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Are genomic evaluations free of bias due to preferential treatment?

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Genomic evaluations now are an essential tool for animal breeding. While young bulls were the initial target, an increasing number of females (both heifers and cows) are been genotyped. Classical genomic evaluations are based on reliable averaged performances of bull's daughters. An incoming issue in the 'genomic world' is whether own performances of females genotyped or present in the pedigree of genotyped animals should be explicitly included in the evaluations. Whereas performances of a bull dam has limited impact on the index of her progeny-tested son, the impact of an own performance on the index of a genotyped cow is much more important. Several countries using genomic selection chose to discard or to correct yield deviations (YD) – i.e., the own performances of cows – from genomic evaluations. The purpose of the study is to assess the impact of including YD in the genomic evaluation model. The 3 main French dairy breeds (Holstein, Montbéliarde, and Normande) were considered. Two traits were studied: milk production (kg), which is the trait most susceptible to preferential treatment and somatic cell count (SCC) which is among the less susceptible ones to such a bias. Data consisted of 2 different groups: 29,701 elite females genotyped by breeding companies and 7,314 cows genotyped in a research project (and considered as randomly selected among the national population). 2 different genomic evaluations were performed, one only included DYD (daughter yield deviations) of proven bulls, and another model including both YD for females, and corrected DYD for males. Correlations between breeding values from evaluations with or without YD were lower for elite females compared to random cows. For elite dams, the average difference between breeding values (including YD or not) was significantly different from 0. To conclude, genomic evaluations may be biased when explicitly including own performances of elite females.