



Reproduction as engine enhancing food security and sustainability

R. Kasarda

Department of Animal Genetics and Breeding Biology, Slovak University of Agriculture in Nitra
Tr. A. Hlinku 2, 94976 Nitra, Slovak Republic

Today's agriculture is faced with many "non-standard" impacts. Some of them have its demographical evidence, others are close to conspiracies. All of them are covered in to one topic "Food security and safety". Most often discussed topics are related to use of biotechnologies in reproduction and genetics, especially issue of GMO, use of genomics and request of sustainable development. Expected growth in global human population, recalculated so many times, but generally speaking, from present 6 billion to 8 bill. in 2020 or up to 9 bill. in 2050 (*United Nations. World Population Prospects, 2002; Nelson et al., 2010*) are emerging argument of increased intensity of agriculture production, ability to produce in less fertile areas, or in development (breeding) of species surviving in such areas even arid parts of the World. We can see increased demand for food sources in most rapidly growing regions. Even in Asia, part of the World's traditionally vegetable based diet, under social development, request for milk, milk products (butter, cheese, yogurt, ..), meat as well as cereals is rapidly increasing. Expected increase of meat production in USA and EU will sustain in present tendency, high increase is expected in China and "developing" world. To the 2020 meat consumption on China will reach 100 mill. ton an in developing world up to 200 mil. ton of meat. Same tendency is expected in milk (milk product) consumption with increase up to 150 mill. and 400 mill. ton in China and developing world, respectively (*UNDP, 2006; FAO 2006*).

From view of traditional breeding we can see higher importance of fertility of animal populations in present and their presence with higher economic value in selection indices. More than before reproduction technologies are discussed to help fulfill demand on food of animal origin. We know today, that orientation solely on production traits brought us in some breeds (populations) of reproduction loss and significant economic expenses of restoring fertility. Insemination as first of broadly used and accepted biotechnologies helped us to fast forward with response in selection in conventional breeding, on the other hand having some inherent limitations due to increase of inbreeding and inability to isolate desirable and undesirable traits. We can state that embryo transfer, cloning or trans-genesis could solve present problems in reproduction and ensure production of animals for desired purposes. But then, specific aspect comes as important issue – public opinion or if you want consumer preferences. Issues of cloning and trans-genesis are in contradiction to clerical or publically accepted ethics.

This aspect is one of most important in present agriculture. Consumer doesn't see that in 1940 one farmer was able to feed only 19 people by its production ability. Today one farm produces food enough for 155 people. No one knows the story, that due to population growth, as well as energy demand and limitation in fossil sources, we produce enough food even using soils not suitable for other purposes (grain production), from materials not suitable for human nutrition, crop residues and by-products from

industry (fiber). These are result of selection, breeding and technological development. Public doesn't understand issues of culling as part of selection of animals better adapted to present technology, they don't understand uniqueness of rumen function and that feeding of by-products is safe and welcome in production process, because saving legumes and cereals, they don't understand that all this is made with one aim to feed growing global human population.

Consumers doesn't see these, they think we are on the wrong track, that produced food does contain suspicious ingredients, that due to mass production it is contaminated and even more that animals under conventional breeding are hurt. That we are wrong and only profit is of our interest. We are responsible for so called "civilization" as obesity and cardiovascular illnesses (*Edelman Insights*, 2012).

Positive influence of genetic on productivity is well proved. Today we don't doubt that phenotype is just result of genetic and environmental factors. We are aware of tools like animal recording, estimation of breeding values, selection tools and mating strategies to push desired population in direction of wish.

Many of the molecular genetic experiments have proved existence of favorable alleles inducing better results in reproduction of all farm species (*Trakovická et al.*, 2006). "Sires of today" (*Alta Genetics*, 2014; *Semex*, 2014) are genetically marked for favorable production traits (CheeseMakers, GenoMax) as well as reproduction traits (Concept+, Repromax, Immunity+). Challenge of today is to identify loci with effect of functional traits as birth difficulty, embryo survival (*Candrák et al.*, 2014) and others increasing longevity of individuals. These are the traits of interest today, because of economic impacts on agriculture branch effectiveness.

