Animal models constructed with hybrid relatedness matrix vs incomplete pedigree: an experimental and simulation approach.

Julie Gauzere, Etienne Klein, Sylvie Oddou-Muratorio, Laurène Gay

To cite this version:

HAL Id: hal-02809584
https://hal.inrae.fr/hal-02809584
Submitted on 6 Jun 2020

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Animal models constructed with hybrid relatedness matrix vs incomplete pedigree in Fagus sylvatica

Julie Gaüzere*, Etienne Klein*, Sylvie Oddou-Muratorio* and Laurène Gay*
* INRA – U.R.F.M. - Mediterranean Forest Ecology – Avignon – France
* INRA – UMR A.G.A.P. – Genetic improvement and adaptation of Mediterranean and tropical plants

Context and aims
To alleviate the effort associated with generating offspring with complete pedigree information, simplified protocols with incomplete pedigrees have been adopted, like open-pollinated schemes. This solution accept untestable assumptions related to the genetic constitution of the families, the numbers of male parents involved and their contributions.

Today, molecular markers provide an alternative way to construct animal models via reconstructed pedigrees or relatedness matrix. However, for some species phenotypic informations are still easier to obtain than molecular informations.

This study aims at judging the estimation errors caused by simplifying assumptions in classical breeding experimentations, and at investigating the efforts that should be allocated to obtain respectively phenotypic and information in quantitative genetic studies in wild population.

Methods and results

a) Results of mating pattern analysis
Cervus analysis with n potential father in each population...and we found x real pollen donor...

b) Quantitative genetics analysis
The VA and h² of the traits were estimated:
(i) using the 6000 phenotyped seedlings, and assuming that they were all half-sibs
(ii) using the sub-sample of 625 individuals, still assuming that they were all half-sibs
(iii) using the same sub-sample and accounting for the paternal relatedness between individuals inferred by Cervus analysis

Discussion
Accounting for complex kinship structure markedly changed VA and h² estimates: for the different studied traits, the estimates of h² varied between 0.22 and 0.45 when using paternal information, versus h² between 0.39 and 0.63 assuming only maternal half-sibs.

The best quantitative genetics model is an intermediate between the models (i) and (iii), i.e. the model which include the most genetic and phenotypic information. However, genetic data are rarely available on sampled of this size.

We can optimize the use of genetic information in creating a hybrid relatedness matrix which should contain: information from paternity assignments (complete pedigree), relatedness estimated from markers (Fi) and mean relatedness estimations within and between families. This last point should allow to consider that the paternal contributions to the fertilization are skewed and that mother-tree can be pollinated by only a few male-trees.

Conclusion
- Mating pattern is highly variable among families
- Quantitative genetics simplified protocols can lead to wrong interpretations since genetic effects can be confuse with maternal effects
- Accounting for paternal relatedness among individuals greatly affect the estimation of VA and h²
- The relevance of constructing a « hybrid » relatedness matrix incorporating several sources of available information (incomplete pedigree, paternity assignments, relatedness estimated from markers) instead of using simplifying assumptions, will be tested by simulation approach.