The genetic gain pattern indicates additive gene effects control alfalfa stem fiber digestibility

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Abstract

Breeding for improved stem fiber digestibility could increase net digestible biomass yield. Two cycles of bidirectional selection for plants with low or high stem 16-h IVNDFD and low or high stem 96-h IVNDFD were carried out. The 96-h IVNDFD trait was highly heritable (H2 = 0.71) with a genetic gain rate of 5.05% per selection cycle. The patterns of continuous increase of stem fiber digestibility from each cycle of selection for high 16-h and high 96-h IVNDFD digestibility and a decrease in digestibility from each cycle in the low 16-h and low 96-h populations suggested that additive gene effects may control stem fiber digestibility. Divergent selection did not alter leaf to stem ratio nor other plant morphological traits. Selection for stem IVNDFD was a highly effective strategy for developing alfalfa cultivars with improved nutritional quality.

Introduction

Alfalfa stem digestibility is lower than that of leaves, but stems are the major portion of the herbage dry matter. Increasing stem digestibility will results in total digestible biomass yield.

In this study, two cycles of bidirectional selection were carried out for 16-h and 96-h IVNDFD of stems. The resulting populations were compared to the parental germplasm in field experiments in two locations over two years, harvesting plants at three maturity stages with four cuts per year. The objective of this research was to evaluate the effectiveness of a recurrent selection of stem fiber digestibility for improving the nutritional value of alfalfa. Specifically, the study aimed to: (i) measure the genetic gain of IVNDFD, detergent fiber components, and cell wall traits from two cycles of divergent selection; (ii) estimate the heritability of each trait; (iii) identify the changes in stem cell wall composition associated with altered IVNDFD.

