

## Evaluation of Progress from Selection for Pectin in Alfalfa Populations

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Recent studies indicate that more than 50% of the total crude protein (CP) in alfalfa is eventually available to ruminants in the form of non-protein nitrogen (NPN), soluble protein, which is utilized only by microbes in the rumen. Soluble protein available in the rumen in excess to the capacity of rumen microbes to assimilate it, is not only underutilized but also associated with detrimental health effects to dairy cows and the environment. Efficiency of utilization of NPN by rumen microbes, and subsequently by the ruminant animal, can be enhanced by increasing the concentration of carbohydrate components that degrade in the rumen in synchrony with the NPN. Recent studies showed that high pectin diets based on dried citrus pulp increased microbial synthesis and performance of dairy cattle due to more efficient use of available nitrogen in the diet. Therefore, animal nutritionists suggest plant breeders to increase pectin concentration in alfalfa. Pectin, localized in the middle lamella and primary cell wall, is a fiber that degrades in the rumen at the same rate as soluble proteins.

At Cornell, recurrent selection to increase pectin concentration in alfalfa forage is in progress. Pectic polysaccharides in alfalfa are the predominant component of neutral detergent soluble fiber (NDSF). Therefore, NDSF concentration, hereafter referred as pectin concentration, was used as a selection criterion for pectin. Evaluation of realized gain from one cycle of bi- or uni-directional selection for pectin, and correlated response in *in vitro* dry matter digestibility (IVDMD) is reported herein as average of three harvests in the spring and summer of 2001 (Experiment I, seeded in 2000) and 2002 (Experiment II, seeded in 2001) in two locations in Ithaca, NY. Pectin concentration and IVDMD are determined based on whole forage samples.

In experiment I, direct divergent responses to selection for pectin in populations I and II were 4.37 ( $P < 0.05$ ) and 12.30 ( $P < 0.0001$ ) g kg<sup>-1</sup> DM, respectively. Unidirectional selection for pectin in populations IV and V increased pectin concentration in the high pectin lines (HPLs) over their respective base populations (BPs) by 3.52 ( $P < 0.05$ ) and 4.76 ( $P < 0.01$ ) g kg<sup>-1</sup> DM, respectively. Pectin concentration in the HPLs vis-à-vis their respective BPs in all the populations was higher by 0.43 to 3.31%. Correlated divergent gains in IVDMD to selection for pectin in populations I and II were 0.99 ( $P < 0.01$ ) and 2.69 percentage units ( $P < 0.0001$ ), respectively. In population IV and V, unidirectional selection for pectin increased IVDMD in the HPLs by 0.30 and 0.31 percentage units, even though insignificantly. Correlated responses in IVDMD in the HPLs compared to their respective BPs in all the populations were in the range of -0.19 to 0.98%.

In experiment II, direct divergent responses to selection for pectin in populations I, II, and III were 6.71 ( $P < 0.01$ ), 3.74 ( $P = 0.08$ ) and 8.17 ( $P < 0.0001$ ) g kg<sup>-1</sup> DM, respectively. Unidirectional selection for pectin in populations IV and V increased pectin concentration in the HPLs over their respective BPs by 5.28 ( $P < 0.05$ ) and 1.44 ( $P > 0.05$ ) g kg<sup>-1</sup> DM, respectively. The corresponding increases in pectin concentration in the HPLs over their respective BPs in all the populations ranged from 0.40 to 3.50%. Correlated divergent gains in IVDMD to selection for pectin in population I, II and III were 0.79 ( $P = 0.06$ ) and 1.63 ( $P < 0.0001$ ), 0.57 ( $P > 0.05$ ) percentage units, respectively. In population IV and V, unidirectional selection for pectin changed IVDMD in the HPLs by 0.12 and -0.26 percentage units, even though insignificantly, respectively. High pectin lines in all the populations had correlated responses in IVDMD in the range of -0.34 to 0.75% in relation to their respective BPs.

In conclusion, genetic improvements for pectin concentration and indirectly for IVDMD in alfalfa appear to be possible, but more than one cycle of selection would need to be done before differences from base populations are statistically significant.