Inbreeding and inbreeding depression: new views from a genomic perspective

Johann Sölkner, University of Natural Resources and Life Sciences, Vienna
johann.soelkner@boku.ac.at

Breeding true to a particular phenotype and careful use of pedigree information have been of key importance in horse breeding since the publication of the first General Stud Book by James Weatherby in 1791. A mix of careful line breeding to important ancestors, increasing inbreeding levels of line bred individuals, and general avoidance of inbreeding otherwise has been practiced in many horse breeds. Breeders know how to calculate inbreeding levels from pedigree information and they use this information in their mating decisions. Pedigree inbreeding coefficients of full sibs are identical because they are calculated from the occurrence of common ancestors shared between their parents. In reality, the inbreeding coefficients of full sibs are not identical because the parents transmit different subsets of their genomes to each offspring.

The ability to visualize what particular parts of the parental genomes have been transmitted to offspring with high throughput genotype (SNP chip) data provides the opportunity to get a much more accurate estimate of the level of inbreeding of an individual. It is also possible to see which particular parts of the genome of an animal have received identical ancestral information from both parents. This presentation introduces the concept of runs of homozygosity for calculation of inbreeding levels of individuals from SNP chip data and compares this information with pedigree inbreeding.

Inbreeding depression is an indication of the reduced fitness of a population due to mating of related individuals. Inbreeding negatively affects individuals mostly due to genetic mechanisms called dominance and overdominance. The improved calculation of inbreeding levels with genomic data also allows better understanding on the effects of inbreeding depression. Genes causing inbreeding depression can be found. This is interesting scientifically because it adds to our knowledge of biology. In practice recessive disorders, which are part of inbreeding depression, can be systematically avoided by genotyping breeding animals and not mating individuals that are both carriers of genetic variants causing a particular recessive disorder.

Genomics has brought a new set of tools to horse breeders, very helpful when making mating decisions at a rather cheap price. They should be used, in my opinion