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A SENSITIVE AND SPECIFIC TOOL FOR THE DETECTION OF *MAL D 1* ALLERGEN GENE TRANSCRIPTS IN APPLE

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While apples are usually recommended for an healthy diet, apple allergenicity is becoming an important issue for a growing number of European citizens. In fact, apples are one of the most allergenic foods, ranking first among the *Rosaceae* fruits. Mild oropharyngeal symptoms to fresh apples, known as Oral Allergy Syndrome, are common in north-west European population. This phenomenon is primarily due to the cross-reactivity between Bet v 1, the major allergen in birch pollen, and its homologue protein in apple, Mal d 1. *Mal d 1* is the most complex allergen gene family of apple, composed by 31 members. *Mal d 1* genes are mainly organized in two clusters on the homeologous LGs 13 and 16 but other sequences have been found also on LG6, 1 and 4. They code for different Mal d 1 isoforms that share a high sequence and structural similarity. These proteins are classified as Pathogenesis Related Proteins of class 10, for which the biological function is not well understood yet. Despite the high similarity, different Mal d 1 proteins have various functional specialisation and different binding affinities to IgE, suggesting a different importance in allergenicity. Therefore, it is necessary to understand each Mal d 1 specific characteristic and function. Up to now a fine resolution was successfully obtained at structural genomic level but functional studies are still poor and not exhaustive, often limited to few genes. The aim of this work was to develop a tool for the specific study of each single *Mal d 1* isoallergen gene from a quantitative point of view. SNPs among genes were exploited to unravel the complexity of *Mal d 1* expression and a complete set of 31 highly specific primer pairs for qPCR with the SYBR Green chemistry was developed. The expression profiling of the *Mal d 1* family in different tissues and in response to stresses will allow a wide comprehension of the feature and putative function of each one, with important implications both for basic research and for apple breeding that, through expression and association studies, can be directed to low allergenic fruits, desirable to meet nutritional needs and to diminish dietary restriction.