

# ***In silico* ANALYSIS OF THE ETHYLENE RESPONSE FACTOR (ERF) GENE FAMILY IN *Malus***

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We have investigated *Malus* genome databases of expressed sequence tags (EST) in order to identify genes coding for functionally characterized proteins sharing sequence similarity to ethylene response factors. Approximately 250,000 EST sequences from 111 libraries were investigated and 66 paralogs of ERF proteins were identified. In *Vitis* and *Populus*, perennial species with complete genome sequence, 197 and 57 predicted ERF orthologs were identified, respectively; thus suggesting that our analyses have uncovered a significant number of apple orthologs. We found evidences of differential sequence evolution in the ERF families from *Arabidopsis* and *Malus*. The presence of conserved motifs distinct from the AP2/ERF DNA binding sequence in apple ERF orthologs allowed clustering into ten groups. Evidence from model species suggests that distinct groups perform distinct ethylene-mediated functions in plant physiology and metabolism. Prediction analysis of apple protein uncovered further differences between *Malus* versus *Arabidopsis* and *Populus* ERFs including its unfoldability prediction, isoelectric point and sub-cellular localization. *In silico* transcriptional profiling was performed with a sub-set of *Malus* putative proteins and suggested that the identified apple proteins are involved in distinct biological functions in response to ethylene, such as developmental control and stress responses. An association between functional and genetic divergence was observed in the studied apple sequences. These results demonstrate the power of comparative genomics between model systems and economically important crop species to elucidate several aspects of plant physiology and metabolism.