

# **NE-1010: Breeding and Genetics of Forage Crops to Improve Productivity, Quality, and Industrial Uses.**

## **Research Project Description**

**Title:** Replicated clonal selection for improving forage yield of alfalfa.

**Lead Scientist:** Don Viands (NY)

**Collaborating Scientists:** Real Michaud (ACFSF), Charlie Brummer (GA), Surya Acharya (AAFC)

**Objective(s):** Determine if replicated clonal evaluation across multiple environments is effective in improving alfalfa forage yield.

**Justification:** Apart from developing cultivars with resistance to diseases and insects, advances in forage yield potential in alfalfa have been very small. Recurrent phenotypic selection has not been very effective for increasing yield potential of germplasm adapted to North America. The NE-144 project has found that half-sib and testcross methods have not been successful either. Because alfalfa cultivars must be adapted to a broad range of environments, successful breeding methods for improving yield potential must include evaluation of genetic material across multiple environments to account for genotype x environment variability. Rumbaugh et al. (1988) mentions replicated clonal line selection as one approach to eliminating escapes for some traits. Replicated clonal line selection would allow for evaluation across environments while theoretically utilizing all the genetic variability among selection units as the original plant population, in contrast to some types of progeny testing where one-half or less of the additive genetic variability can be exploited (Rowe and Hill, Jr., 1984).

**Brief Description of Methods:** Each scientist will be contributing seed of alfalfa germplasm adapted to their location. The lead scientist will randomly cross-pollinate all of these germplasm sources for two generations to create one genetically broad population. Two hundred plants will be randomly chosen to initiate the clonal evaluation. NY will send a stem cutting from each of

these 200 genotypes to each of the collaborators. The collaborators will further propagate enough ramets for evaluation at their locations. Each collaborator will transplant three replicates of three ramets per replicate of each genotype to a field nursery. Ramets will be established at about .5 m spacing within rows and 1 m spacing between rows.

Each scientist will manage the nursery according to common practices for that location. At each harvest period, scientists will count the number of plants and harvest each plot for forage yield for two production years. At the end of the second production year, the highest yielding 10% (20 genotypes) across locations will be intercrossed to produce Cycle 1 seed. A second cycle of selection will be done like the first. The scientists also will produce their own populations within their locations. The same population will be established in a spaced-plant nursery at each location to also conduct phenotypic selection to ultimately compare selection progress with the clonal evaluation.

After two cycles of selection, the base population and the Syn. 2 generation of the first and second cycles of selection, along with several check cultivars, will be established in replicated plot trails at multiple locations to determine selection progress.

**Expected Impacts:** The results of this research will impact the way that alfalfa breeders improve forage yield potential in the future. Improvements in yield will make significant contributions to economically supplying feed for dairy animals and other livestock. Release of a superior cultivar also is a possibility.