

Bioprospection of the *Artemisia* genus: phytochemical profile and antioxidant activity of five *Artemisia* spp. from the Lessini mountains

Pietrolucci F.^{a,b}, Negri S.^{a,b}, Ramos C.^a, Commisso M.^{a,b}, Sebastiano Andreatta^c, Avesani L.^{a,b}* and Guzzo F.^{a,b}*

^aDepartment of Biotechnology, University of Verona, Verona, 37134, Italy

^bNational Biodiversity Future Center (NBFC), Palermo, 90133, Italy

^cMuseo di Storia Naturale, Comune di Verona, Verona, 37126, Italy

* linda.avesani@univr.it and flavia.guzzo@univr.it

The *Artemisia* genus, belonging to the Asteraceae family, is known for its wide distribution throughout temperate regions of the northern hemisphere and extensive use in traditional medicine. Plants from *Artemisia* genus contain a huge and various number of secondary metabolites, which contribute to a broad spectrum of bioactivities, *i.e.* anti-inflammatory, antimicrobial, and antiparasitic properties. One of the most significant uses of *Artemisia* species is in the treatment of malaria, where the compound artemisinin, isolated from *A. annua* leaves in 1972, has emerged as the most potent antimalarial drug. Nowadays, the discovery of new plant-derived products to be used as food supplements or drugs has been pushed by the exploitation of bioprospection approaches, even including the modern -omics techniques and targeted bioactivity assays.

In this work, we selected and sampled five *Artemisia* species (*A. absinthium* L., *A. alba* Turra, *A. annua* L., *A. verlotiorum* Lamotte and *A. vulgaris* L.), with ascribed medicinal properties, growing wild in the natural areas of the Verona province (Italy). The phytochemical profile of the five species has been characterized through the application of an UPLC-HRMS based on untargeted metabolomics approach and, in order to identify potential bioactive metabolites, we correlated their composition to the *in vitro* antioxidant activity data (FRAP and DPPH). In parallel, the occurrence of the lead drug compound artemisinin was investigated in the five *Artemisia* species. Here, we report for the first time the detection of sesquiterpenoids from the artemisinin biosynthesis pathway in the species *A. alba*. In addition, *Artemisia* spp. were used to generate cell cultures lines. The corresponding phytochemical profiles were characterized by UPLC-HRMS and compared with those of the original plants. *Artemisia* spp. cell cultures showed a simplified but still interesting specialized metabolome, probably resulting from cellular dedifferentiation processes.