



An efficient protocol for tissue sampling and DNA isolation from the stem bark of Leguminosae trees

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ABSTRACT. Traditionally, molecular studies of plant species have used leaves as the source of DNA. However, sampling leaves from tall tree species can be quite difficult and expensive. We developed a sequence of procedures for using stem bark as a source of DNA from Leguminosae trees of the Atlantic Forest and the Cerrado. Leguminosae is an important species-rich family in these two highly diverse and endangered biomes. A modified CTAB protocol for DNA isolation is described, and details of the procedures for sampling and storage of the bark are given. The procedures were initially developed for three species, and then their applicability for 15 other species was evaluated. DNA of satisfactory quality was obtained from the bark of all species. The amounts of DNA obtained from leaves were slightly

higher than from bark samples, while its purity was the same. Storing the bark frozen or by drying in silica gel yielded similar results. Polymerase chain reaction amplification worked for both plastid and nuclear genomes. This alternative for isolating DNA from bark samples of trees facilitates field work with these tree species.

Key words: DNA isolation; Bark; Trunk; Cambium; Trees; Leguminosae