

# Alfalfa Breeding: Yield Trial Results from Selection and Intercrossing for Forage Yield and Quality

J. Hansen, J. Crawford, V. Moore and D. Viands, Cornell University, College of Agriculture and Life Sciences, School of Integrative Plant Science, Plant Breeding and Genetics Section

**INTRODUCTION:** Two alfalfa populations were bred for improved forage yield and for improved forage quality. The objective of the research was to evaluate yield of the sub-populations selected for yield and for forage quality. Additionally, these sub-populations were also compared to populations developed from plants selected at random and to populations developed from crossing two populations. Results for yield, maturity and lodging are presented in this poster.

**MATERIALS AND METHODS:** Alfalfa seedlings of two populations from the Cornell Forage Breeding Project were transplanted to a field in Ithaca NY in replicated half-sib rows in 2011. The two populations were NY1408+NY1410 (hereafter renamed NY-A) and NY1409 (hereafter renamed NY-B). After the establishment year, vigor and disease resistance were noted and superior plants were selected for further evaluation (NY-A: out of 5200 plants, 397 were selected; NY-B out of 4300 plants, 344 were selected), or approximately 8% of the plants were selected based on visual assessment of vigor. At second and third harvest in 2013, these selected plants were hand-harvested and the plant material was dried and weighed. From these harvested pools, the best 10-12% of the plants were selected for high yield based dry matter plant weights (NY-A Yield Select and NY-B Yield Select), the best 10-12% of plants were selected for high forage quality based on lab assessment of forage quality (low neutral detergent fiber and high neutral detergent soluble fiber concentrations at two harvests, NY-A Quality Select and NY-B Quality Select), and 10-12% of plants were selected randomly (NY-A Random Select and NY-B Random Select). Each of these populations had about 50 parent plants. In addition, the two sets of plants selected for high yield were crossed together (Yield Cross or NY-A Yield Select x NY-B Yield Select) and the two sets of plants selected for high forage quality were crossed together (Quality Cross or NY-A Quality Select x NY-B Quality Select). For each of the eight populations, seed was produced in the greenhouse. Then one generation of seed increase was completed so seed quantities were sufficient for planting evaluation trials.

Seed was planted in a trial at Ithaca NY in spring 2018. The trial was harvested three times each production year (2019 – 2021). Samples for forage quality analyses were collected at each harvest in 2019 and 2020. At each sampling, plots were rated for maturity (1 to 8 scale, 1 is immature and 8 is mature). Lodging ratings (1 - no lodging and 4 - lodged) were taken when lodging was present (harvest 3-2019 and harvest 1-2020). This research summary is for the trial total yield over years, average maturity (two years) and average lodging rating (two harvests) (Table 1).

Total yield (tons/acre dry matter), maturity score, and lodging score were analyzed as a randomized complete block with four replications. Populations NY-A and NY-B were averaged together for all planned contrasts. Planned contrasts for yield, maturity and lodging were Quality Select vs. Yield Select, Yield Select vs. Random Select, Quality Select vs. Random Select, Quality Select vs. Quality Cross, and Yield Select vs. Yield Cross.

