QUANTITATIVE ANALYSIS OF GENETIC VARIABILITY IN FLORAL AND GERMINATIVE CHARACTERISTICS OF MEADOWFOAM (*LIMNANTHES ALBA*)

A thesis presented in partial fulfilment
of the requirements for the degree of
Doctor of Philosophy in Plant Science
at Massey University

Canhong Cheng

1997

Abstract

Genetic and physiological aspects of flowering, seeding, seed shattering and dormancy of meadowfoam have been studied to provide information on the new crop meadowfoam, and to assist in its domestication and early breeding.

Two hundred and fifty-nine plants were chosen randomly to form an unbiased sample representing the germplasm of eight divergent meadowfoam accessions, which had been intermated to form a composite. Thirteen characters associated with flowering and seeding were involved. Both principal components and clustering proved to be efficient analyses which maximized the discrimination of differences amongst plants in this segregating population. These procedures recognized 190 phenotypes within this germplasm. A high level of significant genotypic variance in all characters was found. Moreover, environmental variances were generally lower in size, so that most characters had high heritability ($h^2 > 0.800$). Early seed set was an exception, with heritability of only 0.446. The results showed that meadowfoam should respond well to selection.

A special feature of this germplasm analysis was the use of cluster analysis, to define "natural" groups. This involved truncating the cluster dendrogram on the basis of minimum F-probability of amongst-cluster to within cluster mean-squares. Further refinement was based on the maximum genotypic variance (σ_G^2), phenotypic variance (σ_P^2) and heritability (h^2), at or near the original truncation.

Another innovation was the use of principal components analysis to identify patterns of fresh flowers, total flowers and seed set. Variability in floral initiation, general flowering time or seed set was randomly distribution, which indicated that the base population was panmictic: one large segregating gamodeme. This pattern analysis was superior to regressions (over time), because there were few time-nodes, and it avoided the need to find optimum functions.

Next, germination and dormancy of this gene-pool were studied, requiring extensive use of the Richards functions and MANOVA. These analyses provided better discrimination amongst treatments than did the univariate character "final germination level".

Dormancy-breaking for meadowfoam was found to be possible by using KNO_3 and/or GA_{4+7} in darkness at 10/5°C, without prechilling. This special test assesses whole-seed germinative maturity; the difference between this and standard germination provides an estimate of dormancy. The results indicated that biosynthesis of GAs and/or sensitivity to GAs were probably involved in meadowfoam germination.

A representative sample gene-pool for study of seed development was established using principal components, giving eight half-sib lines. Harvest ripeness (decline in seed moisture to 12.5%) was compared with seed growth (dry mass), and line differences were found. Standard and special germination tests showed that primary dormancy developed in seeds before they were harvest ripe. Dormancy varied in the eight lines.

ABA content was assayed by ELISA, and principal components and cluster analyses followed using ABA peak measurements (peak height, width and time reaching peak). There were four ABA groups for the eight lines. However, a clear link between ABA pattern and dormancy breaking was not established. Difference in sensitivity to ABA may explain why this was the case.

The results indicated the presence of considerable genotypic variation, allowing estimates of heritability for the development traits. Although the contrast of variance from $\hat{Y}$ (regression) with pooled $\sigma^2_{\hat{Y}}$ was novel, it conformed with biological expectation, and compared well with results from wheat. Heritability was high for harvest-ripe seed mass (0.9238), showing a strong genetic control. In contrast, seed moisture heritability was low (0.3292), indicating considerable environmental influence. Heritability of germinative maturity (dormancy-breaking test on 5 weeks storage seed) was very high (0.9437), indicating that this is a credible measure of true physiological maturity. The heritability of dormancy-breaking was also high (0.9306) after 5 weeks storage. Conversely, after 15 weeks storage, both germinative maturity and dormancy-breaking heritability were low. This indicated that prolonged storage effects were more environmental than genetic.

The general levels of genetic influences (variances and heritabilities) indicate that there is much potential for changing (domesticating) meadowfoam in these characters.

Acknowledgments

I gratefully acknowledge the untiring advice, understanding, constructive criticism and encouragement from Dr. I. L. Gordon, my chief supervisor.

My gratitude and appreciation is also extended to the following people for their contributions toward the completion of this thesis.

My supervisor, Dr. D. J. Woolley for his advice, understanding, criticism and readiness to help.

Dr. P. Coolbear for helpful advice and discussion, especially in the planning of the treatments of seed germination.

Mrs. K.A. Hill, Messers C. R. McGill, M. Currie, C. Rawlingson for occasional technical assistance. Mr. G. Oliver, Ms. L. Barton, B. Rodgers, and G. Gielen, for proof-reading of this thesis.

Past and present members and postgraduate students of the Plant Science, and fellow Chinese students for their friendship and encouragement.

The National Climate Laboratory, HortResearch-Batchelar, for providing one of the controlled environment rooms for me to conduct the experiment of seed development. The Doctoral Scholarship and Graduate Research Awards of Massey University, AGMART and the Department of Plant Science for financial and facility support.

My husband, Hailong, my son, Samuel, and my parents for their love, understanding and encouragement during my PhD study.

Table of contents

List of tables

List of figures