SUPPLEMENTAL DATA LEGENDS

Figure 1S. Sequence of *NtDES1*. Nucleotides are numbered as in the DES1A clone. The 16 first bases, absent from the DES1A clone as determined in a 5'RACE PCR experiment, are in italics. The targets of the HPCEf and HPCEr primers used for initial amplification of DESB3 are indicated by arrows. An asterisk denotes the position of the Thr residue conserved in the O_2-binding pocket (boxed) of P450 monoxygenases, but not in CYP74 enzymes. Other conserved P450s features are the peptide sequences ETLR and PDDFIPDRF (underlined) and the heme-binding Cys (#) in the heme-binding domain (boxed). The modified O_2-binding pocket (domain A) and the heme-binding domain typified by a conserved Cys (Cys-432 in NtDES1, domain D) are found in the C-terminal half of the protein. ETLR and PDDFIPDRF sequences, characteristic of domains B and C of eukaryotic P450s, respectively, are correctly located between domains A and D. In NtDES1, as in other members of the CYP74D subfamily, a characteristic Thr in the O_2-binding pocket is replaced by Ala (Ala-290), obeying the *consensus* AGxx**A**. The sequence surrounding Cys-432 in the heme-binding domain follows the CYP74 *consensus* NKQ**C**(A/P)(G/A)K(D/N)xV as proposed (Chapple, 1998).

Figure 2S. *NtDES1* transcript accumulation upon biotic stress. Northern analysis was performed on 20 µg total RNA isolated from: **A** tobacco cells treated for the indicated time with 30 µg/ml *Ppn* elicitor or untreated control cells; **B** stem and closest adjacent leaf from plants of WT and *NtLOX1*-antisense *N. tabacum* stem-infected with *Ppn* race 0, or stem from mock-inoculated plants (control). Ethidium bromide staining of the gels is shown in lower panels. The experiments were repeated twice; one representative image is shown.