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Genetic data could become more accessible to owners and researchers as scientists discover new techniques that offer more "value for money." And this, one British research group says, could lead to a higher number of horses being genotyped and a better understanding of diseases and disease processes.

This added value is related to the genotyping "density"—essentially, how detailed the genotyping is. By using a combination of low- and high-density genotyping, research costs could be considerably reduced while still maintaining an acceptable level of accuracy, said Laura Corbin, PhD, and colleagues at the Roslin Institute and Royal (Dick) School of Veterinary Studies at the University of Edinburgh.

"Recent developments in the field of genomics have enabled researchers to interrogate the genome of individual animals to a level of detail not previously possible," said Corbin. "However, this 'high-density genotyping' can be costly, leaving researchers struggling to generate the large sample sizes needed for most studies."

All horses in a particular breed are related to some degree—their genomes are made up of the same fragments but in different combinations, she said. As such, it might not be necessary to have the high levels of detail for each genotyping scan within that breed. In fact, researchers can choose to genotype only certain genetic variants called single nucleotide polymorphisms (SNPs) and then fill in the "missing" information based on existing equine genomes.

"This means that if you have a group of horses genotyped at high density, additional horses can be genotyped more cheaply at lower density and missing genotypes filled in or 'imputed' based on existing data," Corbin said.

The trick, of course, is to know which SNPs scientists should—and shouldn't—skip in individual horses. That's why Corbin and colleagues looked at genotype information on 1,201 Thoroughbreds that had already been genotyped with a high-density genotyping chip that classifies 50,000 SNPs in each horse. By masking selected SNPs in a subset of the horses, researchers were able to test how accurately they could predict those missing genotypes based on the genotype information from the remaining horses. Using data on only four of the 32 chromosomes (for a "proof-of-concept" study), they masked the equivalent of 48,000 SNPs genome-wide.

Based on their results, Corbin and her colleagues found they could potentially achieve accuracy rates of 84% with only 2,000 "visible" SNPs left across the genome. The remainder would be imputed (filled in by the researchers). Overall, it's a procedure that would cost only 29% of the price of high-density genotyping.

Using 6,000 SNPs, the team's accuracy reached 96%. However, such high accuracy probably isn't necessary on a practical level. "Using 2,000 SNPs spread across the genome would likely be sufficient for many purposes and provide the best value for money," Corbin said. "By enabling three times the number of horses to be genotyped for the same budget, this approach could lead to faster progress in equine research and the translation of that research into practice."

One example of this, Corbin said, is the genomic prediction of disease risk: "Genomic prediction can offer more than just the potential to accurately select breeding stock based on underlying genetic potential," she said. "It can help researchers investigate the impact of different management practices on the incidence and severity of disease by allowing them to select cohorts of horses which have a similar genetic risk of disease."

"Furthermore, by allowing the prediction of disease risk at birth, genomic prediction can aid management decisions throughout a horse's lifetime," she continued. "For example, if you know that your horse has a high genetic predisposition to osteochondrosis (a developmental orthopedic disease that results from a disruption in the growth of articular cartilage), you can manage his environment to minimize the risk of the condition occurring, or at least minimize its severity."

In addition to reducing costs, Corbin said researchers (together with the equine industry) should also focus on developing a strategy for recording and sharing genotype (genetic makeup of a physical trait) and phenotype (physical characteristics) data.

"What is potentially more important at this stage is to develop ways of comprehensively and consistently recording phenotypic information about the horses from which DNA samples are taken," she noted. "In this way, we will be able to make much better use of the samples we collect."