

Determining Genetic Factors That Influence Forage Quality In Alfalfa

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This integrated project is using 200 diverse alfalfa varieties to determine molecular markers and other genetic information that predict hay quality based on the linkage of these traits with Total Tract Neutral Detergent Fiber Digestibility (TTNDFD). Our overall goal is to implement the resulting data into breeding programs so that new varieties of alfalfa can be generated that maximize that availability of nutrients in ruminant digestion – this will necessarily involve: i) quantifying alfalfa genetic diversity in forage quality in a diverse germplasm, ii) quantifying the relationship between alfalfa quality and other possible confounding and important agronomic parameters; and iii) identifying genetic information associated with forage quality. To accomplish these goals we have developed four objectives: 1) Determine quality and stage of maturity at first harvest of 200 alfalfa varieties at four locations in the PNW. Fall dormancy and yield for all cuttings will be determined to identify and reduce confounding factors with quality. 2) Quantify the genetic diversity of alfalfa that is related to forage quality to understand the potential to breed new alfalfa varieties for higher forage quality. 3) Identify molecular markers associated with forage quality (NDF, NDFD24, NDFD30, NDFD48, kd, iNDF, TTNDFD) traits in alfalfa to aid alfalfa breeders. 4) Extend the knowledge gained from project to positively impact alfalfa producers, breeders and others in the alfalfa industry. Breeding programs from industry stakeholders are cooperators on this project which will impact both alfalfa and dairy producers by improving the reliability of access to more digestive alfalfa feed sources.