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## Description of the French genomic evaluation approach

Pascal Croiseau, Chris Hoze, S. Fritz, F. Guillaume, Carine Colombani,  
Andres Legarra, Aurélia Baur, Christèle Robert-Granié, Didier Boichard,  
Vincent Ducrocq

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**Accuracy of genomic predictions using subsets of SNP markers in dual purpose Fleckvieh cattle**

*Gredler, B.<sup>1</sup>, Anche, M.T.<sup>1</sup>, Schwarzenbacher, H.<sup>2</sup>, Egger-Danner, C.<sup>2</sup> and Sölkner, J.<sup>1</sup>, <sup>1</sup>University of Natural Resources and Life Sciences Vienna, Gregor Mendel Str. 33, 1180 Vienna, Austria, <sup>2</sup>ZuchtData EDV-Dienstleistungen GmbH, Dresdner Str. 89/19, 1200 Vienna, Austria; birgit.gredler@boku.ac.at*

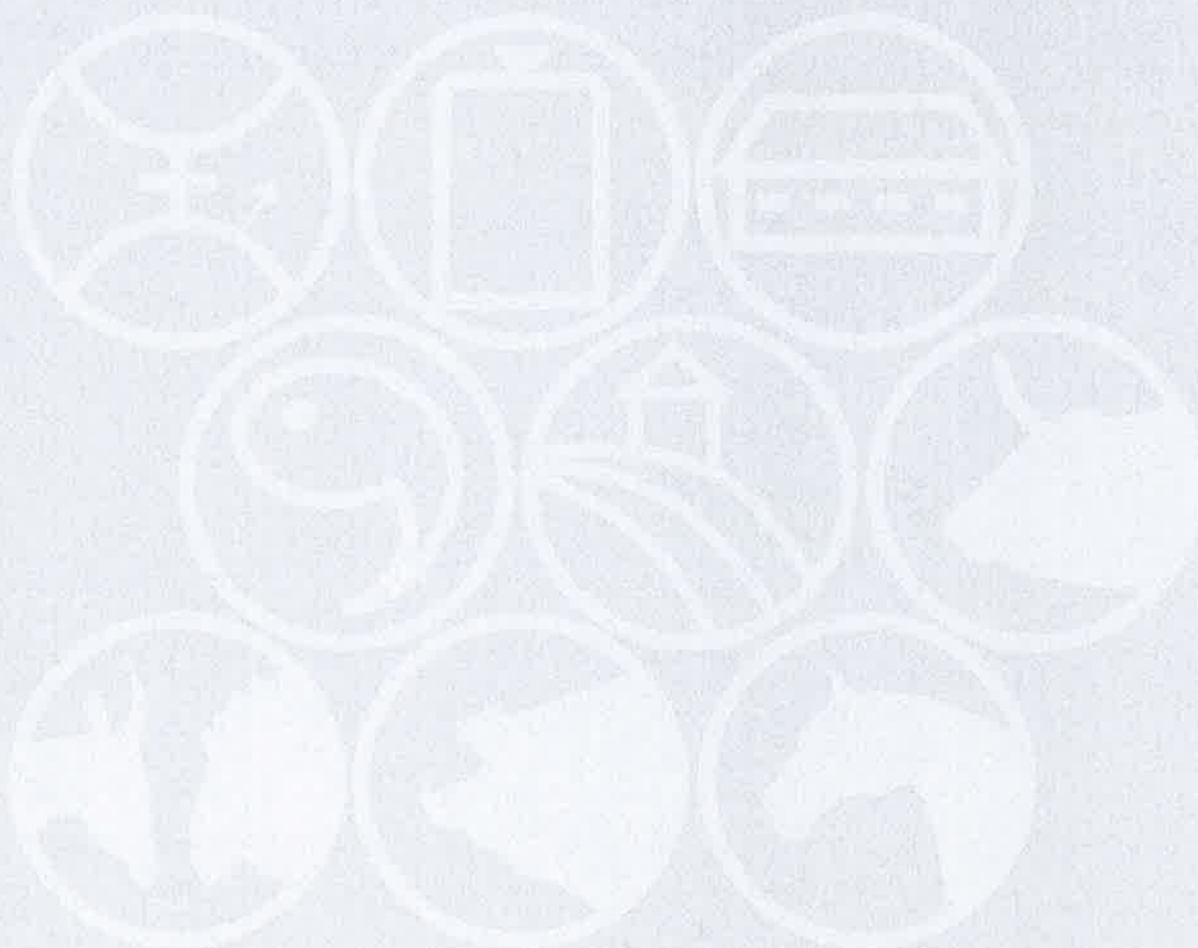
SNP-selection strategies to generate subsets of SNP were evaluated for estimation of direct genomic breeding values (DGV) in dual purpose Fleckvieh cattle in Austria and Germany. 5,556 Fleckvieh bulls genotyped with the Illumina Bovine SNP50TM Beadchip were used in the analysis. The reference set consists of bulls born before 2003 and the validation set of bulls born 2003 to 2006. The full set of SNP contained 41,008 SNPs. DGV were estimated using SNP-BLUP and BayesB methodology. De-regressed breeding values of the traits total merit index, milk yield, fat percentage, protein yield, length of productive life, female fertility, male calving ease and somatic cell count were used as dependant variables in genomic predictions. The 100, 300, 500, 1,000, and 3,000 most influential SNP were selected according to their absolute size of the estimated regression coefficient using the full set of 41,008 SNP estimated with BayesB. In addition, genomic predictions were performed using the SNP included on the Illumina GoldenGate Bovine3K Genotyping Beadchip. Furthermore, subsets of 5K, 10K, 20K, and 30K consisting of the Illumina 3K chip plus 2K, 7K, 17K and 27K randomly selected SNP, respectively, were used. Accuracy of direct genomic breeding values was calculated as the correlation between DGV and the estimated breeding values from routine genetic evaluations in Austria and Germany of bulls in the validation set. Results show that BayesB slightly out performed SNP-BLUP for almost all traits independent of subset of SNP. Using the Illumina 3K chip accuracies were in the range of 67 to 94% of the accuracies achieved using the full set of SNP for all traits applying BayesB. Highest accuracies were always achieved with the full set of SNP. However, accuracies of some combinations of traits and subsets of SNP were close to the full set results.

