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

Dr. Ky Mathews PhD[1*], Dr. Katie O'Connor PhD[1] and Dr. Jodi Neal PhD[1]

[1*]Department of Primary Industries, Queensland Government, Nambour, Australia, 4560, Queensland, Maroochy Research Facility, 47 Mayers Road.

*Corresponding author(s). E-mail(s): ky.mathews@daf.qld.gov.au; Contributing authors: katie.oconnor@daf.qld.gov.au; Jodi.Neal@daf.qld.gov.au;

Abstract

Key message: Less than 30 words summarising the main achievement. Abstract should be around 200 words.

Keywords: A matrix, relatedness, yield

1 Introduction

Ways of finding the best depth. What other people have found.

Atkin 2009 and Yang 2016

Katie's musings, ignore for now: Others' results "In principle, more complete pedigree will lead to more efficient use of phenotypic information of relatives. But the distant ancestors have very little impact on the construction of relationships between candidates and their relatives with records. Thus it may be not necessary to keep distant ancestors in pedigree data. Moreover, the depth of pedigree could have a big

impact on estimates of genetic parameters. Genetic parameters estimated using a linear mixed model reflect the genetic parameters of conceptual base population in which there is no genetic relationship between individuals (Kennedy and Moxley, 1975; Van Der Werf and De Boer, 1990; Bijma et al., 1997). When pedigree is traced back to distant ancestors, the base population will shift to an early generation, and the inbreeding coefficient in the resulting relationship matrix will increase. This implies that in a closed population, additive genetic variance estimated using a deeper pedigree could be larger than that obtained using a shallow pedigree. For each population, genetic parameters and breeding values were estimated using various datasets which differed in number of generations in phenotypic data and pedigree data. Six phenotypic data sets were created; each included recent 1, 2, 3, 5, 10 or 20 generations of records. The pedigree datasets included the generations in phenotypic data and plus 1, 2, 3, 5, 10 or all ancestral generations, depending on the corresponding phenotypic data set. For example, for phenotypic data set comprising 20 generations, the pedigree data was possible to include 5 more generations at maximum, since the total number of generations available was 25. For each scenario of data set, 50 replicates were analyzed. The effect of phenotypic information from previous generations and pedigree depth on EBV was assessed by reliability and unbiasedness of EBV for animals in the last generation. Reliability of EBV ($rEBV^2$) was measured as squared correlation between EBV and true breeding value (TBV)." - Yang and Su (2016).

In their study of the impact of pedigree depth on model convergence in pigs, Pocrnic et al (2017) investigated A matrices with depths of 1 to 5 (where a depth of 3 included all animals with phenotypes or genotypes plus 3 generations of ancestors). They found that.... (Pocrnic et al, 2017). Across different study organisms, optimal pedigree depth varies, for example, results found that three generations of phenotypic records plus an additional two generations was sufficient in simulated pig populations (Yang and Su, 2016), whilst Atkin et al (2009) found that a minimum of three sugarcane generations was required to accurately estimate BVs of parents.

2 Materials and methods

3 Results

Figures and tables are labeled with a prefix (fig or tab, respectively) plus the chunk label. Other environments such as equation and align can be labelled via the \label{#label} command inside or just below the \caption{} command. You can then use the label for cross-reference. As an example, consider the chunk label declared for Figure ?? which is fig1. To cross-reference it, use the command Figure \ref{fig:fig1}, for which it comes up as "Figure ??".

To reference line numbers in an algorithm, consider the label declared for the line number 2 of Algorithm ?? is \label{algln2}. To cross-reference it, use the command \ref{algln2} for which it comes up as line ?? of Algorithm ??.

4 Discussion

5 Conclusions

We found. . .

Supplementary information. If your article has accompanying supplementary file/s please state so here.

Declarations

5.1 Funding

5.2 Competing Interestions

The authors have no relevant financial or non-financial interests to disclose.

5.3 Authors' Contributions

KM and KO developed the idea. KM wrote analytical R code. etc etc.

5.4 Data Availability

The datasets generated during and/or analysed during the current study are available from the corresponding author on reasonable request.

References

Atkin FC, Dieters MJ, Stringer JK (2009) Impact of depth of pedigree and inclusion of historical data on the estimation of additive variance and breeding values in a sugarcane breeding program. Theoretical and Applied Genetics 119(3):555–565. https://doi.org/10.1007/s00122-009-1065-7, URL http://dx.doi.org/10.1007/s00122-009-1065-7

Pocrnic I, Lourenco DAL, Bradford HL, et al (2017) Technical note: Impact of pedigree depth on convergence of single-step genomic blup in a purebred swine population. Journal of Animal Science 95(8):3391–3395. https://doi.org/10.2527/jas.2017.1581, URL https://doi.org/10.2527/jas.2017.1581, https://academic.oup.com/jas/article-pdf/95/8/3391/23805403/3391.pdf

Yang H, Su G (2016) Impact of phenotypic information of previous generations and depth of pedigree on estimates of genetic parameters and breeding values. Livestock Science 187:61–67. https://doi.org/10.1016/j.livsci.2016.03.001, URL http://dx.doi.org/10.1016/j.livsci.2016.03.001