

Table 1 Suppl. Primers used in this study (F - forward, R - reverse).

Name	Sequence
DXR-F	5'-GGYTCYATTGGMACYCAGAC-3'
DXR-R	5'-AACCGCA TATCRGGCCAWCC-3'
DXR-GSP1	5'-CCCTCTGGCAAACCCTGGATACT-3'
DXR-GSP2	5'-TGGGAATGAACATGGTGTCCAAGG-3'
DZR(ORF)-F	5'-AACTGCAGATG GATTGAGGCTTCCCTTCTCG-3' (the start codon was boxed and <i>Pst</i> I was underlined)
DXR(ORF)-R	5'-ATGCGGCCGC TAA GCAGGGACAGGACTTAAACC-3' (the stop codon was boxed and <i>Not</i> I was underlined)
DzDXR(RT)-F	5'-GAAGTGAAGGTTGCTGATG-3'
DzDXR(RT)-R	5'-GATAGACTGTGGGTGTATG-3'
GAPDH-F	5'-TTTGGTGAAAAGTCAG TCGCA-3'
GAPDH-R	5'-TCGGAGCAGAAATGACAACCT-3'

[illegible]

Fig. 1 Suppl. Multiple sequence alignment of DzDXR, *E. coli* DXR, and other plant DXRs. Gaps in the sequence are represented with a *dash*. The putative cleavage site of plastidial signal peptide in DzDXR is indicated by an *arrow*. The P(P/Q) PAWPG(R/T) A motif, two NADPH binding motifs GSTGS(I/V)GT and LAAGSN(V/I), and two substrate binding motifs LPADSEHSAI and NKGLEVIEAHY were *overlined* and marked with I, II, III, IV, and V, respectively. The sequences of DXRs are accessible at the GenBank with the following accession numbers: *Arabidopsis thaliana* (AF148852), *Artemisia annua* (AF182287), *Catharanthus roseus* (AAF65154), *Dioscorea zingiberensis* (KY131955), *Escherichia coli* (NP_414715), *Hevea brasiliensis* (ABD92702), *Nicotiana tabacum* (NP_001312964), *Solanum lycopersicum* (NP_001234553), *Solanum tuberosum* (XM_006344994), *Oryza sativa* (AAL37560), *Withania somnifera* (GQ921844), and *Zea mays* (DAA53825).