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Korean mother's breast milk proteomic analysis; Postpartum 1, 3, and 6 weeks

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Purpose: This study is for monitoring proteome expression patterns and detecting specifically expressed proteins in breast milk among Korean postpartum 1 week, 3 week, and 6 weeks mothers. A quantitative shotgun proteomic approach was used in identifying breast milk proteins and revealing their relative expression amount.

Methods: For each representing week sample, two independent breast milk samples from two mothers were pooled then three replicated shotgun proteomic analysis were conducted. Casein which is highly abundant proteins in breast milk was removed and then trypsin was treated to produce digested peptides. The peptide were loaded in the home-made 15cm revers phase C18 (5μm) fused-silica capillary column and then through LC-MS/MS (LTQ finnigan (Thermo Fisher Scientific, Waltham, MA, USA)), the eluted peptide were analyzed. Through SEQUEST, the MS/MS spectra were used in protein identification by searching against human database in UNIPROT.

Results: For relative amount of proteins were estimated from the normalized spectral count. For each sample, 92~122 non-redundant proteins were identified. In the casein removed breast milk, glycoproteins, metabolic enzyme, and chaperon enzyme such as lactoferrin, tenascin, Carboxylic ester hydrolase, Xanthine dehydrogenase, Fatty acid synthase and Clusterin were highly presented.

Conclusions: The comparison analysis for the 43 proteins which were reproducibly identified in all three replication revealed that 20 proteins were statically significant differentially expressed. Among the differentially expressed proteins, Ig lambda-7 chain C region and Tenascin were drastically decreased with time.

Biography

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Notes:

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