Genomic selection in small populations with reduced effective size: example of oil palm

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Abstract

Genomic selection is expected to increase genetic gain per unit time in oil palm (*Elaeis guineensis*) but currently only simulation results exist (Wong and Bernardo 2008). We applied cross-validation on real data of progeny-tested individuals to estimate the accuracy of genomic selection in oil palm. This study used the largest dataset of estimated breeding values reported in oil palm breeding. It included two breeding populations of 100 and 130 individuals, genotyped with 200 SSR and phenotyped for five traits with a wide range of heritability. Deregressed estimated breeding values were used as observations in a weighted analysis to derive genomic estimated breeding values (Garrick et al. 2009). Two strategies were used for sampling training populations: within population structure based on K-means clustering (Saatchi et al. 2011) and across population structure. Several statistical methods were compared. The accuracy of genomic selection was estimated in the test population. Our results will be valuable for all breeding programs where populations are small and have a very small effective size.

References

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