Global Proteome Analysis of Developing Seeds of *Jatropha curcas*

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The potential of *J. curcas* seeds as a source of raw material for the production of biodiesel is being hampered by a lack of understanding regarding the enzymatic machinery responsible for the biosynthesis of fatty acids, tryacylglycerols and toxic phorbol esters. Using a GelLC-MS/MS approach, we undertook a global proteome analysis of the sub-proteomes of isolated plastids, inner integument and endosperm from developing seeds which resulted in the identification of 1250, 895, and 679 protein groups respectively. These results allowed us to reconstitute most of the enzymatic steps of the biosynthesis of fatty acid and amino acids, as well as several metabolic pathways related to the secondary metabolism of plants, including key enzymes of the biosynthetic pathway of phorbol esters, the main toxic constituents of the seeds. Apart from curcin, no other protein of known toxic properties was identified in either of the sub-proteomes. Besides providing the first picture of the *J. curcas* seeds proteome these results will also give us the possibility of devising experimental approaches for tailoring the fatty acid composition of the seeds to suit specific industrial applications, as well as to obtain varieties which do not accumulate phorbol esters in the seeds.

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