CHR is an enzyme that co-acts with CHS to produce a branch in the first step of the flavonoid pathway. CHS acting alone catalyzes the sequential coupling of three malonyl-CoA molecules with coumaroyl-CoA to produce 4,2',4',6'-tetrahydroxychalcone (Heller and Hahlbrock, 1980). However, in the presence of CHR and NADPH the oxygen function of the polyketide intermediate, which would produce the 6'-hydroxyl of the chalcone, is reduced and then eliminated as water prior to cyclization, resulting in the formation of 4,2',4'-trihydroxychalcone (6'-deoxychalcone). This chalcone is the precursor of the 5-deoxy series of flavonoids and isoflavonoids (Harborne, 1988), which includes nodulation induction factors (Maxwell et al., 1989) as well as pterocarpan phytoalexins of the Leguminosae (Dixon et al., 1983).

In alfalfa (*Medicago sativa*) increased phytoalexin production in response to elicitation or infection is a consequence of the induction of genes encoding enzymes for this pathway (Dixon et al., 1992). Although CHR is an essential first step in the synthesis of 5-deoxy isoflavonoids, CHR transcript induction has been demonstrated only in soybean (Welle and Grisebach, 1989), this being the source of the first and only other CHR gene isolated to date.

An alfalfa cDNA library (Gowri et al., 1991) representing mRNA from elicited suspension-cultured cells was screened for CHR. A 650-nucleotide probe was generated by PCR from soybean genomic DNA and 20-mer primers based on the soybean CHR sequence (Welle et al., 1989) as well as pterocarpan phytoalexins of the Leguminosae (Dixon et al., 1983).

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Table I. Characteristics of alfalfa cDNAs encoding CHR

| Organism: | *Medicago sativa* cv Apollo. |
| Gene Product Function: | Presumed to co-act with CHS in the synthesis of 6'-deoxychalcone. |
| Source: | cDNA library in λZapII prepared from poly(A)+ RNA isolated from elicited suspension-cultured cells (Gowri et al., 1991). |
| Sequencing Technique: | Both strands sequenced from Bluescript plasmid by the automated dideoxy chain termination sequencing technique using oligonucleotide primers. |
| Gene Identification: | DNA sequence comparison to published sequence of a soybean CHR gene (GenBank accession number X55730). |
| Structural Features of cDNAs: | CHR7 is 1142 nucleotides in length, with a 47-nucleotide 5' untranslated region, a 936-nucleotide open reading frame, and a 159-nucleotide 3' untranslated region. CHR12 is 1201 nucleotides in length, with an 18-nucleotide 5' untranslated region, a 936-nucleotide open reading frame, and a 257-nucleotide 3' untranslated region. |
| Features of the Deduced Protein: | Open reading frames for CHR7 and CHR12 each encode a polypeptide of 312 amino acids. Both polypeptides have Leu zipper motifs between amino acid residues 102 and 123 and have sequences conforming to signature sequences for the aldose-keto reductase superfamily. |
| Expression Characteristics: | Run-on transcription analysis confirms that CHR induction in elicited cells results from increased transcriptional activation, which is closely coordinated to that of CHS. |
reported here. Southern blots indicated that alfalfa CHR is encoded by three to five genes (data not shown).

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The EMBL/GenBank/DDBT accession numbers for the sequences reported in this article are U13924 (CHR12) and U13925 (CHR7).

LITERATURE CITED


