ABSTRACT

*Picrorhiza kurrooa* is a medicinally important endangered herb known to yield hepatoprotective terpene derivative picrosides. The present study was carried out to understand the molecular basis of picrosides biosynthetic pathway wherein the objectives were to clone and characterize various genes involved in picrosides biosynthetic pathway and understanding their spatio-temporal regulation. The work showed the unequivocal presence of these compounds in leaf tissue, as opposed to the previous reports emphasizing their presence in underground tissue. This observation has implications in conserving this endangered plant species through modifications in harvesting practice. Separate experiments using pathway specific inhibitors, and [1-^{13}C] glucose showed the prominent role of MEP pathway in the biosynthesis of iridoid moiety of picrosides. The present work reported cloning of twelve genes associated with picrosides biosynthetic pathway, out of which, nine were cloned to full-length and three were partial genes. Full-length genes were *Pkdcs* (2317 bp), *Pkdcr* (1767 bp), *Pkcme* (1674 bp), *Pkhdr* (1701 bp), *Pkacth* (1545 bp), *Pkhmgr* (2241 bp), *Pkippi* (987 bp), *Pkgdps* (1434 bp) and *Pktih* (1545 bp) and partial genes were *Pkhmgs*, *Pkpal* and *Pkcaff*. Picrosides biosynthetic pathway was up-regulated by osmotic stress as evidenced from picrosides content and gene expression analysis, Other cues namely light, MeJA, ABA, H_{2}O_{2} and SA modulated the picrosides content and few genes of the pathway. Data suggested that of all the twelve genes analysed, *Pkcaff* always exhibited modulation in response to cues that modulated picrosides content.