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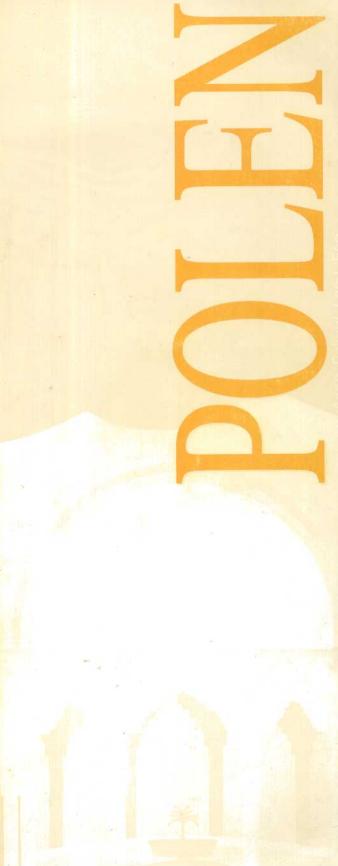
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Sequence polymorphism of the major olive pollen allergen (Ole e 1) in defined cultivars

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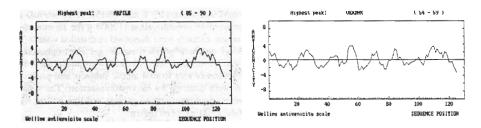
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Ole e 1 is considered to be the major allergen from olive pollen. The protein presents several glycosylation forms, and its amino acid sequence displays relevant homology to pollen proteins from maize, tomato, ryegrass, birch, rice, *Arabidopsis* etc. This identity rises to >85% when compared to Ole e 1-like proteins from members of the *Oleaceae* family (lilac, privet, ash, forsythia) (see review of Rodríguez et al., 2002). Ole e 1 itself exhibits microheterogeneities at several positions of its amino acid sequence (Villalba et al., 1994; Lombardero et al., 1994).

In this work, Ole e 1 sequences were amplified by RT-PCR procedures using total RNA from mature pollen of eight different cultivars of olive (Olea europaea L.). Ole e 1 amplified sequences were cloned and sequenced. The sequences obtained were submitted to the GenBankTM/EMBL Database. The analysis of the obtained sequences showed the existence of a high number of microheterogeneities in the analysed sequences, which were particularly profuse in the 5' and the 3' coding regions. Tree-view analysis of microheterogeneities showed that the inter-cultivar viariability detected was higher than the intra-cultivar variability present in at least three clones of Ole e 1 for each cultivar. An additional N glycosylation motif was detected in one of the cultivars examined. The changes detected within the Ole e 1 molecule affect in many cases immunodominant T-cell epitopes, and produce differences in the hydrophilicity and antigenecity profiles, also affecting the predicted secondary structures of the allergen in the majority of the cultivars studied.

The procedure described here offers a very useful molecular tool to establish discrimination between olive tree cultivars, and to study the basis of the interaction between the allergens and the human immune system. The expression of the obtained clones could be used to define homogeneous Ole e 1 molecules valuable for the improvement of clinical diagnosis and therapy of olive pollen allergy.



Figs. 1 and 2: Antigenicity profiles of the Ole e 1 allergen deduced sequences in two olive cultivars.

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LOMBARDERO, M.; BARBAS, J.A.; MOSCOSO DEL PRADO, J. & CARREIRA, J. 1994. cDNA sequence analysis of the main olive allergen, Ole e 1. Clin. Exp. Allergy 24: 765-770.

RODRÍGUEZ, R.; VILLALBA, M.; BATANERO, E.; GONZÁLEZ, E.M.; MONSALVE, R.I.; HUECAS, S.; TEJERA, M.L. & LEDESMA, A. 2002. Allergenic diversity of the olive pollen. Allergy 57(Suppl. 71): 6-16.

VILLALBA, M.; BATANERO, E.; MONSALVE, R.I.; GONZÁLEZ DE LA PEÑA, M.A.; LAHOZ, C. & RODRÍGUEZ, R. 1994 Cloning and Expression of Ole e I, the major allergen from olive tree pollen. J. Biol. Chem. 269: 15217-15222.