Breeding by DNA

Dr Stephen Harrison explains how genetic technology can be used practically to give breeders advice on their mating plans

What is does your company do?

Thoroughbred Genetics Ltd (TGL) is a racehorse DNA and data analysis company based in Canterbury, UK. It was founded by in 2000 off the back of family interests in thoroughbred racing and a PhD and career in genetics research. It's tests and databases are now supplied to a range of breeders and owners, both large and small and on a global basis. TGL's objective is to help bring black-type success to clients.

So how is this achieved?

This is done by direct DNA testing of horses and data and observations derived from 15 years of testing of thousands of thoroughbreds.

Correlations are made with performance and breeding outcomes, and advice is given on breeding, sales and racing strategies.

TGL is more an agency or consultancy than a mass DNA testing body so all clients' results are thoroughly interpreted. The production and selection of thoroughbred racehorses is clearly multi-factorial processes. We work closely with owners, agents, vets and trainers to provide a bespoke service and help create the best possible outcome.

Specifically, TGL contributes quantifiable, objective genetic information to the melting pot and provides a genetics-based probability model for thoroughbred breeding and selection.

What's the underlying genetic theory?

The rationale behind our breeding and selection processes is that the thoroughbred, rather than being too inbred, is in fact something of a "mongrel breed".

We use a series of genetic tests and data to help manage this "mongrelism" to ensure that horses are bred or selected to do a specific job in the best possible genetic health.

Unlike strictly agricultural animals, thoroughbreds aren't selected for specific characteristics such as live weight gain, milk yields etc. Successful horses come in variable shapes and sizes, run over different distances and it's usually difficult to argue a common genetic reason for their success.

This means no uniform selection pressure and therefore, higher genetic variability.

Contributing further to genetic variability is the fact that in reality many broodmares haven't been "selected" at all.

Many have entered breeding careers early because they've broken down, have physical problems or haven't performed well.

Positive gene selection is done generally via a limited number of top-class colts entering stud. Breeding from comparatively lesser mares diminishes selection and fixation of positive gene versions in the breed as a whole.

Dr Stephen Harrison has combined a love of thoroughbreds, racing and breeding with his scientific prowess

Genetic variability is a good thing in terms of genetic health, but it doesn't do much for job specialisation or the fixing of genes to do these jobs. If it's based partly on retaining lower quality animals in the population, it's counter-productive.

What can be done about genetic variability?

Fortunately, poor quality genetic fixation and mongrelism isn't rife throughout the breed.

Wealthier, established or more organised breeders naturally retain better race mares for breeding – they've been selected properly. Typically, the likes of the Aga Khan and Juddmonte use highly structured breeding programmes over a number of horse generations.

As well as having the best race mares, they also have access to proven and more expensive sires. Individuals not conforming to higher standards are also "culled".

Therefore, unlike the general population, there is extensive genetic fixation within this elite premier division.

Although thoroughbreds do all belong to the same stud book, there is effectively more than one thoroughbred gene pool in existence. Smaller breeders could do worse than buy into affordable breeding stock coming to the sales from the premier organisations.

You analyse both genetics and pedigrees?

