
Impact of preselection varies across genetic evaluation models

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Accurate and unbiased evaluation of genetic merits of animals is of utmost importance in animal breeding. This is mainly to identify the animals that resemble the breeding goal the most, so that these animals are selected to become parents of the next generation. There are two categories of genetic evaluation models: pedigree-based and genome-based models. Pedigree-based models use pedigree information, and genome-based models use genomic information, for estimating genetic relationships among animals. Historically, an animal is genetically evaluated shortly before selection to become a parent, based on its performance record supplemented with performance records of its relatives. Because it is expensive to raise all selection candidates to this age, breeding companies, based on some information available at young ages, preselect a proportion of young selection candidates and raise them until selection of future parents. This practice is called preselection. Genetic evaluations assume that the animals to be evaluated are a true representation of the entire population of the animals at birth. Preselection clearly violates this assumption. It is known that evaluations produced by genome-based models are less affected by preselection than evaluations produced by pedigree-based models. However, the reason for this is not fully understood. In order to be able to adapt the models to better handle the impact of preselection, it is important to understand this reason through understanding the impact of preselection on components of genetic evaluation models. This reason is most likely associated with a component that is different between pedigree-based and genome-based models: the genetic relationship matrix. We hypothesise that in genome-based models, average relationships among preselected selection candidates are higher than average relationships among selection candidates without preselection. Therefore, the aim of this study was to investigate the impact of preselection on average pedigree and genomic relationships among selection candidates. A breeding programme was then simulated, with features of pig and poultry breeding programmes. Impact of various combinations of forms and intensities of preselection on average pedigree and genomic relationships among selection candidates were investigated. Preliminary results show that average genomic relationships among preselected selection candidates are indeed higher than average genomic relationships among unselected and randomly preselected selection candidates. Further results will be presented and discussed at the conference.