Data Quality Control & Spatial Adjustment

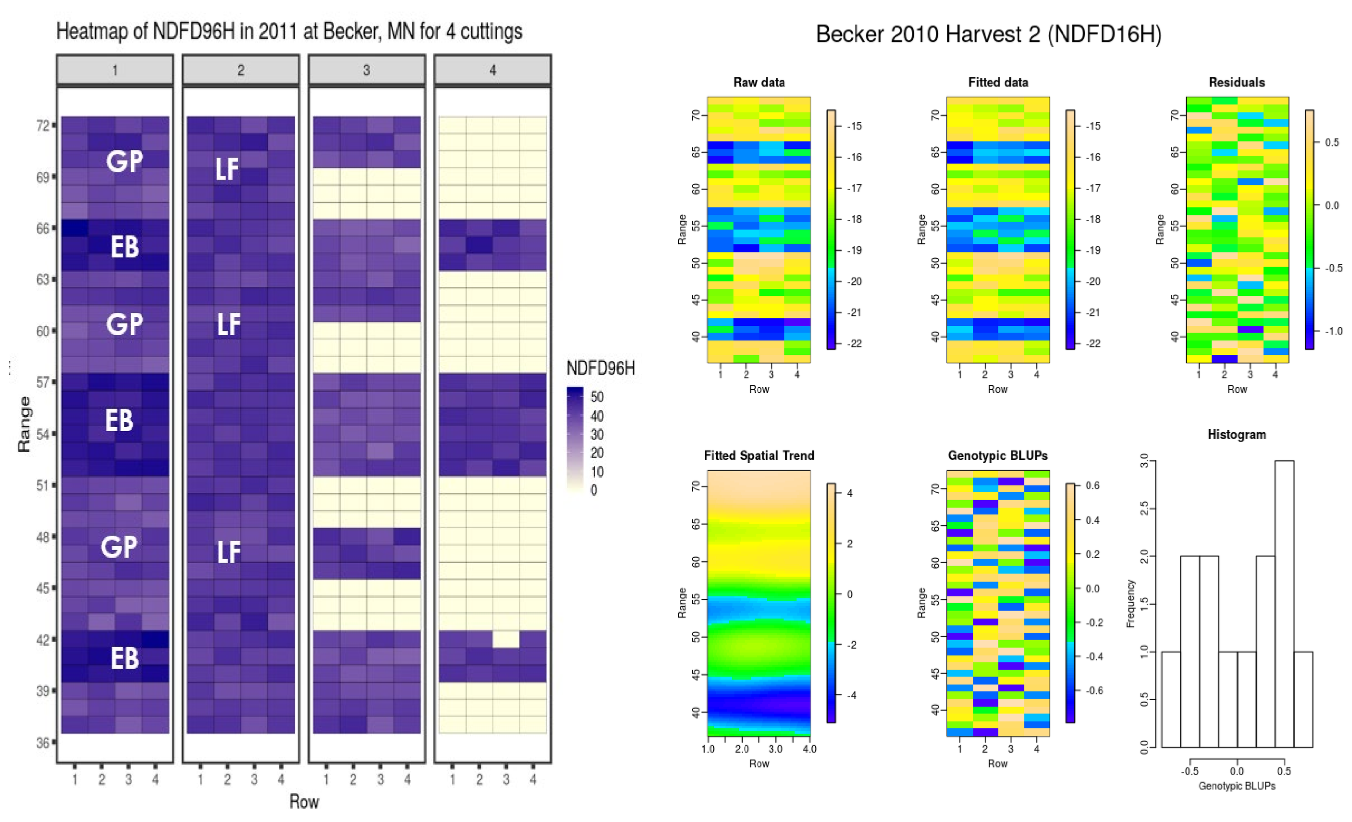

Fig 1. Digestibility raw data at three maturity stages (early bud, EB, late flowering, LF and green pod , GP), spatial adjustment, and their BLUPs

Materials & Methods

Table 1. Materials used for the study

Population Name	Cross type	Cycle number	Number of plants intermated
UMN3097	Parental	C0	
UMN3355	H16 x H96	C1	117
UMN3356	H16 x L96	C1	28
UMN3357	L16 x H96	C1	26
UMN3358	L16 x L96	C1	33
UMN4016	H16 x H96	C2	60
UMN4017	H16 x L96	C2	30
UMN4018	L16 x H96	C2	30
UMN4019	L16 x L96	C2	30

$$\textit{Genetic gain}(\%) = \frac{BLUP_{Cycle2} - BLUP_{Cycle1}}{BLUP_{Cycle1}} * 100$$

$$\textit{Broad Sense Heritability}(H) = \frac{\sigma_G^2}{\sigma_G^2 + \sigma_{Gx\,E}^2 + \sigma_{e/r}^2}$$

