



## W404

## Genomic Selection in Forage Breeding: Designing an Estimation Population

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Time: 10:40 AM

Room: Esquire

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The benefits of genomic selection to livestock, crops and forest tree breeding can be extended to forage grasses and legumes. The main benefits expected are increase selection accuracy and reducing both costs per unit of genotype evaluated and breeding cycle length. Aiming at designing a training population, deterministic equations were used to estimate the impact of sample size (N individuals), effective population size ( $N_e$ ), number of markers per centimorgan ( $L_s$  per cM) and heritability ( $h^2$ ) on accuracy considering *Panicum virgatum* (switchgrass, genome size ~1,600 Mpb for 'Alamo' genotypes) as a model. Simulations were based on  $N_e = 50, 100$  or  $150$ ,  $L_s = 0.3, 3, 6, 10$  and  $20$  markers per cM and,  $N = 500, 2000, 6000$  individuals phenotyped and genotyped, or more. Trait heritability was considered as ranging from high (0.70) to very low (0.01). The selection method was based on individual selection. Taking the benchmark accuracy of traditional BLUP-based phenotypic selection ( $r \geq 0.80$ ) as a reference, accuracy for genomic selection was similar when  $h^2 \geq 0.4$ , using 20 markers per cM,  $N_e = 50$  and 6,000 individuals. As  $h^2$  increases, fewer individuals ( $\leq 2000$ ) and fewer markers (10 per cM) are needed to achieve the same accuracy. Low heritability traits ( $= 0.1$ ) can require 20,000 genotyped and phenotyped individuals, 20 markers per cM and  $N_e = 50$ . Considering the declining of genotyping costs, an expected reduction in generation time, and a potential increase in accuracy, genomic selection is a valuable new tool for use in forage improvement.

[Back to: Grasslands \(Lolium Genome Initiative\)](#)

[<< Previous Abstract](#) | [Next Abstract >>](#)

[Home/Search](#)

[Browse by Day](#)

[Browse by Type](#)

[Author Index](#)

[Exhibitor Index](#)

[Poster Categories](#)

[Personal Scheduler](#)

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