0.006	(0.0403) *****	-0.007	(0.0478) *****
DP%	0.048	(0.0449) 0.9269	0.049	(0.0456) 0.9286
VP%2	0.394	(0.1072) 0.2723	0.398	(0.1079) 0.2710
VP%3	0.173	(0.0786) 0.4546	0.188	(0.0838) 0.4469
AP1	0.234	(0.0934) 0.3997	0.300	(0.1037) 0.3456
AP2	0.190	(0.0865) 0.4542	0.195	(0.0884) 0.4530
AP3	0.158	(0.0769) 0.4876	0.164	(0.0794) 0.4856
AVP1	0.091	(0.0652) 0.7186	0.100	(0.0716) 0.7136
AVP3	0.231	(0.0843) 0.3655	0.250	(0.0889) 0.3555
TAVP	0.272	(0.0967) 0.3552	0.294	(0.1013) 0.3450
RSEXPA	0.174	(0.0766) 0.4405	0.194	(0.0830) 0.4276
RCTEXPA	0.202	(0.0783) 0.3867	0.221	(0.0833) 0.3760
RPEXPA	0.053	(0.0355) 0.6751	0.053	(0.0360) 0.6759
RSEXPO	0.354	(0.1066) 0.3014	0.361	(0.1081) 0.2991
ROSETTE	0.135	(0.0780) 0.5794	0.424	(0.1143) 0.2693
FL	0.067	(0.0412) 0.6122	0.146	(0.0700) 0.4804
QUART	0.567	(0.1184) 0.2108	0.597	(0.1154) 0.1932
QUIN	0.474	(0.1161) 0.2450	0.469	(0.1165) 0.2485
TNH	0.514	(0.1242) 0.2419	0.613	(0.1083) 0.1767
FCOL	0.138	(0.0861) 0.6253	0.595	(0.1212) 0.2037
NCOL	0.696	(0.1011) 0.1453	0.787	(0.0701) 0.0891
DFCOL	0.584	(0.1267) 0.2168	0.732	(0.0847) 0.1158
FLWID	0.121	(0.0715) 0.5921	0.359	(0.1143) 0.3186
AC	0.243	(0.1023) 0.4209	0.371	(0.1148) 0.3093
FDENS	0.352	(0.1287) 0.3661	0.541	(0.1152) 0.2131

APPENDIX 10.3 continued

	$\hat{h}^2$(full)		$\hat{h}^2$(restricted)	
FE	0.619	(0.1294) 0.2090	0.772	(0.0810) 0.1050
AMTPOL	0.268	(0.1087) 0.4054	0.410	(0.1148) 0.2797
ARPOLAD	0.016	(0.0125) 0.7879	0.174	(0.0814) 0.4668
NSTIG	0.001	(0.0009) 0.7895	0.188	(0.0749) 0.3990
DEXT	0.310	(0.1283) 0.4143	0.576	(0.1076) 0.1867
ESTA	-0.040	(0.0379) -0.9479	-0.042	(0.0394) -0.9391
SELF1	0.310	(0.0997) 0.3221	0.350	(0.1044) 0.2979
SELF2	0.115	(0.0666) 0.5776	0.162	(0.0859) 0.5308
SELF1%	0.275	(0.0958) 0.3481	0.302	(0.1006) 0.3326

APPENDIX 10.4 Genotpye means in the pooled environment with their standard error, F-test significance for genotypes, and least significant difference. (Standardised data)

