



# *Chloris roxburghiana* schult Grass genetic variation - The need for *in situ* Seed Multiplication

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## Introduction

Pasture farming is the best way to use many areas where cropping is unsustainable because of insufficient rainfall or risk of soil erosion (Boonman 1993; Skerman & Riveros 1990). Unfortunately livestock production under extensive system in the semi-arid rangelands is threatened by degradation in the form of reduction or total loss of perennial grasses. Contributing to this degradation are long-term continuous use, overstocking, drought, termites and cessation of seasonal burning. (Long, Jones & Roberts 1992; Steiner 1996). Where land degradation has occurred there is need for restoration accompanied by a judicious utilization package. Experience with reseeding has shown that the species most likely to be successful in reseeding are native species found on sites similar to those to be re-seeded. This is mostly understood to mean similar ecological zones (Pratt & Gwynne 1977). Unfortunately, reseeding efforts in Kenya have been met with minimal success (Bogdan & Pratt 1967; Mnene, Wandera & Lebbie 2000). Seeds obtained from localized government institutions are used for re-seeding programmes country-wide due to lack of range grass seeds in the market. It is therefore hypothesized that use of seeds from populations not adapted to the degraded areas is a possible cause of the low reseeding success rate. This paper is based on trials with *Chloris roxburghiana* grass establishment under different on-farm sites and presents results of genotyping the grass's four naturally occurring populations found in the rangelands of Kenya.

## Materials and Methods

### Re-seeding

Three degraded sites were selected within ecological zone V (Pratt & Gwynne 1977) namely Kavatini, Merueshi and Kimala, situated approximately 25 km northeast, 30 km west and 150 km south of Kiboko, respectively. Seeds of four grass species including *C. roxburghiana* selected by the local communities were collected from Kiboko following the procedures of Herbage Seed Unit (HSU) (1994). A known mixture of the seeds was used in re-seeding the three sites with four treatments involving range pitting, deferment, over-sowing, pitting, and pitting with over-sowing. Data was seasonally collected on seedling population and subsequently biomass production for two years.

### Genotyping

Five young entire leaves of *C. roxburghiana* were picked from 25 plants from the research centre at Kiboko and the three re-seeding trial sites. Collections at each site were confined within a homogeneous area measuring approximately 50 m<sup>2</sup>. Genotyping was done at the International Livestock Research Institute (ILRI) laboratory in Nairobi. The CTAB DNA extraction technique was used (Doyle & Doyle 1990). Random amplified polymorphic DNA (RAPD) analysis was undertaken according to Dawson *et al.* (1999). Nine primers that revealed clear polymorphisms were selected for analysis of all 96 individuals. Amplified fragments were separated in a 2% agarose gel using 1X TBE buffer stained with ethidium bromide. Gels were visually inspected and scored for presence or absence of bands and band base pairs were estimated. Estimates of similarity were based on Nei's (1987) definition of similarity.

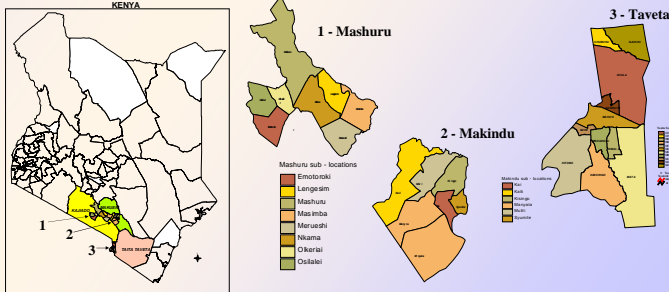


Figure 1

## Results and Discussion

### *Chloris roxburghiana* establishment

Seedling population and subsequent biomass estimates varied between the sites, treatments and sampling dates. Consistently, Kavatini had more seedlings and biomass than both Merueshi and Kimala. The seedling population was least at the beginning but tended to increase over time and varied from site to site, ranging from 0 to 30 m<sup>2</sup>. Biomass ranged from 2.0 to 125.6 gm<sup>2</sup>. Biomass estimates were within the range reported previously (Kinyamario and Imbamba reported in Long *et al.* 1992). The effect of date of sampling on biomass was expected due to the seasonal nature of growing conditions; two rainy seasons are experienced annually with intervening dry seasons. Seed germination and seedling emergence are also predominantly controlled by wet conditions. Thus, dry season sampling did not capture new seedlings while every wet season resulted in recruitment of new cohorts of seedlings into the population. However, the magnitude of new seedlings was not directly related to wet weather conditions but rather depended on the sites suggesting possible existence of other factors.

