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Genomic selection in a purebred pig breeding scheme: a simulation study

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HAL Authorization

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Stochastic simulation was used to compare the efficiency of 3 pig breeding schemes based on traditional or genomic evaluations. The simulated population (1,000 females, 50 males) was selected during 10 years for a synthetic breeding goal including 2 traits with equal heritability ($h^2=0.4$) and economic weights.

The reference breeding scheme (BLUP-AM) was based on BLUP-Animal Model evaluations and the phenotyping of 13,770 candidates per year for trait 1 and of 270 relatives per year for trait 2. Under the GE-1TP scenario, selection was based on genomic breeding values (GBV) estimated with one training population (TP) made up of candidate relatives phenotyped for both traits, whose number increased from 1,000 to 3,430 over time. Under the GE-2TP scenario, the GBV for trait 2 were estimated using a TP identical to that of GE-1TP, but the GBV for trait 1 were estimated using a large TP made up of candidates whose number increased from 13,770 to 55,080 over time. Concerning trait 2, GE-1TP and GE-2TP generated 125% higher reliabilities, and therefore respectively 116% and 84% higher average annual genetic trends than BLUP-AM. Concerning trait 1, GE-1TP generated 34% lower reliabilities and 37% lower annual genetic trends than BLUP-AM, whereas GE-2TP generated 80% higher reliabilities and 12% higher annual genetic trends than BLUP-AM. Consequently, GE-2TP was 29% more efficient in improving the global breeding goal than BLUP-AM, whereas GE-1TP was only as efficient as the reference scheme. At last, GE-1TP and GE-2TP reduced the inbreeding rate by 22% and 55%, respectively. In conclusion, genomic selection could substantially and durably improve the efficiency of pig breeding schemes, even for traits with currently limited phenotyping capacity resulting in small TP. Conversely, large TP are required to remain as efficient as traditional schemes for traits recorded on numerous candidates.