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PARALLEL USE OF CID, HCD AND ETD FOR CHARACTERIZATION OF PROTEIC ALLERGENS FOUND IN POLLENSOMES

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In Mediterranean countries, olive (*Olea europaea*) pollen constitutes one of the most important causes of allergy, a major health problem of most modern societies. Recently, it has been shown that allergenic pollen-derived submicronic particles can be present in the air. These pollen-derived particles can reach the respiratory lower airways, eliciting allergic symptoms in susceptible subjects. In the context of studying the mechanism for the release of respirable allergen-bearing particles from olive pollen on hydration, we analyzed the protein content of these novel particles, named by us as pollensomes. In order to identify the highest possible number of proteins present in pollensomes, we analyzed tryptic-derived peptides by nHPLC coupled to LTQ-Orbitrap XL, where peptides were fragmented combining three different types of fragmentation, *i.e.* collision induced dissociation (CID), higher energy collision induced dissociation (HCD) and electron transfer dissociation (ETD).

As a result, pollensomes display a discrete set of proteins, some of which previously described in exosomes derived from animal cells. In addition, two major allergens of olive pollen were detected. These findings indicate that pollensomes from germinated pollen serve as vehicles for allergens, with a potential role on the induction of allergic reactions. The performance of the LTQ-Orbitrap XL for these analyses and the complementarity of the parallel detection method proposed here are also discussed.