Character	1	2	3	4	5	6	7	8	9	10	11	12	se	Sig	$LSD_{0.05}$
VP%1	1.9868	2.7503	2.0107	2.6645	2.7539	2.3163	3.0443	3.0168	2.4643	2.8803	2.7096	2.0179	0.3991	NS	-
DP%	0.2626	1.2349	0.4579	0.3250	0.3789	0.3958	1.1741	0.5907	1.1916	0.3422	0.4280	0.5216	0.2759	(NS)	-
VP%2	1.8858	0.8950	2.5711	2.9814	1.3187	2.8983	1.7902	1.4109	3.3851	2.4275	0.6800	0.7728	0.2906	****	0.8054
VP%3	1.5940	0.8954	1.9093	2.0426	0.7741	1.8996	1.5782	0.6743	2.1205	1.2128	0.5738	0.5183	0.3058	***	0.8477
AP1	3.2302	5.6907	4.0450	6.2009	4.8450	5.1653	4.0801	5.0470	5.2708	4.1953	4.6883	5.1723	0.3333	****	0.9238
AP2	3.1988	5.4027	4.1630	5.4180	4.6737	5.2146	4.4060	5.1666	5.0457	4.1607	4.6654	5.0258	0.3338	****	0.9253
AP3	2.4571	4.1595	3.8982	4.6059	3.4818	4.4162	3.5110	4.1369	4.1958	3.5795	3.7143	4.3054	0.3100	***	0.8594
AVP1	1.1733	2.7597	1.4760	2.9840	2.4405	2.0941	2.3581	2.7878	2.3468	2.0617	2.3785	1.8782	0.3624	****	1.0046
AVP3	0.9249	0.7875	1.6683	2.2436	0.5625	1.9350	1.2094	0.5730	2.0363	0.9358	0.4959	0.5030	0.2468	****	0.6841
TAVP	1.5538	2.2498	2.4035	3.9908	2.0580	3.2388	2.5165	2.3955	3.6121	2.4544	1.7120	1.5428	0.3146	****	0.8721
RSEXPA	3.3030	2.6300	3.1358	1.4553	2.5717	2.9431	3.2122	1.5308	2.2650	2.7655	2.3000	2.3053	0.2875	****	0.7968
RCTEXPA	2.5648	1.1695	2.6810	1.3291	1.3340	1.5872	1.2046	0.6684	1.8224	2.0333	1.1783	1.2706	0.2404	****	0.6663
RPEXPA	0.1037	0.1713	-0.1383	0.2892	0.4195	0.0808	0.1507	1.0488	0.1688	0.2803	0.6799	0.1891	0.2018	*	0.5593
RSEXPO	2.0834	2.4218	2.1899	0.8275	2.2846	2.7695	4.4255	1.3546	1.3908	1.9926	1.7452	1.8141	0.3216	****	0.8914
ROSETTE	12.4793	12.0517	15.1333	12.8882	13.5641	11.9119	12.0703	12.4886	10.7705	13.6095	13.0065	12.6040	0.3757	****	1.0413
FL	6.9494	7.3174	6.9604	7.6459	7.5434	8.0473	7.7223	8.1915	8.0298	6.9140	6.7308	7.0019	0.2655	***	0.7359
QUART	0.0883	0.4098	0.1782	0.8082	0.5656	0.3043	0.3594	0.4525	2.9508	7.5472	0.8680	0.3592	0.6875	****	1.9058

Continued

APPENDIX 10.4 continued (std data)

Character	1	2	3	4	5	6	7	8	9	10	11	12	s e	Sig	$LSD_{0.05}$
QUIN	0.0000	0.2453	0.0000	0.0946	0.0000	0.0000	0.0000	0.0000	0.6495	4.3265	0.0000	0.0000	0.4195	****	-
TNH	1.3283	2.4418	1.9903	2.2557	1.6389	1.8957	1.8025	2.1815	3.8784	8.0811	2.7720	1.9890	0.5199	****	1.4412
FCOL	8.1783	8.1733	8.1268	9.0873	9.5420	8.9486	8.3079	8.1673	16.0825	14.1958	7.8547	6.6193	0.9755	****	2.7039
NCOL	6.8144	6.7530	6.6918	7.0716	7.1308	7.1171	6.9774	6.6485	13.0473	11.7141	6.6070	5.5046	0.3584	****	0.9935
DFCOL	5.7242	5.1720	5.7519	6.6915	7.3235	6.1650	5.5285	5.6908	10.9873	10.4008	4.9276	3.6798	0.4462	****	1.2367
FLWID	9.3263	10.2631	10.7540	10.9729	10.4040	10.5180	8.7280	9.6521	9.1625	10.7364	10.8090	12.4695	0.4063	****	1.1262
AC	4.3790	5.2428	5.7435	5.9312	5.3564	5.5217	3.8137	4.6399	4.2096	5.7452	5.8000	7.6938	0.4054	****	1.1238
FDENS	6.2301	7.1740	8.1048	4.1733	7.6559	5.7303	6.6398	6.7825	3.8493	6.9264	8.2173	8.7134	0.4792	****	1.3283
FE	8.9118	2.8060	11.5680	8.9713	3.3686	6.8350	2.5308	2.6012	11.1085	9.2763	3.0533	3.3363	0.8333	****	2.3097
AMTPOL	2.2893	4.3323	2.9317	5.8308	2.8588	3.6680	2.7340	5.0403	2.9922	4.3415	4.0432	4.5633	0.3868	****	1.0723
ARPOLAD	6.8137	8.1963	7.7336	8.2512	7.9999	8.0848	7.6241	8.2198	6.4226	7.9684	8.2146	8.1046	0.3077	***	0.8528
NSTIG	12.0940	13.8300	13.6584	13.8300	13.4569	13.6081	13.4916	13.8300	12.6169	13.5298	13.7428	13.7118	0.2255	****	0.6251
DEXT	6.8923	7.8881	6.4535	2.8288	7.7029	7.3320	7.3328	5.9545	6.0205	5.6935	7.8475	7.7155	0.3787	****	1.0498
ESTA	0.2778	0.1189	0.0010	0.3753	0.0171	1.0695	0.5720	0.4616	0.3818	0.7338	0.2911	0.8605	0.4133	NS	-
SELF1	2.8851	0.4758	0.6074	0.9861	0.5177	0.2767	0.1008	1.2497	0.1183	2.1058	0.6870	0.5611	0.2833	****	0.7851
SELF2	2.8786	2.0675	1.7846	2.4944	1.4637	1.9437	1.0965	2.6298	1.8587	2.5253	3.1800	2.9050	0.3682	**	1.0205
SELF1%	2.7696	1.0903	0.8029	0.8495	0.5527	0.2465	0.1154	1.4221	0.1300	1.7642	0.5953	0.4755	0.2950	***	0.8177

