

# Discussion

## Outline

1. Introductory paragraph contextualising the past chapters (1-2 paragraphs)
  - i) In this general discussion, we provide a synthesis of the previous four chapters with two major aims. First, we wish to identify the direct implications of our research in diploid potato on broader hybrid potato.
2. Summarising the past few chapters (6-8 paragraphs)
  - i) Hybrid yield can be adequately represented by their parental combinations ( chapter 2)
  - ii) In hybrid potato populations, we can decompose genetic correlations into their predominately additive and dominance components (GCA and SCA as proxies) (chapter 2)
  - iii) These same models can be overlaid with marker data for genomic prediction/selection applications. (chapter 3)
  - iv) Marker data showed little evidence of structure in population. (chapter 3)
  - v) For both phenotypic and genomic models, some traits showed higher genetic variance.
  - vi) Multiple molecular selection strategies were viable for several traits (chapter 4).
  - vii) Potential for multiallelic marker information in predictive modelling (chapter 5).
3. Implications of these results (6 paragraphs)
  - i) SCA is a genetic residual (Bernardo 2016) (chapter 2)
    - A. Not something worth trying to predict in diploids.
    - B. Using GCA's for selection in young potato populations. C. (Labroo2024)
  - ii) Tuber size and dry matter content are better candidates for selection than tuber number
    - A. Sensitivity of tuber number.
    - B. Larger residual variance
  - iii) Multi-trait models a benefit for potato breeders. (Chapter 2)
    - A. Index selection can be of direct use to breeders.
    - B. Technical problems applying this in production.
  - iv) Technologies like genomic prediction can be applied quite simply
    - A. Require smaller training set sizes relative to tetraploids
  - v) Crossing schema for training set development (chapter 3).
    - A.
  - vi) Model choice is useful but not the most important factor for selection.
  - vii) Multiallelism likely a benefit for major QTL, and little else
  - viii) Flexibility in Spatial modelling.
4. Future applications of statistical models (3 - 4 paragraphs)
  - i) Multi-trait modelling to estimate genetic correlation between tuber generations
    - A. (Gopal 1998): GCA does not appear to be very repeatable in early generations, suggesting that even

- family-based analyses do not give stable components across generations.
- B. (Davies and Johnston 1974): Also examines the lack of suitability in selection in 1-hill stage C. (Maris 1988): Excellent paper looking at the lack of correlation between seedling, first, and second clonal generations.
- ii) IBD founder tracing in pre-breeding generations in potato
- A. Link to Genome Design (Zhang et al. 2021).
- B. Access and assessment of tetraploid material.
- (Wilson et al. 2021)
- iii) Genomic prediction as a vehicle for population change
- A. You are driving selection of parent development
- B. Hybrid prediction for coming cycles (Zhao, Mette, and Reif 2015).
- iv) Risk-based approach for estimating potato sensitivity. A. Traditional stability indeces (random regression)
- B. (Yazdi et al. 2002): Example of hazard models in studying longevity of a potential candidate based upon a sire's genetic value.
5. Wrapping up / Conclusions about hybrid breeding in potato (2 paragraphs)
- i) Current status of statistical methods in potato
- ii) This thesis' place in advancing knowledge about hybrid potato

## References

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