Unknown-parent groups and incomplete pedigrees in single-step genomic evaluation

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Session 34 — Theatre 13

Unknown-parent groups and incomplete pedigrees in single-step genomic evaluation

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In single-step genomic evaluation using best linear unbiased prediction (ssGBLUP), genomic predictions are calculated with a relationship matrix that combines pedigree and genomic information. For missing pedigrees, unknown selection processes, or inclusion of several populations, a BLUP model can include unknown-parent groups (UPG) in the animal effect. For ssGBLUP, UPG equations also involve contributions from genomic relationships. When those contributions are ignored, UPG solutions and genetic predictions can be biased. Several options exist to eliminate or reduce such biases. First, mixed model equations can be modified to include contributions to UPG elements from genomic relationships (greater software complexity). Second, UPG can be implemented as separate effects (higher cost of computing and data processing). Third, contributions can be ignored when they are relatively small but they may be small only after refinements to UPG definitions. Fourth, contributions may approximately cancel out when genomic and pedigree relationships are constructed for compatibility; however, different construction steps are required for unknown parents from the same or different populations. Finally, an additional polygenic effect that also includes UPG can be added to the model (slower convergence rate). Chosen options need to reflect different origins of UPGs: missing pedigrees in a closely selected population, multiple breeds, external lines or combinations of origins. Incomplete pedigrees may also cause biases and convergence problems even when UPGs are not in the model. In such cases, choices include restoration or truncation of pedigrees. Severity of problems with UPG and incomplete pedigrees greatly depends on the population structure.

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Effect of project 'YoungTrain' on participants` career

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The main aim of the project 'YoungTrain' was to train a group of 40 early carrier scientists from new Member States and countries in Southern and Central Europe, the Newly Independent States (former Soviet Republics) and the Mediterranean rim in transparency of the food chain and quality in meat products. The animal scientists were supported by mentors and a new network that includes regional experts. By means of e-learning packages and workshops, they learned to pass on the safe and high-quality food message and to develop RTD projects in the field. The group received full attention from specialists in the field of meat quality and quality of meat products as well as about procedures of preparing a proposal in framework of RTD projects. One very important issue was the selection of participants. Project leaders made balanced selection according gender, age, regions, ability to communicate and willingness to cooperate. Support action YT enabled young scientists to meet not only specialists in the field of meat and product quality, but also persons actively involved in support managing and creating ideas of new call for RTD projects. Participants of YT project started or continued their scientific career in field of animal science during or after the project with support of skills and contacts obtained as result of the project. Lot of them finished PhD study, became assistant professor or heads of department in home universities or institutes. One of the more important outputs from the project is networking and dissemination of knowledge among participants and their working places. It is not surprising that quite a visible part of participants have started to work actively in structures of EAAP, in Scientific Commissions, Working Groups or on organising annual meetings. Nowadays participants communicate and cooperate on creating international projects using skills and personal contacts established on the base of the YT project.

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