A New 1-Deoxy-D-xylulose 5-Phosphate Reductoisomerase Gene Encoding the Committed-Step Enzyme in the MEP Pathway from *Rauvolfia verticillata*

Zhihua Liao[a], Rong Chen[a], Min Chen[a,*], Chunxian Yang[a], Qiang Wang[b], and Yifu Gong[c]

[a] Laboratory of Natural Products and Metabolic Engineering, Institute of Biotechnology, Key Laboratory of Eco-environments in Three Gorges Reservoir Region (Ministry of Education), School of Life Sciences, Southwest University, Chongqing 400715, China. Fax: 86-23-68 36 71 46. E-mail: mminchen@swu.edu.cn
[b] China Rural Technology Development Center, Beijing 100045, China
[c] Faculty of Life Science and Biotechnology, Ningbo University, Ningbo 315211, China

* Author for correspondence and reprint requests

Z. Naturforsch. **62 c**, 296–304 (2007); received August 14/October 13, 2006

1-Deoxy-D-xylulose 5-phosphate (DXP) reductoisomerase (DXR; EC 1.1.1.267) catalyzes a committed step of the methylerythritol phosphate (MEP) pathway for the biosynthesis of pharmaceutical terpenoid indole alkaloid (TIA) precursors. The full-length cDNA sequence was cloned and characterized from a TIA-producing species, *Rauvolfia verticillata*, using rapid amplification of cDNA ends (RACE) technique. The new cDNA was named as *RvDXR* and submitted to GenBank® to be assigned with an accession number (DQ779286). The full-length cDNA of RvDXR was 1804 bp containing a 1425 bp open reading frame (ORF) encoding a polypeptide of 474 amino acids with a calculated molecular mass of 51.3 kDa and an isoelectric point of 5.88. Comparative and bioinformatic analyses revealed that RvDXR showed extensive homology with DXRs from other plant species and contained a conserved transit peptide for plastids, an extended Pro-rich region and a highly conserved NADPH-binding motif in its *N*-terminal region owned by all plant DXRs. The phylogenetic analysis revealed that DXRs had two groups including a plant and bacterial group; RvDXR belonged to angiosperm DXRs that were obtained from *Synechocystis* through gene transfer according to the phylogenetic analysis. The structural modeling of RvDXR showed that RvDXR had the typical V-shaped structure of DXR proteins. The tissue expression pattern analysis indicated that *RvDXR* expressed in all tissues including roots, stems, leaves, fruits and followers but at different levels. The lowest transcription level was observed in followers and the highest transcription was found in fruits of *R. verticillata*; the transcription level of *RvDXR* was a little higher in roots and stems than in leaves. The cloning and characterization of *RvDXR* will be helpful to understand more about the role of *DXR* involved in *R. verticillata* TIA biosynthesis at the molecular level and provides a candidate gene for metabolic engineering of the TIAs pathway in *R. verticillata*.

Key words: Cloning, Characterization, *DXR* Gene, *Rauvolfia verticillata*