Gene organization of the TRG locus in *Equus caballus* as deduced from the genomic assembly

A. Caputi Jambrenghi[1], G. Linguiti[2], F. Giannico[3], R. Antonacci[4] and S. Massari[5]
[1]University of Bari – DiSAAT, Via G. Amendola, 165/A, 70126, Italy, [2]University of Bari, Department of Biology, Via E. Orabona, 4, 70126, Italy, [3]University of Bari – DiMeV, S.P. 62 per Casamassima Km 3, 70010, Italy, [4]University of Bari, Department of Biology, Via E. Orabona 4, 70126, Italy, [5]University of Salento, Department of Biological and Environmental Science and Technologies, Via per Monteroni, 73100, Italy; francesco.giannico@uniba.it

The domestic horse, *Equus caballus*, belongs to the Perissodactyla order, Equidae family, and Equus genus, which also includes zebras, and African and Asian asses. Since its domestication, humans have selectively bred horses for performance traits causing a drastic reduction of the wild population and the develop of multiple breeds with a wide range of phenotypic peculiarities. As a result, most horse breeds today are closed populations with high phenotypic and genetic uniformity of individuals within the breed, but with great variation between breeds. Many of the phenotypic traits found in breeds have been successfully mapped into genomic regions, facilitated by recent methodological advances in horse genomics. Taking advantage of the latest release of the genome assembly, we studied, for the first time in an organism belonging to Perissodactyla order, the horse TRG locus encoding the gamma chain of the γδ T cell receptor. The horse TRG locus spans about 1,130 kb, from AMPH and STARD3NL genes that flank this locus in all mammalian species studied so far. It contains 38 Variable (V), 23 Joining (J) and 16 Constant (C) genes organized in 16 V-J-C gene clusters, in tandem aligned in the same transcriptional orientation. The horse TRG results the locus with the greatest extension and with a significantly higher number of genes than the orthologous locus of the other mammalian species. However, despite the dynamic evolution of the horse TRG genomic region, our phylogenetic analyses show a tight relationship of the genes encoding the variable domain with those of other mammalian species, indicating that they have been preserved as a result of a strong functional constrain. The genomic organization of the horse TRG confirms the great evolutionary plasticity of the TRG locus among the different species and the important role of the gamma chain in the adaptive immune response.

Genomic predictions including unknown parent groups for milk traits in Portuguese Holstein cattle

A.A. Silva[1], D.A. Silva[1], P.S. Lopes[2], H.T. Silva[2], R. Veroneze[2], G. Thompson[3,4], J. Carvalheira[3,4] and C.N. Costa[5]
[1]FCAV-UNESP, R. Prof. P.D. Castellane, 14884-900 Jaboticabal SP, Brazil, [2]U. F. Viçosa, Av. P. H. Rolfs, 36570-000 Viçosa MG, Brazil, [3]ICBAS, U.Porto, R. J.V. Ferreira, 4050-313 Porto, Portugal, [4]BIOPOLIS-CIBIO, U. Porto, R. Padre A. Quintas, 4485-661, Vairão, Portugal, [5]Embrapa Gado de Leite, Rua Eugenio Nascimento, 36038-330 Juiz de Fora MG, Brazil; claudio.napolis@embrapa.br

In Portugal, the autoregressive test-day (TD) model for multiple lactations has been successfully applied to predict genomic breeding values (GEBV) in the national genetic evaluation. Missing pedigree information is a recurrent issue and the objective of this study was to compare the reliability and bias of GEBV predicted with ssGBLUP with and without unknown parent groups (UPG). The Portuguese Dairy Cattle Breeders Association provided a total of 12,982,057 TD records from the first 3 lactations of milk, fat, and protein yields, and somatic cell score (SCS) of Portuguese Holstein cattle. Data from 4,485 genotyped animals were used in ssGBLUP including a total of 35,970 SNPs. To evaluate the impact of UPG on the prediction ability, the validation population included more than 860 cows and 160 bulls (>19 daughters). The bulls and cows' pseudo-phenotypes (DYD and YD) predicted in the full data set (records up to 2021) were regressed on the GEBV predicted in the reduced data set (with records truncated at 2017) for all traits. The use of UPG in the pedigree relationship led to better regression coefficients, therefore, less bias. For bulls, the b1 values with UPG (without UPG) were 0.83 (0.73) for milk yield, 0.7 (0.49) for fat yield, 0.86 (0.65) for protein yield, and 1.07 (1.02) for SCS. For cows, these values were higher than 0.85 in both approaches, probably due to the larger amount of information available for them. For bulls, the validation reliability values were 0.44 (0.38) for milk yield, 0.30 (0.20) for fat yield, 0.40 (0.30) for protein yield, and 0.42 (0.41) for SCS, respectively. The increases up to 0.10 in bull reliability achieved by fitting UPG shows the importance of including this step in ssGBLUP. In conclusion, genomic predictions for milk related traits in Portuguese Holstein cattle using ssGBLUP were more reliable and nearly unbiased when using UPG.