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**Quantitative genetics in apple (*Malus*  
*x domestica* (Borkh.)) breeding:**

**Fruit shape traits, genetic parameter estimation and  
breeding strategy development**

A thesis presented in partial fulfilment of the requirements  
for the degree of  
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## Abstract

The aim of this thesis was to investigate some aspects of breeding for quantitative traits in apple. First, this study explored the measurement and inheritance of a complex quantitative trait (fruit shape). Fourier analysis was used to mathematically describe apple fruit shape in an objective manner and principal component analysis grouped the Fourier descriptors into meaningful shape traits. Heritabilities were estimated to determine genetically inherited shape traits, and genotype by environment interactions were estimated to determine the stability of the trait expression across environments. Fruit aspect ratio accounted for over 76% of the phenotypic variation in shape, fruit conicity for 6% and fruit squareness for only 2%. These traits had moderate to high narrow-sense heritabilities (0.79, 0.38 and 0.38 respectively), which indicated that individual selection would be efficient. High between-site genetic correlation ( $r_A > 0.8$ ), indicated low genotype-by-environment interaction and suggests breeding based at one site would be efficient for altering shape at other sites. A shape chart was constructed to enable these three apple shape traits to be evaluated quickly and accurately in the field, avoiding the need for image capture and Fourier analysis.

Second, heritabilities and genetic correlations were estimated for a range of apple traits from a genetically broad-based apple breeding population of 71 families. Narrow-sense heritability was estimated at each of two sites and across sites for fruit acidity (0.17-0.22), fruit sugars (0.25-0.26), and tree growth habit (0.19-0.41). Higher heritabilities were estimated for fruit squareness (0.32-0.43), fruit conicity (0.32-0.46), powdery mildew incidence (0.40), vigour (0.28-0.62), fruit firmness (0.44-0.53), harvest time (0.66-0.82), leafing (0.60-0.83), fruit aspect ratio (0.74-0.89), flowering (0.92) and fruit size (0.90-1.01). Traits with a high narrow-sense heritability could be selected for efficiently with individual selection. High genetic correlation between sites ( $r_A \geq 0.64$ ) indicated low genotype by environment interaction and that breeding based at one site would be efficient for improving these traits at other sites. High positive genetic correlations between traits at site 1 were estimated for leafing with flowering (0.95), harvest time with fruit firmness (0.92), leafing with harvest time (0.69), and fruit acidity with fruit firmness (0.61). High negative genetic correlations were reported for vigour with fruit squareness (-0.82) and tree growth habit with leafing (-0.53). Rapid gains can

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be made with positively correlated traits, but high negatively correlated traits will make simultaneous gain in both traits difficult. Caution must be applied when interpreting genetic correlations between traits due to high standard errors and the possible influence of environmental interaction between traits (dependence) and linkage disequilibrium.

Third, the traditional apple breeding strategy (mass selection) was compared to an option based on recurrent selection for general combining ability (RS-GCA). The excessively long generation interval of the traditional breeding strategy meant negligible gains were made. However, the traditional breeding strategy generated greater gains per generation than the RS-GCA strategy but at a greater cost in terms of eroding genetic diversity, thereby reducing the potential for long-term gain. The slower rate of gain in the RS-GCA was due to the slower rate of gain in the breeding population. However, the RS-GCA strategy made greater gains in the cultivars relative to the breeding population despite similar selection intensities due to better utilisation of the between-family genetic variance as well as the within-family genetic variance.

Breeding strategies based on quantitative genetics have been applied with success to animal, crop and forest tree breeding, but only recently in apple breeding. It is clear that future breeding programmes would benefit from the application of quantitative genetic theory.

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*Two are better than one, because they have a good return for their work:*

*If one falls down, his friend can help him up.*

*But pity the man who falls and has no one to help him up!*

*Ecc 4: 9-10*

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