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Weak cation magnetic separation technology and MALDI-TOF-MS in screening serum protein markers in primary type I osteoporosis

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ABSTRACT. We investigated weak cation magnetic separation technology and matrix-assisted laser desorption ionization-time of flight-mass spectrometry (MALDI-TOF-MS) in screening serum protein markers of primary type I osteoporosis. We selected 16 postmenopausal women with osteoporosis and nine postmenopausal women as controls to find a new method for screening biomarkers and establishing a diagnostic model for primary type I osteoporosis. Serum samples were obtained from controls and patients. Serum protein was extracted with the WCX protein chip system; protein fingerprints were examined using MALDI-TOF-MS. The preprocessed and model construction data were handled by the ProteinChip system. The diagnostic models were

established using a genetic arithmetic model combined with a support vector machine (SVM). The SVM model with the highest Youden index was selected. Combinations with the highest accuracy in distinguishing different groups of data were selected as potential biomarkers. From the two groups of serum proteins, 123 cumulative MS protein peaks were selected. Significant intensity differences in the protein peaks of 16 postmenopausal women with osteoporosis were screened. The difference in Youden index between the four groups of protein peaks showed that the highest peaks had mass-to-charge ratios of 8909.047, 8690.658, 13745.48, and 15114.52. A diagnosis model was established with these four markers as the candidates, and the model specificity and sensitivity were found to be 100%. Two groups of specimens in the SVM results on the scatterplot were distinguishable. We established a diagnosis model, and provided a new serological method for screening and diagnosis of osteoporosis with high sensitivity and specificity.

Key words: Primary type I osteoporosis; Proteomics;
Weak cation magnetic separation technology; Biomarker;
Matrix-assisted laser desorption ionization-time of flight-mass spectrometry

