

**Title** A peanut seed lipoxygenase responsive to *Aspergillus* colonization  
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### Abstract

Several lines of evidence have indicated that lipoxygenase enzymes (LOX) and their products, especially 9S- and 13S-hydroperoxy fatty acids, could play a role in the *Aspergillus*/seed interaction. Both hydroperoxides exhibit sporogenic effects on *Aspergillus* spp. (Calvo, A., Hinze, L., Gardner, H.W. and Keller, N.P. 1999. Appl. Environ. Microbiol. 65: 3668–3673) and differentially modulate aflatoxin pathway gene transcription (Burow, G.B., Nesbitt, T.C., Dunlap, J. and Keller, N.P. 1997. Mol. Plant-Microbe Interact. 10: 380–387). To examine the role of seed LOXs at the molecular level, a peanut (*Arachis hypogaea* L.) seed gene, PnLOX1, was cloned and characterized. Analysis of nucleotide sequence suggests that PnLOX1 encodes a predicted 98 kDa protein highly similar in sequence and biochemical properties to soybean LOX2. The full-length PnLOX1 cDNA was subcloned into an expression vector to determine the type(s) of hydroperoxide products the enzyme produces. Analysis of the oxidation products of PnLOX1 revealed that it produced a mixture of 30% 9S-HPODE (9S-hydroperoxy-10E, 12Z-octadecadienoic acid) and 70% 13S-HPODE (13S-hydroperoxy-9Z, 11E-octadecadienoic acid) at pH 7. PnLOX1 is an organ-specific gene which is constitutively expressed in immature cotyledons but is highly induced by methyl jasmonate, wounding and *Aspergillus* infections in mature cotyledons. Examination of HPODE production in infected cotyledons suggests PnLOX1 expression may lead to an increase in 9S-HPODE in the seed.