Strategic issues solved in our research are to develop tools for breeding value estimation in dairy cattle as well as tools for estimation of breeding values of functional length of production life. Tools and research is based on official milk recording system running in Slovakia under gesture of Breeding Services of Slovak Republic s. e. Those subjects have long, now we can say 20 years old history by us. Even not very well known, due to this we have been first country in the world (*Candrák et al.*, 1997) using test-day animal model under commercial conditions. On the other hand, we are proud having people like G. Mészáros, who was developing tools in breeding value estimation of fLPL for population of Pinzgau cattle in Slovakia (*Mészáros et al.*, 2008), than preparing and consulting of system for the whole dairy cattle population and finally future development of method to the full animal model (*Mészáros et al.*, 2013). Length of productive life was analyzed by the use of methodology of the survival analysis. Studied fixed effects were the herd and year of calving, relative milk production, parity and stage of lactation, herd size change, age at first calving. The results for fixed effects in both models (sire vs. animal) were comparable. In separate models two genetic effects were considered: the sire of the cow and the animal itself with the corresponding pedigree records. The heritability estimates from the two models were different: $h^2=0.08$ for sire model and $h^2=0.11$ for the animal model. As the animal model accounts for all relationships in the population, including those between cows, it is the favorable alternative for a genetic evaluation. It is also a pre-requisite for a potential total merit index for Slovak Pinzgau cattle, where breeding values for functional length of productive life could play a decisive role when accounting for the functional traits. In present research accent is given to development of tools for other functional traits, mainly connected with reproduction.

In the field of diversity (sustainability) protection, we are not only concerning on traits of interest but also developing tools for monitoring and managing population for

future use. Intra-population diversity is an important part of the global diversity of farm animals. To prevent deterioration of genetic diversity, minimizing inbreeding in small populations is of prime importance.

Main cattle (Holstein, Simmental, Pinzgau) and horse (Hucul, Lipizan, Shagya-Arab, Slovak sport pony) breeds in Slovakia have their present status defined (Kadlečík *et al.*, 2011, 2012; Pjontek *et al.*, 2012; Pavlík *et al.*, 2014). Determination of genetic variability based on pedigree information in Slovak Spotted breed was made based on pedigree completeness, characteristics based on probability of identity by descent and gene origin. The level of inbreeding it's gain per generation and relatedness were low, under 1%. The average value of relatedness coefficient in reference as well as in the whole pedigree file was higher than inbreeding coefficient. Therefore it is assumed that number of inbred individuals will increase in the next generation. The analysed horse populations consisted of 656 Hucul horses, 2052 Lipizan horses, 1951 Shagya Arabian horses and 220 Slovak Sport Ponies. The pedigree completeness of the reference population was evaluated for each animal based on the number of fully traced generations, the maximum number of generations traced and the equivalent complete generations. The equivalent complete generations ranged from 4.93, for the Slovak Sport Pony, to 10.25, for the Lipizan horses. The average value of inbreeding ranged from 2.67%, for the Slovak Sport Pony, to 6.26%, for the Hucul horses. The average relationship coefficients were from 3.08%, for the Shagya Arabians, to 9.34%, for the Huculs. Individual increases in inbreeding ranged from 0.43 %, for the Lipizans, to 1.06%, for the Huculs, while the realised effective sizes were from 117.14 to 47.67 animals. The analyzed populations were derived from 80 to 499 founders. The effective number of founders ranged from 26 to 160, while the effective number of ancestors was from 7 to 32. There is increased demand for sustain monitoring of populations of "genetic preserves". In particular, mating program with control of inbreeding in horses is under development in experimental horse population. Optimization of breeding plans according sustainability, includes systems of breeding value estimation, pedigree structure development as well as estimation of expected genetic improvement (Kasarda *et al.*, 2004, 2007, 2014). It has been shown that increasing the number of sires to breed sires results in decreased response to selection in all alternatives. At the same number of sires a *MOET* schemes yield the highest gain but also highest inbreeding. When restricting the rate of inbreeding to a value between 0.5-1 % per generation the highest gain was obtained by using five progeny tested sires per year under young sires breeding scheme design. Observed was inbreeding depression -39.60 SKK (1€ = 30.128SKK) of SPI, -8.95 kg in EBV of milk, -0.37 kg in EBV of fat and -0.36 kg in EBV of protein, respectively. We simulate scenarios of possible development in population when constraining inbreeding further. In classical approach a maximum avoidance of inbreeding (MAI) mating strategy is used and compared with a random mating alternative. The parameters of the simulation were based on the structure the Slovak Pinzgau active population of 2868 animals (930 purebred cows). Simulated was selection under a total merit index (TMI) covering the milk production, functional LPL and the live weight breeding value estimation results. The heritability of TMI ($h^2 = 0.09$) was estimated using a REML single trait animal model. Alternatives were build respecting theoretical assumptions of a closed population structure, fixed number of mating per parent, and equal use of sires in insemination. Animals in generation 0 were set as founders without pedigree information. In separate simulation runs, the number of sires of sires varied with 40 dams of sires in all cases. The sex ratio of the offspring was assumed to be 50/50 male/female. Minimum ten (due to achievement of Bulmer

