

Development and proof-of-concept application of genome-enabled selection for alfalfa biomass yield in Northern Italy: preliminary results

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In a previous study, alfalfa genomic selection (GS) for a Northern Italy genetic base displayed a predictive ability of 0.32 along with a predicted advantage over phenotypic selection (PS) (Annicchiarico et al. 2015), based on a training set of 124 parents undergoing genotyping-by-sequencing (GBS) and phenotyped according to 3-year biomass yield under limited supplemental irrigation of their half-sib progenies. This study provides a comparison of GS vs PS for the same genetic base in terms of actual genetic gain for biomass yield, envisaging three possible GS models, namely, rrBLUP and linear Support Vector Regression (SVRLin), which emerged as best statistical models in the earlier study, and rrBLUP restricted to 150 markers that displayed odd score > 1.5 in a GWAS. GS selected 18 parent genotypes out of 1536 belonging to the elite, widely-adapted landrace MSP017 from Northern Italy. Because of budget constraints, GS relied on GBS using half of the genotyping effort applied to the original training set, thereby reducing the available markers (from over 11000 to 6780) and the predictive ability of the actually adopted GS models. While rrBLUP and SVRLin issued correlated breeding values ($r = 0.89$) and shared 11 of the 18 selected parents, neither of them shared any selected parent with rrBLUP limited to GWAS-selected SNPs. PS implied the selection under limited supplemental irrigation of 18 parent genotypes out of 1776 plants of MSP017, using two stages of multi-year selection for biomass yield. The Syn-2 generation of the four synthetic varieties issued by GS or PS, the unselected landrace MSP017, and the recent reference cultivar Alfitalia were evaluated for two-year dry biomass yield in two growing environments represented by a rainfed (with 237 mm and 171 mm April-September rainfall in 2021 and 2022, respectively) and an irrigated (with additional 320 mm during the summer period of each year) water regime. We adopted a randomized complete block design with six replicates per environment, using 4.5 m² plots. Rainfed cropping halved the number of harvests relative to irrigated cropping (3 vs 6). However, genotype × environment interaction was not significant ($P > 0.10$), in agreement with the wide-adaptation target of producing phenotyping data for GS and performing PS under limited supplemental irrigation. GS based

Table 1: Two-year dry biomass yield across two water regimes of alfalfa experimental populations derived from three genomic selection (GS) models or phenotypic selection (PS), the reference landrace MSP017 (acting as genetic base), and the reference cultivar Alfitalia.

Material	Biomass yield (t/ha)
GS based on the rrBLUP model	5.72 a
GS based on SVRLin model	5.43 ab
Alfitalia	4.99 bc
Landrace MSP017 (genetic base)	4.97 bc
GS based on rrBLUP model using 150 SNPs from GWAS	4.97 bc
PS	4.47 c

Column means followed by different letters differ at $P < 0.05$ according to Duncan's test

on rrBLUP displayed a manifest yield advantage (>14.5%) over the unselected landrace, the elite cultivar Alfitalia, and GS based on rrBLUP limited to GWAS-selected SNPs (Table 1). GS based on SVRLin was somewhat less efficient but not significantly inferior to that based on rrBLUP. PS failed to improve biomass yield relative to the genetic base, despite its considerable investment in time and resources (Table 1).

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References

Annicchiarico et al. (2015) Accuracy of genomic selection for alfalfa biomass yield in different reference populations. *BMC Genomics* 16:1020.