

# Identifying Molecular Markers Associated With Quality & Quantifying Their Potential to Increase Alfalfa Value

*Steve Norberg, Washington State University*

*Sen Lin, Purdue University*

*Cesar Medina-Culma, USDA-ARS*

*Long-Xi Yu, USDA-ARS*

*David Combs, USDA-ARS*

*Glenn Shewmaker, University of Idaho*

*Guojie Wang, Oregon State University*

*Don Llewellyn, Washington State University*

*Steve Fransen, Washington State University*

Dairy producers purchase feed to meet protein, energy, and fiber requirements for their cows. Alfalfa is a viable feedstuff that contributes to those nutrient needs. Our research was conducted on the evaluated first cut of 200 diverse alfalfa accessions ranging in fall dormancy from 2 to 6 in the field trials of 2018 and 2019 at Prosser, WA, Union, OR, and Kimberly, ID. Forage quality analyses were conducted and calculated. Nutrient values were determined using information from Northwest United States from November 2017 to August 2019 to determine dollar value  $\text{Mg}^{-1}$  of first cut alfalfa. Forage quality traits were analyzed using empirical best linear unbiased prediction (EBLUP) and covariate was used for fall dormancy variation. Optimum forage quality constituents found in the trial were placed into protein, energy, fiber, and fiber fill calculations to determine dollar values to dairy nutrition. Greatest potential to increase dollar per ton hay value followed sequentially in order of importance by: increasing metabolizable protein, decreasing ash content, decreasing lignin, increasing fat, decreasing acid detergent insoluble crude protein, and increasing neutral detergent insoluble crude protein. If all constituents were maximized, it increased in alfalfa hay from an average value of \$274 to \$364 / ton for an increase of \$90/ton. The same panel of accessions were genotyped using genotyping by sequencing and the genotypic data was used for marker-trait association analysis in combination of phenotypic data described above. Genome-wide association studies (GWAS) identified 28 SNP markers associated with 16 quality traits. Among them, most of the markers were associated with fiber digestibility and protein content. Among different sets of markers identified by location, two markers were associated with nine traits of fiber digestibility. After validation, these markers can be used for marker-assisted breeding to improve alfalfa quality.