



W528

Factors controlling accuracy of genomic selection in oil palm (*Elaeis guineensis*)

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Wong and Bernardo (2008) showed in a simulation study that genomic selection could increase the rate of genetic gain in oil palm (*Elaeis guineensis*). In order to estimate the accuracy of genomic selection in a real breeding program, we applied a cross-validation approach to the largest dataset of progeny tests reported in oil palm breeding. It included two breeding populations of 100 and 130 individuals, genotyped with 225 SSR and evaluated for ten traits. 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. Five statistical methods were compared. The strategy for sampling training populations had the strongest effect on the accuracy of genomic selection in the test population. Its effect was related to the maximum relationship coefficient between test and training individuals. Also, trait, population and trait by population interaction had a significant effect on accuracy. We hypothesized the trait effect was related to the genetic architecture of each trait. The population effect was correlated to the effective size of each population. The trait by population interaction was correlated with the trait variability existing in each population. Finally, our real data confirmed the usefulness of genomic selection for oil palm breeding. Our results should be valuable for all breeding programs where populations are small and have a reduced effective size.