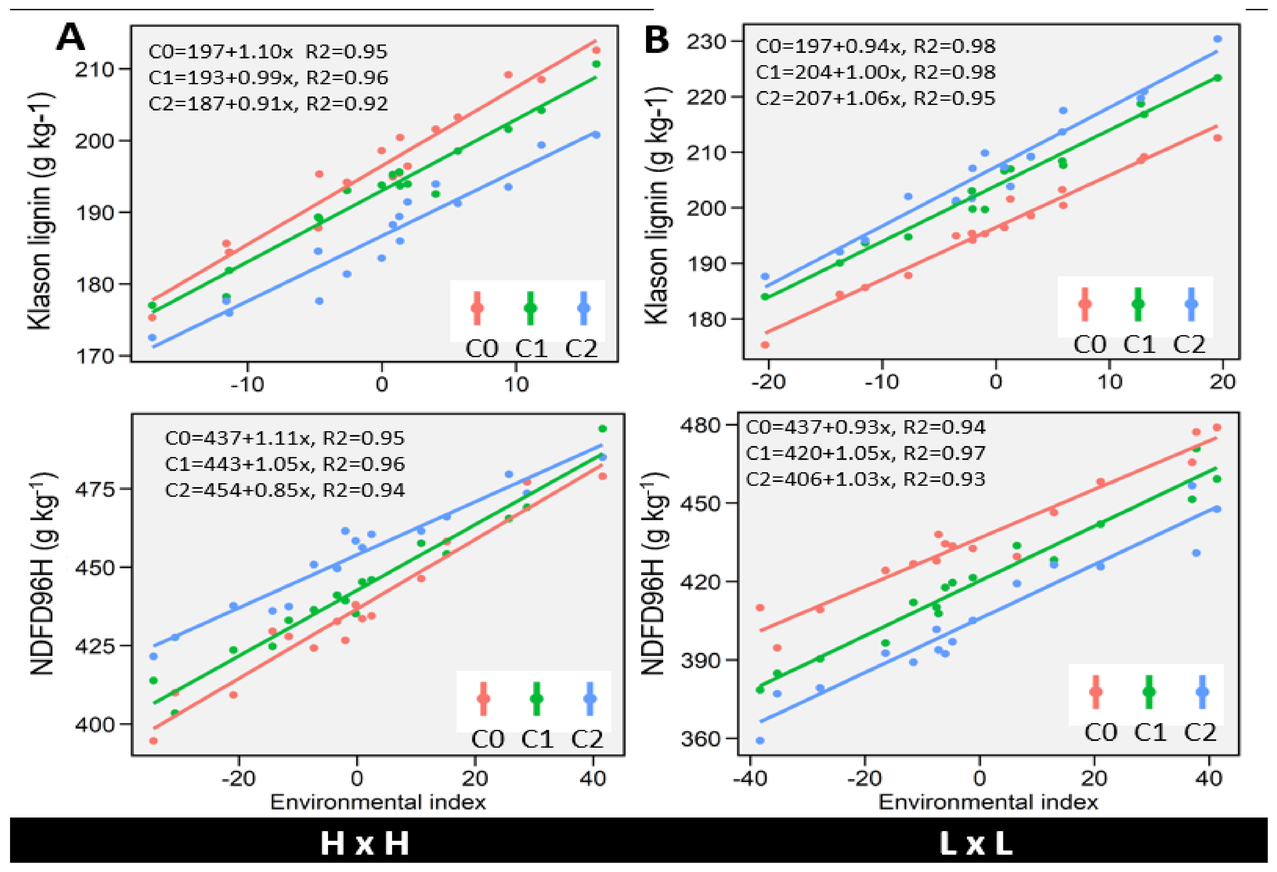

Fig 3. Environmental stability of Klason lignin and 96-h IVNDFD across all harvest environments. (A) H x H, intermating of plants with high 16-h IVDFD and high 96-h IVNDFD. (B) L x L, intermating of plants with low 16-h IVDFD and low 96-h IVNDFD.