Significance NS not significant 8 $0.050 \geq P > 0.010$ *** $0.005 \geq P > 0.001$

(NS) $0.100 \geq p > 0.050$ ** $0.010 \geq P > 0.005$ **** $P \leq 0.001$

APPENDIX 11 Stigma receptivity in safflower

A small unreplicated experiment was conducted to find out approximate lengths of stigma receptivity.

Method

Florets were emasculated using the method outlined in Section 3.4.4 Samples were taken at

1. afternoon prior to dehiscence (at emasculation)
2. morning of style elongation
3. late afternoon of the day of style elongation
4. second morning of style turgidity
5. third morning of style turgidity
6. fourth morning when turgidity was lost.

Styles were stained with α-napthyl acetate substrate and fast blue salt B (as outlined in Section 3.4.4); and 2,3,5-triphenyl tetrazolium chloride (as outlined in Section 3.4.1). The first stain detecting esterase activity, and the second detecting dehydrogenase activity.

Results and discussion

Esterase activity was most pronounced in the afternoon after extrusion. Tetrazolium staining indicated that the region of high enzyme activity at the tip of the stigma in the morning had moved to the base in the afternoon (Plate A2 and A3). High enzyme activity in the wilted florets probably resulted from cellular breakdown with aging.

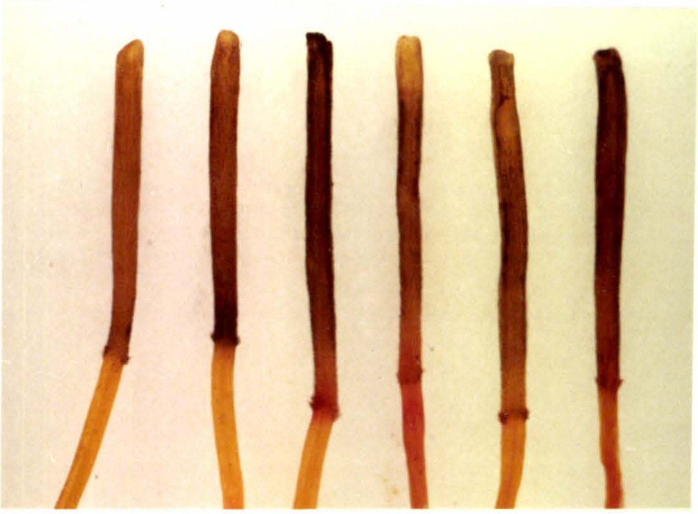

Plate A 2 Esterase activity in safflower stigmas sampled on different days (as specified in the Appendix 11)

Plate A. 3 Stigmas sampled on different days (as specified in Appendix 11) stained with 2,3,5-triphenyl tetrazolium chloride.

High enzyme activity at the base of the stigma in the afternoon following extrusion may indicate a mechanism of shifting receptivity to a zone where insects are likely to brush pollen.

Enzyme activity on other days while stigmas were still turgid did not appear to be high.

(Refer to Bibliography for References)