Relative acceptability of new leucaenas for grazing cattle

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The *Leucaena* genus is one of the most important sources of forage trees for the tropics and includes a number of agronomically promising but lesser–known species. An experiment was undertaken to examine the relative acceptance by grazing cattle of 24 forage tree genotypes in a field trial at Mt Cotton in South–east Queensland.

The genotypes, including 3 non-Leucaena species, were planted as paired trees in a 3 x 6m grid and replicated 16 times. Genotypes were Leucaena collinsii 52/88(1), 56/88 (2); L. diversifolia 82/92(3), 83/92 (4); L. esculenta 47/87 (5); L. lanceolata 43/85 (6); L. lempirana 6/91 (7); L. leucocephala cv. Cunningham (8), cv. Tarramba (9); L. macrophylla 47/85 (10); L. pallida 52/ 87(11), 79/92(12), CQ3439(13); L. salvadorensis 36/88 (14); L. shannonii 19/84 (15); L. trichandra 4/9 1 (16), 53/88(17), CP146568 (18); L. trichodes 61/88 (19); L. pallida x L. leucocephala K376 x K8 (20), (K806 x K748) x K636 (2 1); Gliricidia sepium cv. Retaluleu (22); Calliandra calothyrsus CPI115690 (23); and Sesbania sesban cv. Mt Cotton (24). Four steers, naive to forage trees and with one previous exposure to cuttings of each genotype, were allowed to graze one replicate per day for 2 hours. Before and after grazing of each replicate, the leaves of each genotype were counted. The pattern of defoliation within the 2-hour period was determined every 20 seconds by recording which genotype was grazed. The pattern was expressed as the number of grazing observations on each genotype in four 30 minute periods over the total observations, for the 2 hours. In the analysis of % leaf defoliated (Figure 1) the replicates were treated as consecutive grazing occasions in time, while for the analysis of grazing observations per 30 minute period (Figure 2) data were averaged across replicates. Cluster analysis was used to identify groups of genotypes that behaved similarly for both attributes.

Three groupings were identified from leaf defoliation data (Figure 1). The non-leucaena genotypes were minimally grazed, 2 genotypes of leucaena were accepted to an increasing extent with time and the remaining 19 leucaena genotypes were almost completely defoliated **from** the beginning. Analysis of grazing observation data identified 4 groups within the leucaena genotypes (Figure 2). The most acceptable group comprised genotypes that were grazed to the greatest extent at the beginning of the **2–hour**

Recent Advances in Animal Nutrition in Australia 7997 University of New England, Armidale NSW 2351, Australia period. The least acceptable group comprised genotypes that were mainly grazed towards the end of the **2-hours**.

We conclude that, for naive cattle, the leucaena genotypes were more readily accepted than the **non**– leucaena genotypes tested. Within the leucaena genotypes, there were differences in their relative **short**– term acceptability to cattle.

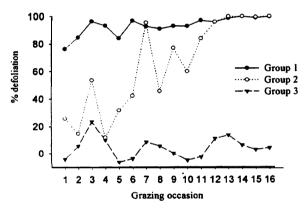


Figure 1 Mean % leaf number removed by grazing cattle for genotype groups over 16 grazing occasions. Group 1 comprised genotypes 1–.9, 11–.15, 17–.21; Group 2 comprised genotypes 10, 16; and Group 3 comprised genotypes 22, 23, 24.

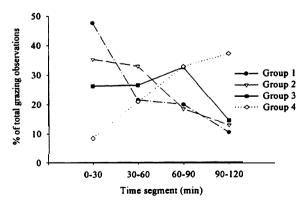


Figure 2. Mean % total grazing observations/Leucaena genotype group, for each 30 minute time segment within a 2 hour period. Group 1 comprised genotypes 6, 8, 9, 11, 15, 18, 19; Group 2 comprised genotypes 1,2, 3, 4, 7, 17, 20, 21; Group 3 comprised genotypes 5, 12, 13, 14; and Group 4 comprised genotypes 10, 16.