Results

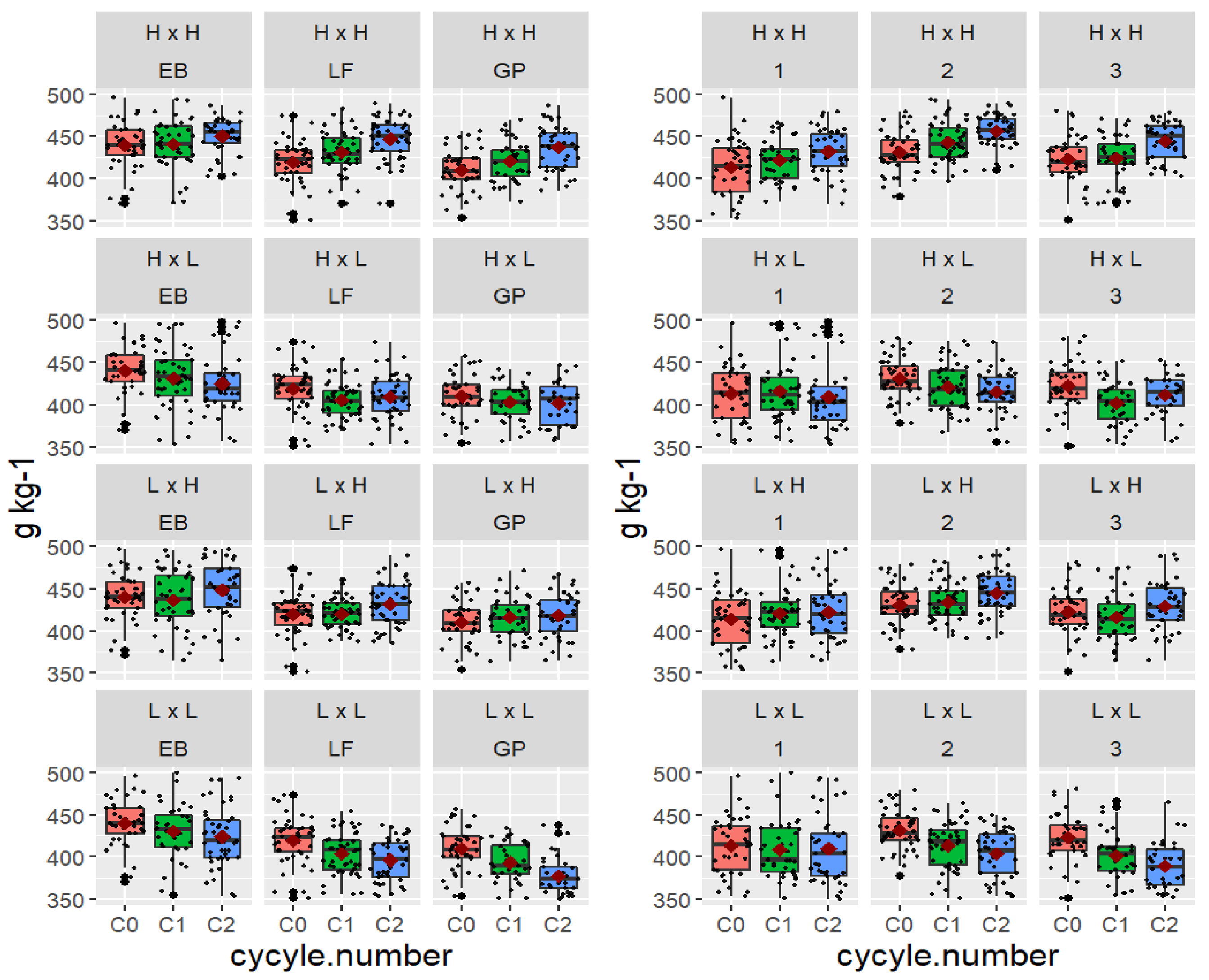

Fig 2. 96-h IVNDFD patterns in populations from Cycle 0, 1, and 2. Left panels, digestibility by maturity. Right panels, digestibility by harvest

Table 2. Summary of the heritability, genetic gain (GG), regression slope, and the p-values of the regression slope for digestibility traits

Trait	Heritability	Genetic Gain	Slope	P-value of GG
Klason lignin	0.74	-5.20	-3.77	4.15E-02
96-h IVNDFD	0.71	5.05	7.75	1.89E-02
Xylose	0.58	-4.69	-1.45	3.25E-02
16-h IVNDFD	0.46	4.10	2.79	4.30E-02
Hemicellulose	0.42	-1.82	-1.01	5.44E-03
Fucose	0.42	7.20	0.04	3.29E-02
Uronic acids	0.41	1.39	0.48	2.91E-02
Cellulose	0.32	1.11	1.62	6.55E-03

Discussion

These results suggest that IVNDFD was improved in the H x H populations by accumulation of favorable alleles from selection cycles C0 to C2, while in the L x L populations undesired alleles accumulated with each cycle. In contrast, there are no unidirectional increase/decrease patterns from the H x L and L x H populations. Additional cycles of selection for IVNDFD should be expected to continue to improve digestibility with concomitant changes in cell wall components. The selection methodology resulted in populations with the desired characteristics at later maturities and across harvests, reducing seasonal variation in forage quality. Plants from each population were genotyped by the Breeding Insight genotyping platform with 3,000 SNPs, and dominance and epistasis gene effects size will be estimated and used, together with additive effects, to increase the genetic gain of digestibility of alfalfa stems.

Conclusions

Recurrent selection for alfalfa stem IVNDFD was a successful strategy for improving fiber digestibility and reducing stem lignin without changing the proportion of leaves to stems in total herbage. Increased digestibility and decreased lignin occurred in later maturity stages, which would increase biomass yields while maintaining forage quality.

High digestibility plants in the field

Sampling for digestibility

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Postdoc position available for alfalfa breeding, please scan it

The postdoc will focus on Crop Genetics and Genomics with genome wide markers for winterkill and persistence tolerance in alfalfa. We are using cutting-edge phenomics and genomic approaches to screen for stress resilience and linking these traits to the genes/alleles. Skills in R or Python programming are highly desired. If interested, please email zhanyou.xu@usda.gov or call 515-708-2858. Please notice, no citizenship or green card is required for this position.