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ANTHROPIC INFLUENCE IN THE METABOLIC COMPOSITION OF MANGROVE ESPECIES

Gibson Gomes de Oliveira, Marina Bertini, Fausto Carnevale Neto, Norberto Peporine Lopes

Núcleo de Pesquisa em Produtos Naturais e Sintéticos (NPPNS), Faculdade de Ciências Farmacêuticas de Ribeirão Preto da Universidade de São Paulo (FCFRP-USP), Ribeirão Preto, SP, Brazil.

gibson-oliveira@hotmail.com

Abstract: Mangrove forest, composed by salt tolerant trees that live in rough coastal conditions, is one of the most diverse biomes on planet. A total of 349 secondary metabolites have been reported so far from mangrove species worldwide, including triterpenes, diterpenes, steroids, flavonoids, naphtoquinones and iridoid glucosides.[1] Despite its importance, human activities as aquaculture, agriculture, and urban land have threatened its survival.[1] In order to stimulate its conservation, this work aim to evalutate the anthropic influence in metabolic composition of mangrove species (*Rhizophora mangle*, *Laguncularia racemosa* and *Avicennia schaueriana*) from Pernambuco State -Brazil. Stems and leaves of *A. schaueriana* (Black mangrove), *L. racemosa* (White mangrove) and *R. mangle* (Red mangrove), were collected at three regions of Pernambuco-Brazil during 2014 and extracted by maceration using MeOH and MeOH:H2O (3:7, v/v). The extracts were analyzed by HPLC-DAD-TOF and HPLC-DAD-IT in both ESI positive and negative modes. MS-based dereplication was performed by on-flow detection of high resolution molecular formula of the molecules and collision induced MS/MS technique for fragmentation of molecular ions, assisted by molecular networking workflow, according to figure 1.[2] DAD detector was set to record between 200 and 800 nm. Preliminary results led to the in situ identification of mono, di, tri-*O*-glucosyl flavonoids, methoxy-flavonoids, and proanthocyanidins, previously described in mangrove forest. The metabolites were distributed among all three collected plant species. Molecular networking organized MS/MS data based on chemical similarity and allowed dereplication of known molecules and detection of related analogues. HPLC-MS data will also be employed in multivariate data analyses as hierarchical clustering analysis (HCA) and principal component analysis (PCA) to identify the anthropic influence in terms of metabolic variation.

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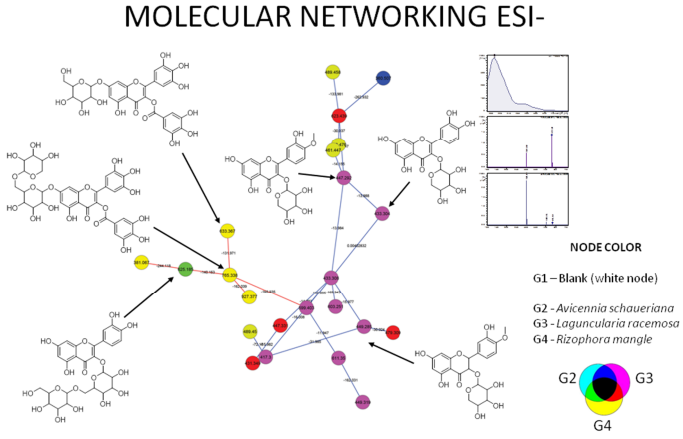

Figure 1. Detection of flavonoids based on molecular networking workflow and MS/MS spectra similarity.