equilibrium) to twenty consecutive generations were simulated for both random and maximum avoidance of inbreeding. Simulation results showed that the use of a maximum avoidance of inbreeding mating strategy would lead to significantly decreased rates of inbreeding while maintaining suitable levels of genetic gain in the Slovak Pinzgau population.

REFERENCES

- Edelman Insights (2012). Field to Fork 2012: Consumers Feel America's Approach to Food Production Is on the Wrong Track [on-line]
<http://www.edelman.com/insights/intellectual-property/field-to-fork/>
- United Nations (2003). World Population Prospects. The 2002 revision [on-line]
<http://www.un.org/esa/population/publications/wpp2002/WPP2002-HIGHLIGHTSrev1.PDF>
- Nelson et al. (2010). Food security, farming, and climate change to 2050 : scenarios, results, policy options. IFPRI research monograph. ISBN 978-0-89629-186-7
- UNDP, 2006 World agriculture: towards 2030/2050 – Interim report. Rome. [on-line]
http://www.fao.org/fileadmin/user_upload/esag/docs/Interim_report_AT2050web.pdf
- FAO (2006). The state of the Food Insecurity in the World. Report. Rome.
- Trakovická et al. (2006). Analysis of polymorphism of ESR gene of pigs by use of PCR-RFLP. Acta fytotechnica et zootechnica. 9. 18-19.
- Alta Genetics (2014) [on-line] www.altagenetics.com
- Semex (2014) [on-line] www.semex.com
- Candrák et al. (2014) DNA analyses of cows in Slovak republic... (in Slovak). [on-line]
http://www.holstein.sk/domain/holstein/files/infomagazin/Miniinfo%20April%202014_web.pdf
- Candrák et al. 1997. The use of test-day model for Slovak cattle populations. In: Proc. 48th Annual Meeting of the European Association for Animal Production, Vienna, Austria, August 25-28.
- Mészáros et al. (2008). Evaluation of breeding value for functional length of productive life in Slovak Pinzgau cattle. Arch. Tierzucht, 51. 5. 438-448.
- Mészáros et al. (2013). Analysis of longevity in the Slovak Pinzgau population - extension to animal model. Czech Journal of Animal Science. 58. 7. 289-295.
- Kadlečík et al. (2011). Pedigree analysis of Slovak Pinzgau breed . Agriculturae Conspectus Scientificus. 76. 3. 165-168.
- Kadlečík et al. (2012). The assessment of genetic diversity and analysis of pedigree completeness in purebred Slovak Spotted cattle. Acta Agriculturae Slovenica. 100. 3. 131-135.
- Pjontek et al. (2012). Pedigree analysis in four Slovakian endangered horse breeds Czech Journal of Animal Science. 57. 2. 54-64.
- Pavlík et al. (2014). Joint genealogical analysis as a tool for diversity evaluation in Pinzgau cattle populations. Archiv Tierzucht. 57. 14. 1-12.
- Kasarda et al. (2004). Genetic gain, increase in inbreeding rate and generation interval in alternatives of Pinzgau breeding program. Czech Journal of Animal Science. 49. 12. 524-531.
- Kasarda et al. (2007). An economic impact of inbreeding in the purebred population of Pinzgau cattle in Slovakia on milk production traits. Czech Journal of Animal Science. 52. 1. 7-11.

Kasarda et al. (2014). Influence of mating systems and selection intensity on extent of inbreeding and genetic gain in the Slovakian Pinzgau population. *Czech Journal of Animal Science*. 59. 5. 219-226.

Corresponding author:

doc. Ing. Radovan Kasarda, PhD

Department of Animal Genetics and Breeding Biology

Slovak University of Agriculture in Nitra

Tr. A. Hlinku 2, 94976 Nitra, Slovak Republic

E-mail: Radovan.Kasarda@uniag.sk