

IDENTIFICATION OF CANDIDATE GENES INVOLVED IN POLLEN-PISTIL INTERACTION IN *CITRUS*

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Citrus, laser capture microdissection, microarray, self-incompatibility

Compared to what is known in model species, reproductive biology in citrus is still poorly understood. Although in recent years several efforts have been made to study pollen-pistil interaction and self-incompatibility, little is known about the molecular mechanisms regulating these processes. The understanding of self-incompatibility mechanism in mandarins, which is related to seedlessness, is of outstanding interest for breeding.

Here we report the identification of possible candidate genes regulating pollen-pistil interaction and self-incompatibility in clementine (*Citrus clementina* Hort. ex Tan.). These genes have been identified comparing transcriptomes of laser-microdissected stylar canal cells isolated from two clementine genotypes differing for self-incompatibility response: ‘Comune’, self-incompatible; and ‘Monreal’, a natural self-compatible mutation of ‘Comune’. These genotypes were previously characterized by histological assays, which demonstrated that the mutation leading to self-compatibility in ‘Monreal’ affected the style functions regulating pollen rejection.

Transcriptome profiling was performed using Affymetrix Citrus Genechip representing up to 33,000 citrus transcripts. Among them, only 10 genes resulted overexpressed in ‘Comune’ stylar canals and 6 genes in ‘Monreal’ ones. The results of microarray hybridizations were validated using real time PCR. Most of the differentially expressed genes are not functionally annotated in citrus or other plant species. Interestingly, 3 of the ‘Comune’ overexpressed genes clustered in a range of about 10 kb in the clementine genome. The clustered genes shows similar domains in their predicted protein sequences, and are close to a DELLA gene, previously identified in self-pollinated ‘Comune’ styles with stigmas by cDNA-AFLP transcript profiling. Moreover, a time course analysis showed different expression patterns of selected genes in virgin and self-pollinated styles with stigmas of the two genotypes during pistil maturation and pollen tube elongation (from 0 to 8 days after pollination). Since most of the candidate genes were not previously characterized, further analyses are needed to reveal their specific role in the interaction between pollen tubes and stylar canal cells.