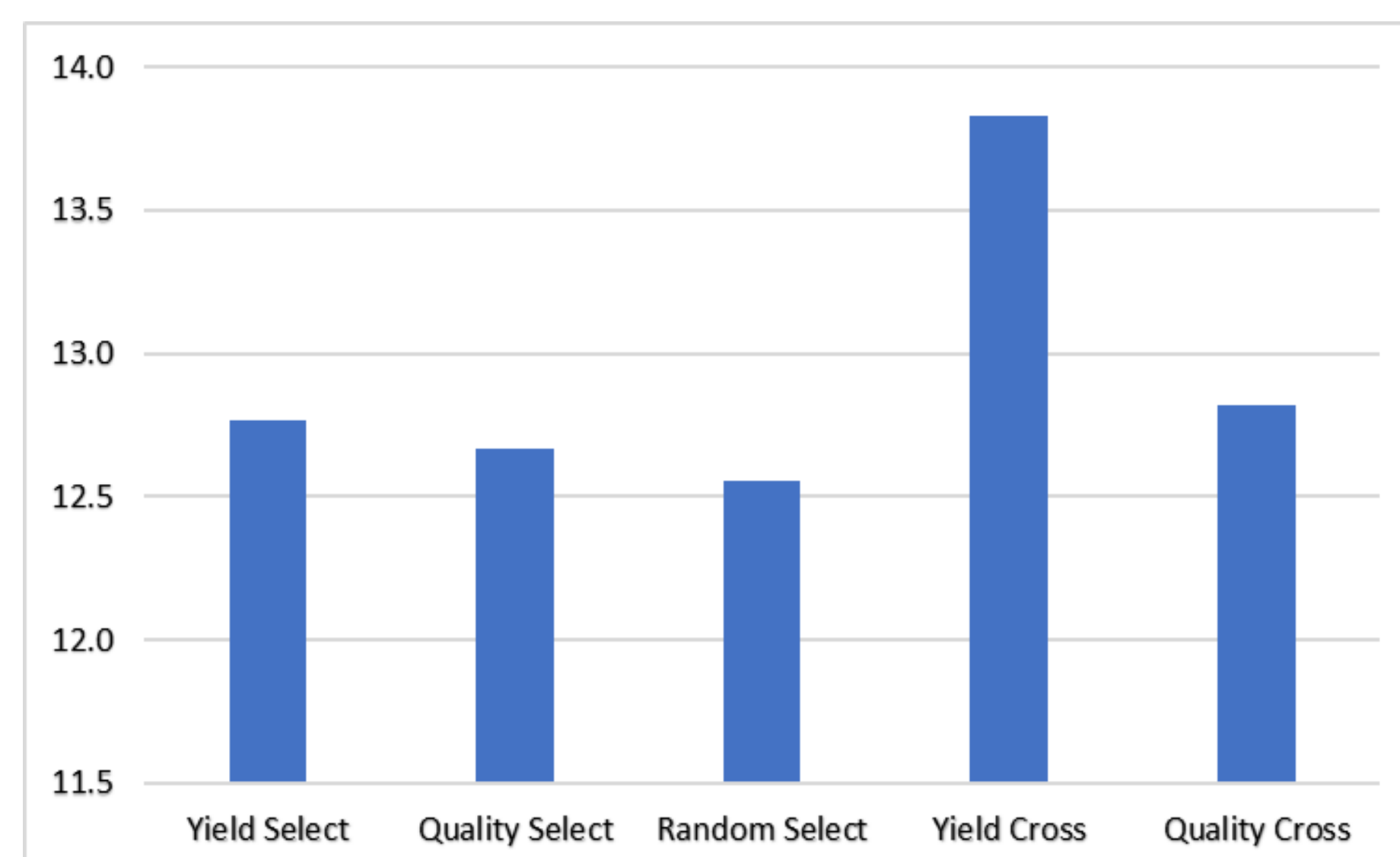


Figure 1: **Total Yield** (tons per acre dry matter) of the alfalfa populations selected for yield, forage quality, random selections, yield cross and forage quality cross.

