Genomic selection for new traits: optimal prediction and reference population design

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Genomic selection (GS) is the most successful application of –omics technologies in livestock production. An important promise is that it allows selection for difficult or expensive to measure traits. Our objective is to review requirements to start GS for such new traits, and possibilities to optimize use of limited reference populations. In practice, size of reference populations may be dictated by required number of records to estimate genetic parameters, phenotypic data availability, phenotyping and genotyping costs, and population size. When cost of measuring phenotypes is very high (e.g. methane emission), the most optimal strategy may be to obtain single phenotypic measurements of genotyped animals. To maximize average accuracy of direct genomic breeding values (DGV) with a small reference population, the following strategies can be used: (1) optimize reference population design in terms of relationship within the reference population and to evaluated animals (selective genotyping); (2) optimize selected set of included phenotypes (selective phenotyping); (3) use a model that optimally fits the architecture of the trait and used marker density; (4) measure indicator traits with higher heritability or a larger scale in the reference population to cheaply increase its power; (5) measure indicator traits on evaluated individuals to increase DGV accuracy; (6) combine national reference populations through international collaboration. Limited size reference populations with up to a few thousand individuals with single records yield DGV with relatively low accuracies, compared to traditional breeding values. Combined with a reduced generation interval and an increase in selection intensity, using such DGV can still lead to considerable genetic gain, compared to progeny testing schemes for easy to record traits.