Major Genes for Important Traits

New gene tests are emerging almost every day. Make the most use of expensive gene test data. Improve the odds in your favour. Don't compromise on other traits or factors in your breeding program.

One gene or many?

Traits may be genetically controlled by a single gene, many genes or a combination of many genes with some having larger effects. Most production traits are the latter and our standard genetic evaluation systems are able to estimate an "average effect" of all the genes for the trait. We call this the Estimated Breeding Value (EBV, but also referred to as BV or EPD). It is a single figure for the trait that tells us how much better or poorer an individual is than others in the same population (and analysis).

When a gene is large enough to "see" or we can find a region of the genome to test for a gene, we have a "gene marker" that we can reliably use to select for this one gene. When a gene marker is very good (it is pointing right to the gene without error), we can select with almost 100% confidence the gene in question and expect to see the predicted phenotypic expression.

If we select only on a single, very predictable gene, we will lose the ability to select for other traits effectively with EBVs. In the most extreme case, this is because we ignore the EBVs and choose only individuals with our gene of interest, and as a consequence we lose many good individuals who may not carry the single gene but have exceptionally good EBVs for other traits. If some of the EBV traits are undesirably correlated with the single gene, we may compound this error by actually selecting against EBV traits.

The best approach is a balanced approach

Just like with balancing traits appropriately in the breeding objective and the selection index, and balancing genetic gain and coancestry in the genetic trade-off, we want to balance selection on gene markers with selection using $Index and EBVs.

Take a balanced approach with TGRM®

And just like with $Index, coancestry, progeny inbreeding, and trait distributions, TGRM® let's you include gene marker analysis data[1] in your mating optimisation giving you the opportunity to balance selection in a way that reflects your breeding goals.
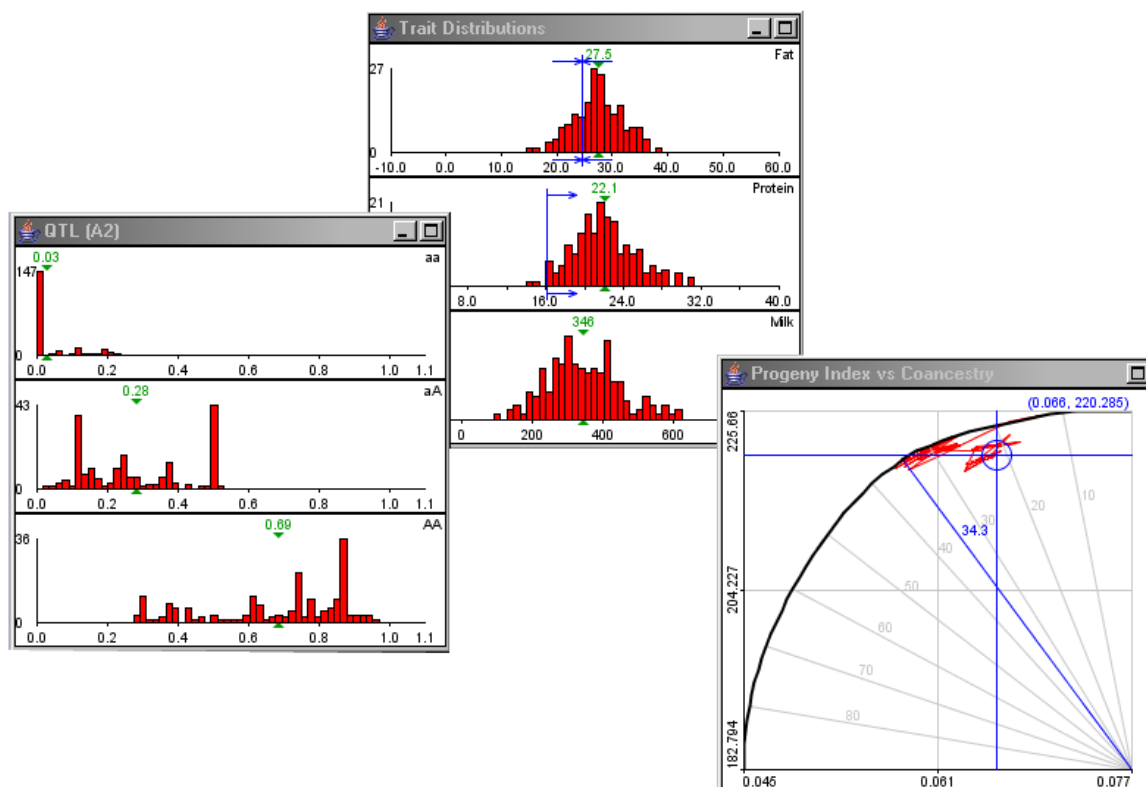
Don't ignore information that is the result of hard-earned data collection practices. And don't put all your eggs into one basket by placing too much emphasis on a single gene marker that "promises" to make large impacts on your bottom line.

> Make selection and mating decisions in an objective framework where you can assess the pros and cons of alternative approaches and make an informed choice.

[1] Using gene tests effectively requires the use of segregation analysis to estimate the probability of having the desirable gene for individuals that have not been tested. With only a few gene tests this analysis can estimate the genotype probabilities for all the individuals in the stud or population. This is a very powerful analysis and may be performed as an optional add-on to your TGRM® analysis.