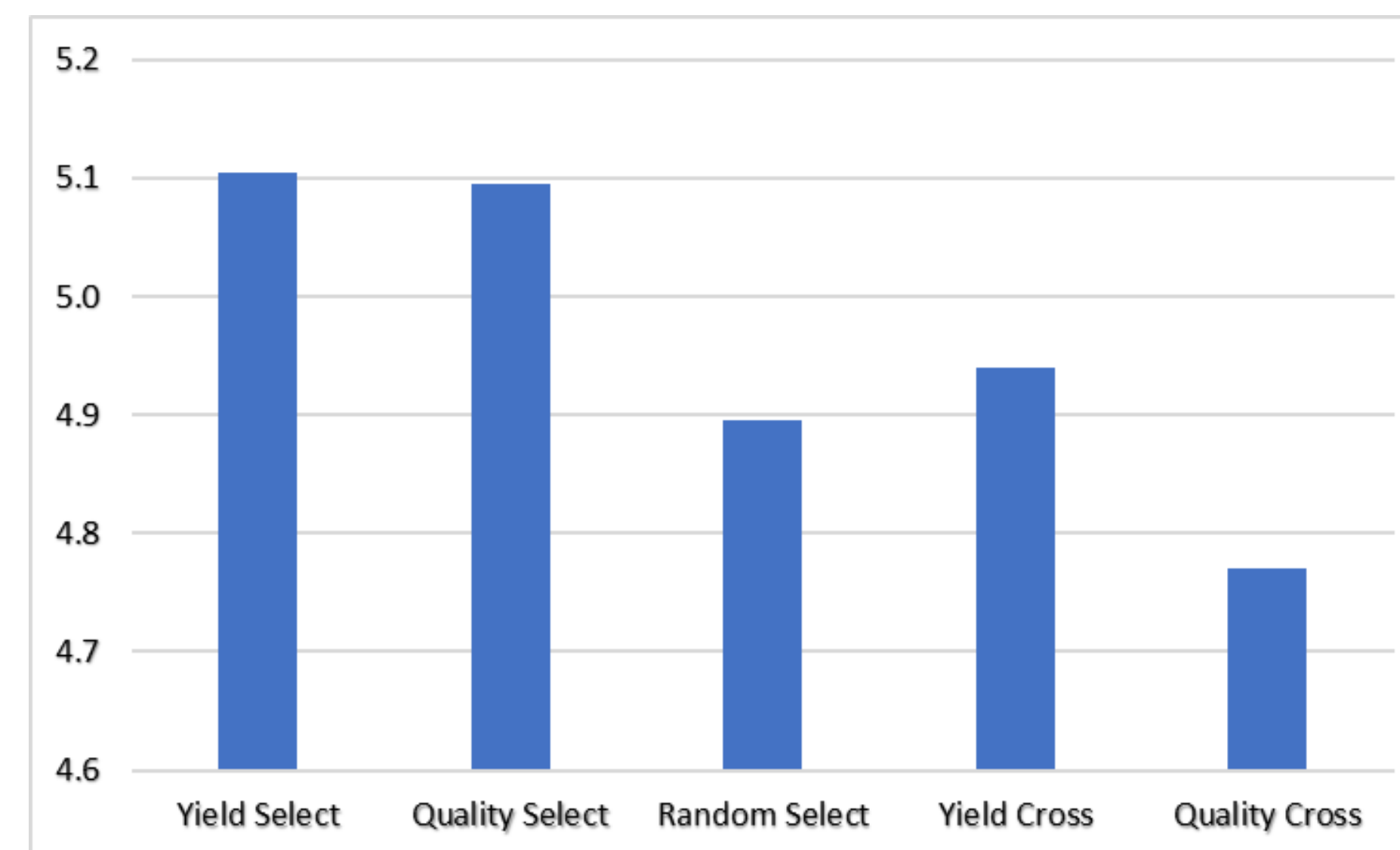


Figure 2: **Maturity** (1 is immature, 8 is mature) of the alfalfa populations selected for yield, forage quality, random selections, yield cross and forage quality cross.