**Description of the French genomic evaluation approach**

*Croiseau, P.<sup>1</sup>, Hozé, C.<sup>1,2</sup>, Fritz, S.<sup>2</sup>, Guillaume, F.<sup>3</sup>, Colombani, C.<sup>4</sup>, Legarra, A.<sup>4</sup>, Baur, A.<sup>2</sup>, Robert-Granié, C.<sup>4</sup>, Boichard, D.<sup>1</sup> and Ducrocq, V.<sup>1</sup>, <sup>1</sup>INRA, UMR1313, GABI, Domaine de vilvert, 78352 Jouy en Josas, France, <sup>2</sup>UNCEIA, 149 rue de Bercy, 75595, Paris, France, <sup>3</sup>Institut de l'élevage, 149 rue de Bercy, 75595, Paris, France, <sup>4</sup>INRA, UMR631, SAGA, Chemin de Borde Rouge, Auzeville, 31320 Castanet-Tolosan, France; pascal.croiseau@jouy.inra.fr*

Worldwide, a large panel of genomic evaluation methodologies has been proposed and compared. When reference populations of adequate size are used, these methods appear to lead to similar accuracies of prediction of future bull's performances. However, computing requirements and time may be different, to such an extent that some of the better methods cannot be applied routinely. In France, a strong experience on Marker Assisted evaluation and Selection (MAS) has been accumulated over the last decade. A major advantage of MA-BLUP used in MAS is that the size of the mixed model equations system is manageable and computing requirements are limited. To build on this experience, a genomic evaluation methodology was developed to combine SNP corresponding to large QTL detected via Linkage Disequilibrium and Linkage analysis (LDLA) or by other genomic selection approaches such as Elastic-Net (EN) or Sparse PLS. Different scenarios were compared for a set of 1172 progeny tested bulls from the Montbéliarde breed. The 222 youngest ones formed the validation population. For six different traits – milk and protein yield, rear udder width, height at sacrum, conception rate and somatic cell counts – the correlations between the predicted and observed phenotypes (daughter yield deviations) were calculated. A MA-BLUP including 400-500 QTL detected by LDLA or by EN and followed by haplotypes of 3-5 SNP provided the best correlations. This leads to computation times of genomic evaluations which are less sensitive to future increases in number of animals or SNP chip densities. This approach has been routinely applied for genomic evaluations in the French Holstein, Montbéliarde and Normande breeds since June 2010.

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