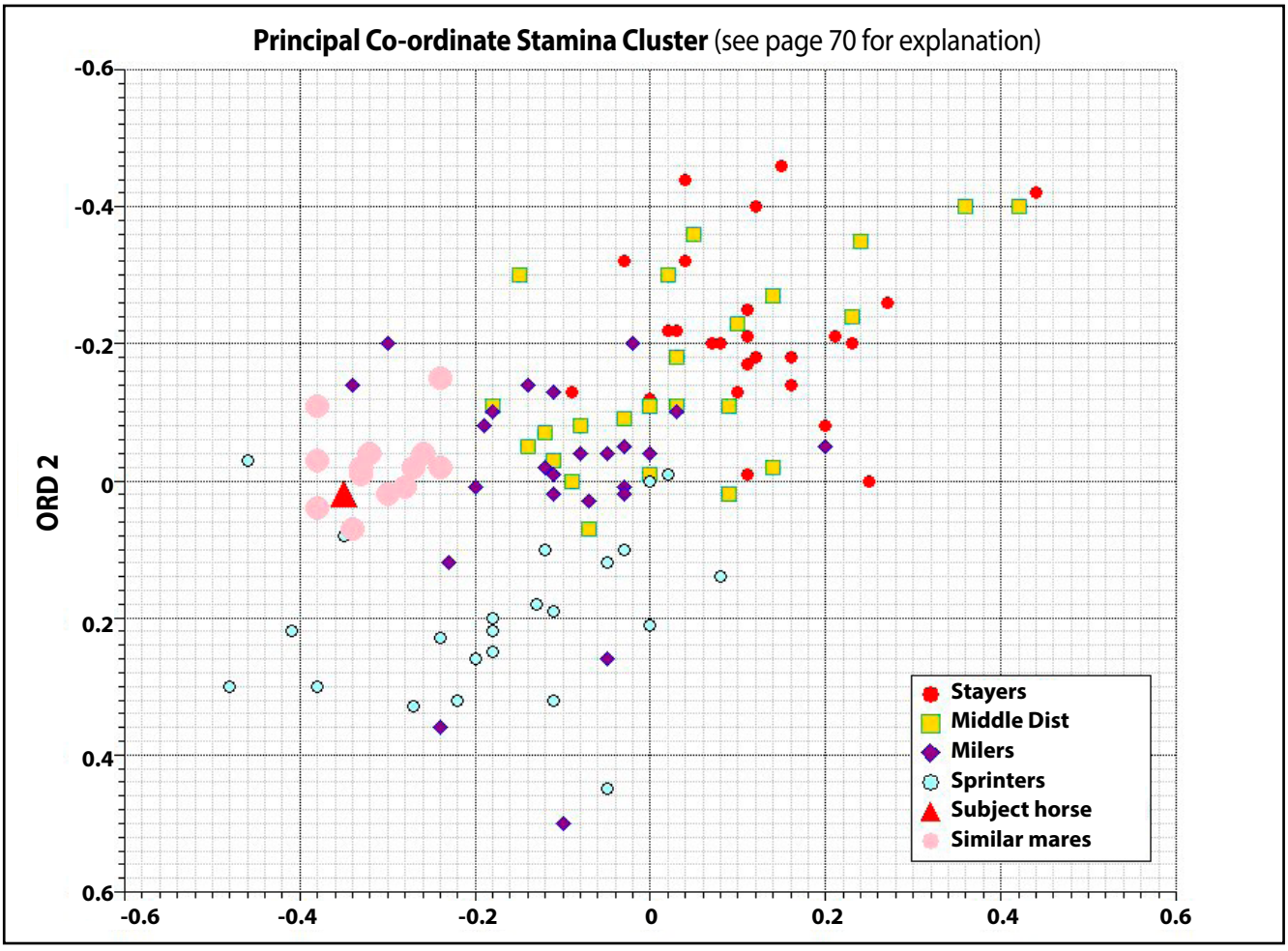
Whether we are talking about helping to breed horses for owners or selecting pre-existing animals from the sales, we work on the basis that we want animals that are not too genetically variable but adapted to do a specific job whilst being healthy.

We seek to consolidate and progress this within the premier breeding division or helping smaller and newer breeders emulate this model in the most effective, quickest and cost-efficient manner.

Pedigree information is also useful and we've found a number of correlations between DNA results and pedigree profiles. Similarly, certain performance and breeding data have strong DNA related correlations.

This has allowed us to develop databases that can relatively predict some genetic characteristics, even in the absence of DNA tests. However, even taking this into consideration, there are numerous instances where "on-paper" information can't predict genetic status or outcomes in the thoroughbred.

Principal Co-ordinate Stamina Cluster (see page 70 for explanation)



Inbreeding is also the best way of fixing consistent useful genetic characteristics, but only if you can avoid duplication of the less desirable ones

Genetic data and DNA analysis is used to follow the inheritance of actual genes and genetic markers of importance.

Following extraction of DNA from blood or hair samples, we employ a series of DNA tests and genetic data to help co-ordinate, fix or identify genetic combinations that support common speed, stamina and precocity objectives – helping to produce or select horses that are complete, targeted and uniform packages assembled to do specific racing jobs with higher levels of success.

Which genetic assessments are employed?

From available evidence in horses and humans it's obvious that athletic performance is controlled by multi-gene complexes, not just single genes.

Generally, we don't believe that single gene approaches for the selection and breeding of horses are appropriate. It could lead to the overlooking of other useful genes, loss of genetic health and, for instance, breeders shying away from using certain stallions with genotypes perceived to be associated with unfashionable characteristics such as extended stamina.

Relatedness / cluster analysis: Using 750 selected primary DNA markers we graphically cluster horses into relatedness, precocity and stamina groups with known animals in our databases.

For example, use of this analysis on a mare gives us an accurate idea of whether she carries an adapted or mixed batch of genes and if she is likely to produce stamina or speed-orientated progeny.

This gives us a better indication of how to fix co-ordinated stamina genes and identify suitable crosses for her.

It's almost like an accurate molecular dosage system. This type of information enables us to genetically recalibrate pedigrees for more accurate study.

In the graph on page 69 we can see the assessed mare (red triangle) compared with a large number of good quality horses of varying stamina and precocity leanings. A useful comparison can be made with mares of known, similar genetic status (pink circles).

For new mares, comparison with those that have already produced runners allows us to see which sires have been producing the best results with similar mares.

Determination of inbreeding levels - heterozygosity and homozygosity: A better indication of the level of inbreeding in a particular horse is provided by use of multiple marker DNA analysis to measure gene duplication. This was one of the first tests we employed back in 2000.

Substantial data has been collected from this and some strong correlations have been observed with various breeding and performance traits. Inbreeding leads to an increase in homozygosity (gene duplication).