### Genetic differentiation among populations

Genetic diversity within *C. roxburghiana* populations varied considerably. The percentage of polymorphic loci ranged from 44.27 in Kiboko to 77.10 in Kimala. The genetic diversity showed that Merueshi population has the greatest level of variability with a *He* value of 0.193 while Kiboko has the least with a value of 0.142. The mean genetic diversity over all four populations was 0.171. A significant level of overall gene divergence (*Gst* value of 0.244) was detected. This means that 24% of the variation observed in this study was due to differentiation among populations of *C. roxburghiana* compared to 76% within populations. Figure 2 shows the dendrogram for the individuals from the four populations. Two main clusters at 72 % similarity were identified. Cluster 1 consisted of two smaller genetically distinct clusters of two sites at 78% similarity index while cluster 2 consisted of a complete mix of individuals from the other two sites.

Distinct variation was observed between two of the populations, Kavatini and Kiboko, indicating that these sites constitute genetically isolated populations, while the other two spatially separated populations, Kimala and Merueshi, were found to be genetically similar. Nonetheless, among all populations, there were a few individuals that were similar to those of other populations, indicating a common ancestry. These results suggest that gene flow between the sites may be limited and genetic drift and/or natural selection may have caused the high divergence observed between individuals of different sites. The populations clustering due to reasons other than geographical isolation obtained in this study could be explained by difference in soils, including fertility of the study sites. Other studies have also reported similar results with different plants (Nevo *et al.* 1983; Huff *et al.* 1998).

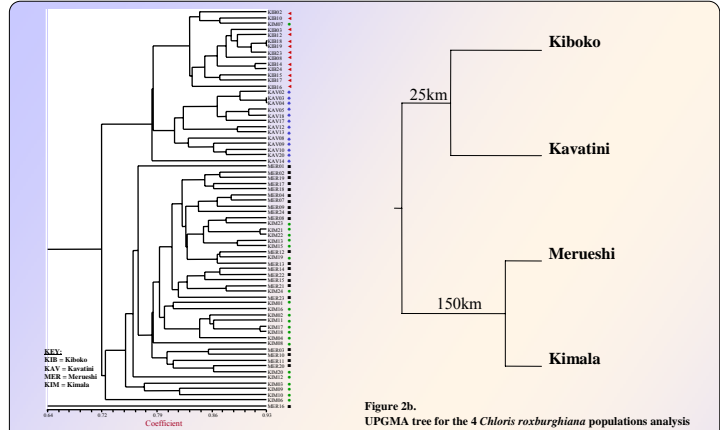


Figure 2a. RAPD analysis of 4 Kenyan populations of *Chloris roxburghiana* Dendrogram based on coefficient of similarity

Figure 2b. UPGMA tree for the 4 *Chloris roxburghiana* populations analysis showing close relationships between Kiboko and Kavatini and Merueshi and Kimala but each as separate groups and unrelated to spatial separation.

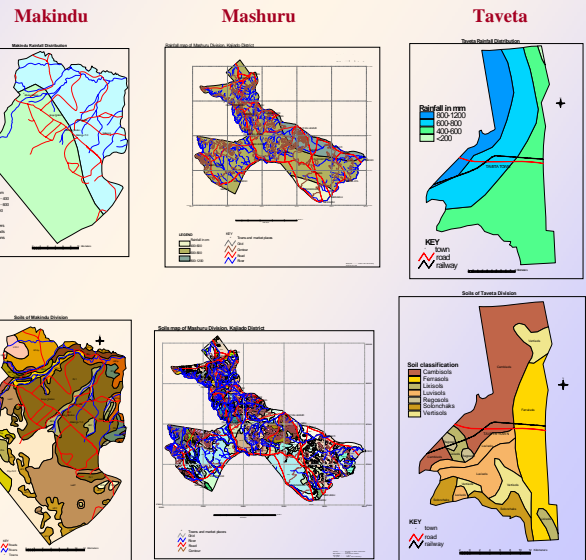


Figure 3

## Conclusions

There is a significant genetic variability within and between natural populations of *C. roxburghiana* found in the southern Kenya rangelands. *Chloris roxburghiana* seed establishment varied by site, probably because lack of adaptation. Therefore, for re-seeding purposes *C. roxburghiana* seeds need to be multiplied *in situ* or in selected habitats with very similar environments.

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