# Impact of pedigree depth in the Australian strawberry breeding program: variance component estimation, prediction accuracies and estimation of clonal and breeding values

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Blurb introducing ASBP and different regions bred for.

The Australian Strawberry Breeding Program (ASBP) uses pedigree information in the routine analysis of all traits to estimate breeding values for parental selection. The total genetic effects for each genotype, the so-called “clonal values”, are also estimated from these models.

The analyses are performed in the linear mixed model framework and follow Oakey et al 2006 and Oakey et al 2007 which uses the numerator relationship matrix generated from pedigree information. The ASBP pedigree records are in good order with genotype name aliases regularly updated and information back to founders mostly complete. Currently, the breeding program uses a standard pedigree depth of 10 generations. It is of interest to determine what an optimal pedigree depth could be and the effect of changing pedigree depth on the genetic variance estimates, the breeding and clonal value estimates and the prediction accuracies these estimates.

Aitken et al (2009) performed a similar study in sugar cane where they also investigated the number of years of trialling that make a difference to the estimates. In the case of the ASBP, they have implemented the contemporary group technology described in Smith et al 2021 to determine that for the subtropical program 5 years was sufficient, and for the temperate program 4 years.

Strawberries are an open-pollinated crop and so crosses are made by…. Description of breeding program here…

Strawberries are considered as diploid for all intents and purposes in the realm of genomics and breeding. However, it is actually a ?? species and the present calculation of the A matrix is based on Henderson (???) and Wright (1922) which is for diploid species.

What is the current total number of generations in the breeding program pedigree?

The purpose of this paper is to investigate the effect of changing the number of generations used to calculate the numerator relationship matrix on the additive and non-additive genetic effects, the breeding and clonal value estimates and their respective accuracies.

## Data set

The proposed datasets are the:

* Subtropical 2020-2024 yldpp, avfrtwt, cumulative yld (cyldpp) and cavfrtwt
* Temperate 2020-2024 yldpp, avfrtwt, cumulative yld (cyldpp) and cavfrtwt
* Pedigree information from Katmandoo, then subset for the following and generate A matrices for each
  + A2: 2 generations (individuals and parents)
  + A3: 3 generations (individuals, parents and grandparents)
  + A4: 4 generations (individuals and parents)
  + A5: 5 generations (individuals and parents)
  + A6: 6 generations (individuals and parents)
  + AF: Back to founders
  + AI: AISweep generated from AF

## Proposed Analyses

1. No pedigree: Single YearWeek analyses for yldpp and avfrtwt
   1. Investigate spatial effects as a side task
2. No pedigree: Single Year analyses of cumulative traits, cyldpp and cavfrtwt
   1. Not sure about spatial for these because they are accumulated over the season– but not difficult to include
3. Develop repeated measures model for yldpp and avfrtwt
4. Investigate different ways of calculating an A matrix for non-diploid species
5. Best model from 1, 2 and 3 above with all 6 x t A matrices, where t = number of types of A matrices (no more than 3), if there are any!)

## Proposed Results

1. Spatial vs non-spatial models
2. Repeated measures versus cumulative – BLUPS
3. Report on number of parents added with each generation
4. Additive vs non-additive genetic variances
5. Clonal and breeding values with accuracies
6. Correlation between CV and BVs for each trait and each matrix type

## Other thoughts

1. Link to simulation of missingness
2. This may not be the place for the repeated measures
3. Find out if the animal model is appropriate for this species, rather than the parental model we use from Oakey et al 2006, 2007.