# Genetic Relationships and Ploidy Levels of Rubus spp. of the Tropical Americas

## Background

Several Rubus species and landraces are grown in Costa Rica and throughout the tropics. These possess important traits such as low acidity, high ORAC values, and dwarfism (Figs. 1 and 5). R. adenotrichos landraces are the most economically important, and are widely grown throughout the country. Little is known about the genetics of these plants, and because there is potential for improved cultivars, we studied the genetic relationships and ploidy for crossing genotypes. From the point of view of genetic resources, it is also important to study this material as these are highland blackberries that can be affected by global climate change.

## **Materials and Methods**

R. adenotrichos, R. urticifolius, R. miser, and R. glaucus are tropical genotypes grown in Central and South America and were obtained from several local growers (Flores-Mora et al. 2005; Fig. 1). Three elite cultivars donated from the Corvallis Clonal Germplasm Repository were used as controls. 12 Genotypes representing 6 species were analyzed using 9 RAPD and 13 SSR markers. Nei's genetic distances were calculated and UPGMA was used to generate a dendrogram. Nuclei were isolated and analyzed by flow cytometry to determine ploidy (Meng and Finn 2002).



Figure 1. Map of regions where genotypes are found naturally (shown in blue), these include *R. adenotrichos, R. urticifolius, R. glaucus,* and *R. miser.* Map of Costa Rice aryanded (red curves). Landraces used in this study were collected from growers in *Zona de los Santos,* San Jose nce (arrow).





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Figure 2, Genetic relationships among 12 Rubus genotypes. Dendrogram was generated by using 13 SSR markers, Nei's genetic distances, and the UPGMA procedure (left). Diversity in colors, shape and fruit sizes of tropical Rubus genotypes (upper right).



Figure 3. Allelic distribution, and marker diversity of 12 Rubus genotypes from 13 SSR markers.

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s-Mora, D., Jiménez-Banilla, V., & Ortiz-Sancho, F. (2005). Mirc tecnológicas (1st ed., pp. 65-75). Cartago: Editorial Tecno ngs, D. (1988). Raspbernies and blackbarries: their breeding, di B. & Elimo, C. (2002). De-B. & Elimo, C. (2002). De-tector of the second incropropagación nológica de Cost disease and gro th, London: Academic Journal of the Am nce, 127(5), 767-775



Figure 4. Genetic profiles of SSR and RAPD molecular markers of *Rubus* genotypes (left). Histograms of relative fluorescence intensities of *Rubus* nuclei that were detected as either 2x or 4x; 'Tulameen' and 'Navaho' cultivars used as 2x, and 4x controls, respectively (right).





Fig. 5. Stems from prickly and non-prickly landraces of *R. adenotrichos* (left). *R. miser* flowers, the only genotype studied with like flowers (left). Enana is a dwarf landrace with short intermodes, 5 to 8 cm, while other landraces range from 15 to 25 cm (right).

#### **Results and Discussion**

Both RAPD and SSR analyses showed very similar genetic distances and arrangements of the genotypes within the dendrogram. R. glaucus has been reported as a blackberry-raspberry hybrid (Jennings 1988). This is also supported by the marker analyses, as it is closest to the raspberry cultivars ('Tulameen', and 'Qualicum'; Fig. 2). Although Caballo and Ratón are the same species, Caballo was closer related to R. adenotrichos (Fig. 2). Additionally, histograms of fluorescent intensities show different ploidy between Caballo and Ratón (Fig. 4). Genetic profiles also suggested higher ploidy in Caballo because number of PCR products were higher in both SSRs and RAPDs (Figs. 3 and 4). Therefore taxonomic classification should be reexamined.

RAPD markers generated ≥100 bands per sample, while SSR markers generated up to 9 alleles per marker. Allelic diversity was low among R. adenotrichos genotypes, and highest within Caballo. For future crosses and study populations, R. adenotrichos landraces should be crossed with other genotypes to increase allelic diversity.