MOLECULAR BIOMARKERS AND INORGANIC PROFILE TO CHARACTERIZE *AMANITA PONDEROSA* MUSHROOMS STRAINS

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Amanita ponderosa strains are wild mushroom eatable species, very appreciated in gastronomy, with a high exportation potential that grow spontaneously in some microclimates, particularly in Alentejo and Andaluzia. Additionally, its mineral and organic composition, depend on the fungal strain and their ecosystem. Moreover, due to symbiotic relation between mushrooms and some plants in its habitats, mushrooms can accumulate high concentrations of some elements, namely metals. Due to positive and negative effects and the toxicity of heavy metals on both human health and the environment, the analysis of trace metal contents of environmental samples is important to estimating the adequacy of intakes of essential nutrients and assessing exposure risks from intake of toxic non-essential heavy metals. Some species as *Amanita* spp. contain mineral and other components with therapeutically properties, therefore others were high toxicity, so is important the improve of a method to characterize different *Amanita* strains.

The aim of this study is to determine the inorganic composition of several *Amanita ponderosa* strains and to found molecular biomarkers to characterise these mushrooms.

Inorganic composition of the strains of A. ponderosa strains were determined by UV-Vis spectrometry (P), by flame atomic absorption spectrometry (Na and K) and by flame emission photometry (Ca, Mg, Fe, Cu, Zn and Mn). CPA analysis performed showed that inorganic elements of A. ponderosa strains were distributed between three different groups and Ca, Mg and Na were the major elements that contribute for this clustering.

The molecular profile of A. ponderosa strains were analyzed by MSP-PCR, with a M13 primer, and compared to other Basidiomycetes species and one Ascomycete strain. Similarity evaluation of the different strains was performed by a phylogenetic tree (UPGMA). Results showed that MSP-PCR is a fast method to characterise the genetic profile of A. ponderosa strains with high reproducibility and similarity for the same specie. The amplified DNA polymorphic sequences analyse allowed to identify at specie level and to differentiate A. ponderosa at strain from each origin sites.