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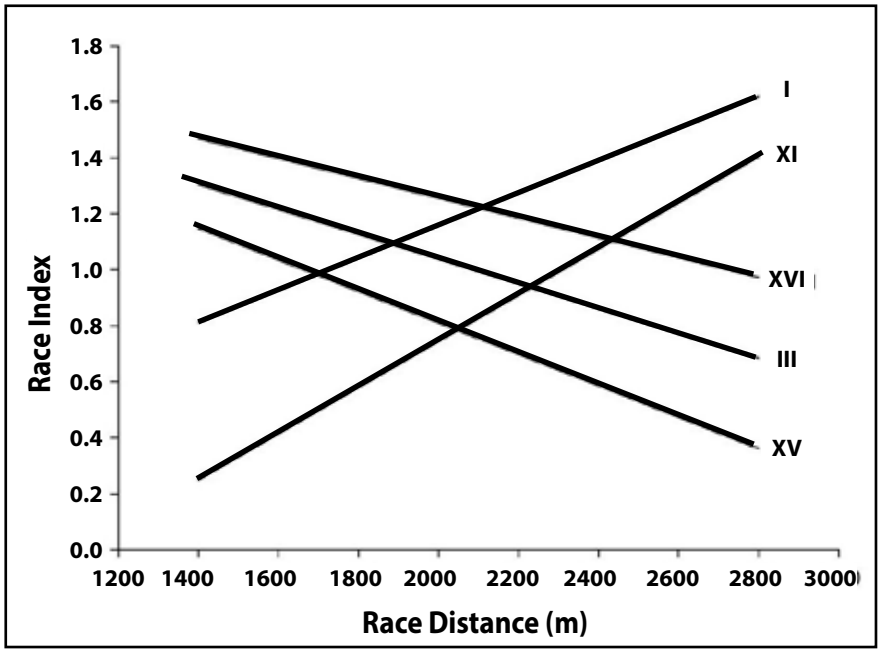
Using DNA markers we have been able to determine that there is an optimum amount of gene duplication that occurs in the best performers and breeders. This varies depending on whether we are talking about stayers or sprinters – the former being more outbred.

A pedigree might indicate that an animal is inbred whereas often the converse exists and vice versa. We believe that inbreeding is beneficial, but only when applied under the right circumstances.

Through use of DNA assessment, we can obtain a clearer picture of how close this can be carried out and whether it should be avoided or increased. It's more accurate to use a DNA sample to determine this, but we've also collected DNA data that allows more accurate prediction of on-paper pedigree inbreeding.

Assessment of respiratory/energy release genes: As first described in our 2006 academic paper*, which links specific genes to racehorse performance, we analyse transmission of eight mitochondrial (structures within cells that convert the energy from food into a form that cells can use) genes, including the important ATPase6 gene.

These genes form part of three muscular



energy-release complexes. Strong stamina and performance correlations exist with the varying gene versions carried by different horses.

From this it is possible to derive DNA-based stamina indices, which have important application to all areas, including breeding and training.

Many stallions also produce better progeny when crossed with mares from specific mitochondrial gene groups. Databases can give indications of which stallions are better used with specific mares and also of the likely effect on the stamina of the progeny.

This is not something that can be derived from a normal pedigree. This is a type of complex "nicking" based on actual genes rather than pedigree and can be refer to as mitochondrial or molecular nicking.

Because we've classified so many horses using mitochondrial DNA, we can identify most family lines and can now do this straight from the pedigree without sampling genetic material.

The graph opposite is taken from a 2006 research publication* and illustrates the correlation in Racing Index with racing distance for five different genetic types of horse.

So how can breeders use this information?

Breeding and progeny: The three DNA test areas listed above make up the panel that we call "EQ Profile".

Applying the tests to mares enables us to determine how genetically variable they are and whether they have particular aptitude strengths that should be re-enforced.

A weighted genetic scoring system has been developed that allows us to provide

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a selection of stallions that will produce offspring that are more adapted, have better genetic fixation and are less genetically variable.

Similarly, application of the tests to existing racing or young stock will tell us how their genetic status will affect racing, aptitude, performance and breeding potential. As far as the northern hemisphere is concerned right now is a busy time of year.

Sales: Sales-specific computer databases have been produced and they score sales lots based on trends viewed from years of DNA testing.

A weighted scoring system classifies animals on a number of factors, including respiratory gene grouping, sire complementation of dams from specific mitochondrial groups and potential inbreeding.

Animals get an overall score for genetic status and racing merit together with distance indices for a range of distances.

Return of Mares: These genetic assessments can be applied to a study of the reproduction records for first and second-season sires.

This has particular application to the winter foal sales. This provides a highly effective tool for early identification of the freshman sires most likely to produce better two-year-old and three-year-old progeny, allowing better pin-hooking selection of foals and prediction of stud-fees.

For example, it is possible to provide genetic scores for all of the potential progeny of new sires with two-year-olds due to run in a coming season. In conjunction with scores for the foal sales, this helps to identify the best pin-hooking or investment opportunities. It also provides us with an indication of the best commercial sire opportunities for future breeding seasons.

Training & Racing: Using our extrapolated and/or actual DNA tests, it is possible to provide owners and trainers with advice on likely optimum racing distances and help in the planning of racing strategies.

www.thoroughbredgenetics.com

***Stephen Paul Harrison & Juan Luis Turrion-Gomez, 2006. Mitochondrial DNA: An important female contribution to Thoroughbred racehorse performance.**