

A proteomics approach to evaluate expression host and downstream recovery compatibility: Analysis of maize proteomics using ion exchange chromatography and 2-D electrophoresis

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Maize is a potentially cost-effective host for production of recombinant proteins. Regardless of host, protein recovery is generally the most costly aspect in the production of recombinant proteins. Proteomics could provide guidance as to what recombinant proteins are best suited to simplify recovery from the native host proteins. The extraction and purification behaviors of native maize proteins will determine favorable matches to recombinant proteins. Our characterization of isoelectric point (pI), molecular weight (MW), and hydrophobicity revealed preferred extraction pH and ion exchange elution profiles for enhanced selection recovery. Based on these results, step elution cation exchange chromatography was selected for further mapping of host protein properties to separation performance because most maize germ proteins have pIs greater than 4, the preferred extraction pH. Since not all recombinant proteins may be effectively extracted at pH 4, we also examined step elution anion exchange chromatography at pH 7. Under these conditions the level of host proteins in the extract is much higher. The combined results will be used for a two-fold purpose of evaluating the ability to correlate the 3-D characterization of the proteins with elution behavior and also to identify conditions where there are fractions of very low native protein content that could be matched to the elution characteristics of potential recombinant proteins. 2-D gel electrophoresis combined with hydrophobic partitioning in an aqueous two-phase system provides our primary 3-D characterization.