

Smarter

SMALL Ruminants breeding for Efficiency and Resilience

Climate change threatens to have severe meteorological, biological and thereby societal effects. We who work in agriculture have to ensure safe food supply for the ever increasing human population under increasingly deteriorating environmental and production conditions, while we also have to strive to manage our resources sustainably and to conserve biological diversity. Since conservation of the genetic diversity of our animal stock is one of the key objectives of both present and future, it is worthwhile for livestock farmers to utilize scientific results in the course of their work.

The genetic makeup and genetic structure of species and varieties as well as their reactions to local environmental conditions are as yet little known, even though they may contain genetic variants that may prove valuable from the aspect of adaptation to changing environmental conditions and various diseases.

Within the framework of the SMARTER project we have had the opportunity to study the genetic diversity of Hungarian and related sheep varieties (the latter living in present-day Romania) using so-called SNP chips, a state-of-the-art tool providing a vast amount of analysable information. The majority of these varieties had not been examined using these tools.



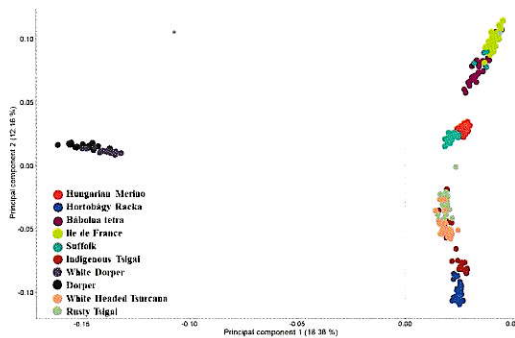
COUNTRY	VARIETY	NUMBER OF INDIVIDUALS
Hungary	Indigenous Tsigai	28
	Hungarian Merino	29
	Dorper	21
	White Dorper	20
	Bábolna Tetra	27
	Île de France	27
	Suffolk	20
	Hortobágy Racka	28
Romania	Rusty Tsigai	30
	White-Headed Tsurcana	30
TOTAL		260

In the course of our analyses we also determined the so-called inbreeding coefficients of the sheep populations studied, which indicated that in the case of certain varieties – such as Dorper and White Dorper – inbreeding depression can be a concern, whereas the inbreeding levels of the indigenous Tsigai, Suffolk and Hortobágy Racka varieties can be considered moderate. Examination of the genetic structure of the varieties showed that the major part of all genetic differences observed exists within the

gene pools of the varieties, and there are much fewer differences that are dependent only on which variety the individual studied belonged to. This result indicates that breeders have broad opportunities for selection within varieties and populations.

Phylogenetic analysis examining the lineages of varieties or populations revealed structuredness, which is statistically confirmed. In other words, the majority of the varieties were well separable from each other and were not characterised by genetic mixing.

Based on a statistical procedure that serves for classification according to genetic characteristics using principal component analysis, we established that Dorper and White Dorper, the two varieties established under tropical conditions and introduced only recently to Hungary are completely separate from the other varieties. On the other hand, the varieties that have long been present in the Carpathian Basin (Indigenous Tsigai, Hortobágy Racka, Rusty Tsigai and Tsurcana) form another group separate from the other varieties included in our study but not indigenous to our region, i.e. Île de France, Hungarian Merino, Suffolk and Bábolna Tetra.



We trust we will have further opportunities in the future to continue building what has been started here within the framework of similar projects. This would serve the interests of all participants.



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