

Proteomic Alteration During Storage of *Curcuma Longa* Rhizomes

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The rhizomes of genus *Curcuma* are extensively used as spices, food preservatives, coloring materials, cosmetics and medicines. The *Curcuma* becomes dormant during the dry season. The changes in proteins during storage of *Curcuma longa* have not been investigated in detail. We employed proteomic technology to study the protein expression from the day of harvest to the commencement of sprouting of *Curcuma longa*. The two dimensional gel electrophoresis patterns (pH 4-7) of the rhizomes showed a high abundance of proteins with pI in the range of 3-5 and low abundance with pI in the range of 5-7. Microscale solution-phase isoelectric focusing (Zoom) was employed to enrich the low abundance proteins in the pH range of 5.4-10 and improve the separation of those proteins in the acidic range from 3-5.4. The total storage period was 77 days. Samples were drawn at an interval of 7 days from the harvest until sprouting. The proteomic patterns of the storage period (0, 7, 14, 21, 35, 42, 49 and 70 days) were studied in these two pH ranges. In the pH range from 3-5.4, the expression of ribulose 1, 5-bisphosphate dehydrogenase, actin, anionic peroxidase swpa4, maturase and photosystem I assembly protein ycf4 were increased and putative oxygen evolving enhance protein I, hypothetical protein MeviPp13 and MLP_like protein 423 were decreased from 0 to 70 days, while in the pH range from 5.4-10, the expression of eight identified proteins were expressed only at 70 days. Sporamin, the major storage protein of the tuberous roots of sweet potato was highly expressed in the dormancy period and lower expression seen in the sprouting period. The expression of 60S ribosomal protein L10, ribosomal protein subunit 2, ribosomal protein S7, Vacuolar ATP synthase

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subunit E and alcohol dehydrogenase II were increased in the visible sprouting (70 days). These results represent the first proteomic patterns during storage period of *Curcuma longa*.

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