Chemical diversity in essential oil of *Eplingiella fruticosa* (Salzm. ex. Benth.) Harley & J.F.B. Pastore genotypes

Anderson de C. Silva, Lenaldo M. de Oliveira, Angélica Maria Lucchese

Universidade Estadual de Feira de Santana - Bahia, Brazil
lenaldo.uefs@gmail.com

Keywords: *Hyptis fruticosa*, medicinal plant, active germplasm bank.

Eplingiella fruticosa (syn *Hyptis fruticosa*) is a native Lamiaceae plant from Brazil who has wide use in folk medicine as an analgesic and anticonvulsant. The biological activity of *E. fruticosa* essential oil was efficient to reduced the pain in rats (1). Recent studies show great variability in the chemical composition of the essential oil from *E. fruticosa*, related to soil and climatic conditions and different plant organs (1,2). The aim of this study was to characterize the composition and the chemical diversity of the essential oils from 12 *E. fruticosa* genotypes kept in active germplasm bank (BAG) deployed in the State University of Feira de Santana (UEFS). Samples of 100g (leaves) per replicate of each genotype were used for hydrodistillation of the essential oil, utilizing a Clevenger type apparatus for three hours, quantifying the content. The identification of the compounds and their contents was performed by GC (FID) and GC/MS, in an Agilent 6890N and an Agilent 5973N systems, both with HP-5MS fused silica capillary columns (30 m X 0.25 mm X 0.25 μm). Hydrogen was used as carrier gas for GC/FID and helium for GC/MS, both with a flow rate of 1.0 mL/minute. Oven temperature was raised from 60 to 240°C at 3°C/minute. Mass detector was operated in electronic ionization mode at 70eV. The percentage composition was obtained by normalization from FID. Oil components were identified by comparison of both mass spectra and linear retention indices with spectral library and literature. We use 15 major compounds data in diversity analysis. Cluster analysis and canonical variables were made, using as dissimilarity measure the Mahalanobis distance (D^2). Identified compounds were classified in two major classes of terpenes, mono and sesquiterpenes, with higher for the latter percentage ranging from 49.80% to 68.73%, while the monoterpenes showed a percentage ranging from 24.03% to 38.75%. The cluster analysis result classify the genotypes in four clusters: 1 - formed by genotypes EF001, EF006, EF007, EF008, EF010, EF011 and EF012 with (*E*)-caryophyllene and bicyclogermacrene as major compounds; 2 - EF002 and EF003 genotypes showed that the same, however, percentage with average about 30% higher; 3 - EF004 and EF005 genotypes that showed a greater production of (*E*)-caryophyllene; and 4 - with EF009 genotype, forming a single group to present α-pinene as balanced majority and percentage among the rest. This result was confirmed by canonical variables, which explained 76% of the variation. The bicyclogermacrene, 1,8-cineole, α-copaene and spathulenol compounds were the most important variables for analysis.

1. Franco, C.R.; et al. Phytother. Res., 2011, **25**, 1693-1699.
2. Franco, C.R.; et al. Braz. J. Pharmacogn., 2011, **21**, 24-32.