Metabolic Control of Taxane Accumulation at the mRNA Level

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Plant cell cultures represent a potential method for the large-scale production of important secondary metabolites. One important example is the anti-cancer agent paclitaxel, a secondary metabolite produced by Taxus. Paclitaxel is a member of a family of related compounds known as taxanes. In *Taxus* suspension cultures, paclitaxel is often less than 10% of the total taxanes present. This low selectivity represents an excellent opportunity to increase overall accumulation. The addition of the enzyme elicitor methyl jasmonate has been shown to increase secondary metabolism in a wide variety of plants, including the Taxus system. Methyl jasmonate increases total taxane accumulation as well as paclitaxel levels. In addition, elicitation with methyl jasmonate can be used as a tool to elucidate biosynthetic pathway regulation. We have examined the distribution of various taxanes produced in *Taxus* suspension cultures with and without methyl jasmonate elicitation. We have also used Northern blot analysis of several known genes in the taxane biosynthetic pathway to determine the relationship between gene expression and the accumulation of taxane metabolites. There is evidence for regulation of taxane biosynthesis occurring at the mRNA level. Work presented here provides the basis for ongoing efforts to understand the regulation of the taxane pathway. In the future, the identification of pathway bottlenecks may lead to the development of directed strategies, such as genetic transformation, to increase paclitaxel accumulation.