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How to use molecular data to account for non random mating in quantitative genetic estimates derived from family structured experiments

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Abstract: Accurate estimates of heritability (h^2) of fitness-related traits are necessary to assess their adaptive response in changing environments. For plants, maternal families are often sampled to estimate h^2 . Estimates thus rely on several assumptions about the mating system and the relatedness among mates (basically offspring are assumed to be half-sibs or unrelated). In particular, when mating events are impossible to observe and sample sizes are large, the paternal relatedness is often neglected, leading to bias in the h^2 estimates.

We performed a simulation study to investigate how molecular markers can be used to analyze more efficiently the family structured designs. We compared the simple method based on a maternal family model assumption with methods using marker-based relatedness coefficients, pedigree or hybrid genetic information (animal models) to account for paternal relatedness. We assessed the effect of unequal male reproductive success, inbreeding and maternal effects on h^2 estimates.

Results showed that in presence of unequal male reproductive success, neglecting the genetic relatedness between families led to bias the h^2 estimates derived from the family model. Regarding the animal model, the method using mean marker-based relatedness coefficients was efficient to deal with non-random mating system and ancestral inbreeding in the parental population. But this method was biased in presence of maternal effects. In such cases, only the use of finest genetic information, like pedigrees, allowed to improve the accuracy of the h^2 estimates. Using a hybrid approach, that uses both the pedigree and mean relatedness information, was efficient to deal with any departures from the family assumptions.

In conclusion, family structure designs are part of the experimental exceptions, with inbred samples, where pedigree-free, or partial pedigree-free (also called hybrid approach), methods can be used to get accurate h^2 estimates, at the condition that mean relatedness coefficients are used (estimated at the family/population level).