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Abstract:

Annotation of the genome sequence of *Arabidopsis thaliana* has identified a diverse array of 245 full-length cytochrome P450 monooxygenase (P450) genes whose known functions span the synthetic gamut from critical structural components (phenylpropanoids, fatty acids, sterols) to signaling molecules (oxylipins, brassinosteroids, abscisic acid, gibberellic acid) and defense compounds (alkaloids, terpenes, coumarins). Numerous others in this collection mediate functions that are now being addressed using microarray and oligoarray technologies, molecular modeling, heterologous expression and insertional mutageneses. Profilings of their constitutive and inducible transcript levels have begun to cluster P450s that are likely to mediate tissue-specific and stress-specific monooxygenations. With proper appreciation of the high identities that exist among some of the most recently-duplicated P450 sequences, these studies have begun to differentiate P450s with early response functions leading to production of stress signaling molecules and late response functions leading to the synthesis of protective compounds. Further functional analyses of these P450 sequences with perspectives on their response profiles rely on a variety of theoretical modeling and experimental approaches that can ultimately be tied to the transcriptional profiles and genetic mutants. This review surveys historical and evolutionary aspects of P450 studies, expression variations among *Arabidopsis* P450 loci, catalytic site regions critical for substrate recognition and, finally, genetic mutations/disruptions that can ultimately tie biochemical reactions to physiological functions in a manner not yet possible in most other organisms.