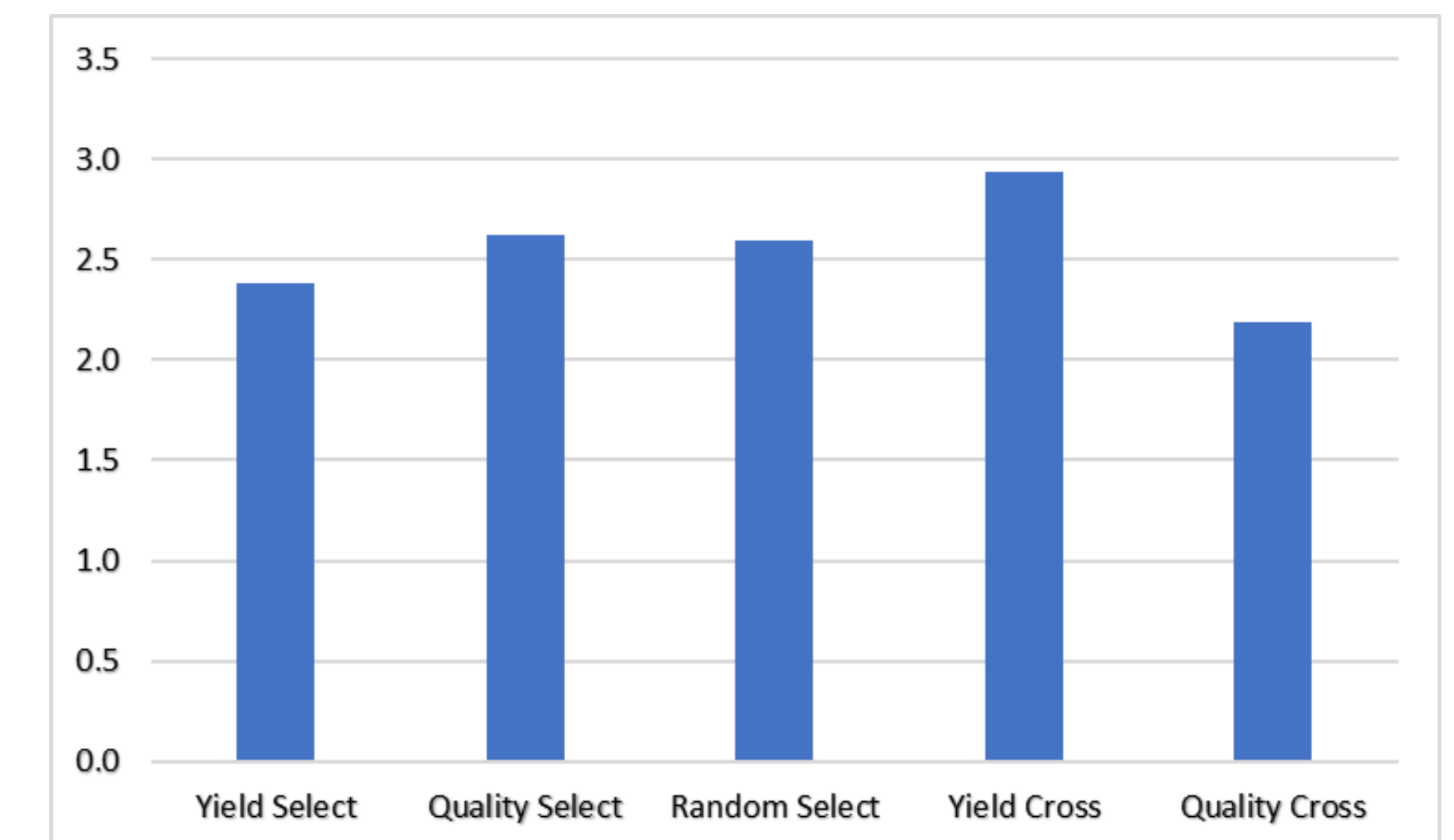


Figure 3: **Lodging** (1 is not lodged, 4 is lodged) of the alfalfa populations selected for yield, forage quality, random selections, yield cross and forage quality cross.

Table 1: Total forage yield (tons per acre dry matter; 9 harvests), average maturity rating (1 to 8 scale, 1 is immature and 8 is mature; 6 harvests) and average lodging rating (1 is no lodging and 4 is lodged; 2 harvests) for eight alfalfa populations in evaluation trial.

Population	Total Forage Yield (dry tons/acre)	Average Maturity Rating	Average Lodging Rating
NY-A Yield Select	13.6	5.3	1.6
NY-A Quality Select	13.0	5.3	2.0
NY-A Random Select	12.9	5.1	1.9
NY-B Yield Select	11.9	4.9	3.1
NY-B Quality Select	12.3	4.9	3.3
NY-B Random Select	12.2	4.7	3.3
Yield Cross	13.8	4.9	2.9
Quality Cross	12.8	4.8	2.2
LSD (0.05)	0.9	0.3	0.5
CV (%)	5.0	3.6	16.2

**RESULTS:** The Yield Cross population had significantly more yield than the Yield Select average ( $P=0.01039$ , Figure 1). The Quality Cross populations did not show a similar yield increase compared to Quality Select average.

Maturity ratings for three of the five planned contrasts were statistically significant (Figure 2). The Yield Select and the Quality Select had greater maturity scores than the Random Select ( $P=0.0240$ ;  $P=0.0312$ , respectively) and the Quality Cross had lower maturity score than the Quality Select ( $P=0.0050$ ).

Lodging rating for two of the five planned contrasts were statistically significant (Figure 3). The Quality Select lodged more than the Quality Cross ( $P=0.0434$ ). The Yield Select lodged less than the Yield Cross ( $P=0.0072$ ).

**CONCLUSION:** One cycle of selection for yield, for quality, and for a random selection of plants did not significantly increase or decrease forage yield or tendency to lodge. For the two alfalfa populations in this study, forage yield was improved by intercrossing two populations selected for forage yield. This yield improvement is possibly due to heterosis for yield alleles. Intercrossing two populations selected for forage quality did not show a similar response in yield improvement. Rather maturity score was improved (was less mature) by intercrossing two populations selected for forage quality possibly due to heterosis for forage maturity alleles associated with forage quality.