

UNDERSTANDING THE SORGOLEONE BIOSYNTHETIC PATHWAY: MOLECULAR AND BIOCHEMICAL APPROACHES TO ENHANCING ALLELOPATHY

Dayan F. E.¹, Rimando A. M.¹, Kagan I. A.¹, Cook D.¹,
Baerson S. R.¹, Pan Z.¹, Nanayakkara N. P. D.²

¹USDA, ARS, NPURU, National Center for Natural Products Research, University of Mississippi, University, MS, 38677, USA; ²National Center for Natural Products Research, University of Mississippi, University, MS 38677, USA.

Sorgoleone is the main allelopathic component produced by sorghum (*Sorghum bicolor*) root hairs. Its biosynthetic pathway, the key genes and their gene products involved in the biosynthesis are being investigated through chemical, biochemical and molecular approaches. ¹³C-NMR analysis of sorgoleone, extracted from seedlings fed with various ¹³C-labeled substrates, indicated that the putative pathway arises from the convergence of the fatty acid and polyketide synthase pathways for the aliphatic tail and quinone ring, respectively. The tail, derived from an unusual C16:3 fatty acid precursor possessing a terminal vinyl bond is probably synthesized in the plastids, exported into the cytosol and converted into 5-pentadecatriene resorcinol by a polyketide synthase. This resorcinol intermediate, which was identified in root hair extracts, is subsequently methylated by a SAM-dependent *O*-methyltransferase and dihydroxylated by a P450 monooxygenase to yield the reduced form of sorgoleone. Sorgoleone converts to the more stable oxidized form in the presence of air. A root hair-specific expressed sequence tag (EST) analysis was performed on approximately 5,500 random sequences from a cDNA library. Highly expressed candidate sequences representing all of the putative target enzyme classes suggested by the retrobiosynthetic study were identified within the root hair EST data set. Functional analysis of some of these genes has thus far led to the characterization of a resorcinol specific *O*-methyltransferase catalyzing a key step in the biosynthetic pathway of sorgoleone. This *O*-methyltransferase is different from all others so far reported in the literature, in that it can use lipid resorcinols as substrates. Genes encoding for enzymes catalyzing other key steps are being characterized.

