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Integration of genomic information into genetic evaluation model :
application in the multi-breed French dairy goat population

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The rapid evolution in sequencing and genotyping raises new challenges in the development of methods of selection for livestock, also called genomic selection. With this genomic information, it is now possible to estimate breeding values of selection candidates at birth without waiting for phenotypic data collection. Genomic selection requires the creation of a reference population made of genotyped animals with precise phenotypes. Genomic evaluations consist in predicting phenotypes in this reference population as the sum of molecular markers. The main methodological challenge is the large number of effects to estimate, usually much larger than the number of available phenotypes. We briefly describe and compare the various families of proposed methods: genomic BLUP (Best Linear Unbiased Prediction) based on relationship computed from marker information, Bayesian methods, variable selection methods and a single step approach which combined pedigree and genomic data and raw phenotypes. The precision of genomic selection is done via cross validation among the youngest animals of the reference population. Several parameters (size of the reference population, relationship between selection candidates and the reference population, genetic parameters of traits analysed, etc) have a significant impact on the efficiency of genomic selection methods. An application on French dairy goat data will be presented. This population consists in 852 males from Alpine and Saanen breeds recently genotyped with 50k chip and born between 1993 and 2011. This population consists of two breed and has different genetic parameters. We then compare the effect of three models (multiple trait model ; one model for each breed or one model combining data for the two breeds) on the efficiency of genomic selection. Traits studied are five milk production traits: milk yield on a lactation (kg), fat and protein yields (g/kg) and fat and protein contents (g/kg); somatic cell score (SCS) and five type traits recorded by scores: udder floor position, udder shape, rear udder attachment, fore udder, teat angle. For milk production traits, 4 178 315 Alpine performances and 3 173 516 Saanen performances of females born between 1970 and 2012 were recorded. Pedigree used consisted in 2 981 809 animals considering up to 29 generations for males and 41 generations for females.