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EVOLUTION OF THE ALLERGENIC POTENTIAL IN PEACH AND NECTARINE FRUITS DURING RIPENING

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According to recent epidemiological studies, food allergies enhanced during recent decades in many countries. Allergies to fruits represent also an increasing problem and studies should be addressed to produce hypoallergenic fruits. In peach the major allergen has been identified as a Lipid Transfer Protein (LTP) and in the present research the evolution of the allergenic potential of different peach and nectarine varieties has been monitored throughout ripening and in relation to postharvest treatments. Fruits of peach cv Royal Gem, Zorzi, of nectarine cv Rita Star, Early Giant and Mariadorata, and of flat type (Platicarpa), were harvested in correspondence of commercial ripeness (T0) and maintained in air for few days at room temperature to reach the full ripe stage or at 4°C for 3 weeks. Treatments with propylene were also performed. Northern blot analyses were carried out on total RNA extracted from epicarp and mesocarp to study *Pp-LTP1* gene expression. Immunological studies were performed by means of a polyclonal antibody raised against the purified protein.

Expression analysis showed that *Pp-LTP1* transcripts accumulated only in the epicarp. With the exception of cv Rita Star the strongest accumulations have been detected in epicarp of all varieties at T0. A decreasing trend of expression was observed in all fruits kept in air and at 4°C, but not in Platicarpa. Excluding Mariadorata fruits, propylene treatment did not appear to affect *Pp-LTP1* gene expression. Western blots revealed the presence of LTP only in epicarp of all varieties, but not in Rita Star, and showed that the protein markedly increased in full ripe fruits maintained in air: this might indicate the presence of a lag between gene transcription and accumulation of secreted functional LTP. According to these results, Rita Star appears to be a variety with a low allergenic potential, opposite to Royal Gem which seems to represent the most allergenic one. Further analyses are currently being directed to study the promoter sequences of Rita Star and Royal Gem *Pp-LTP1* gene by means of *in silico* approaches, to characterize putative elements responsible for the different LTP transcript accumulation profile during the ripening process.