Background: In the past decades, there is no single clinical chemical marker meets both the sensitivity and specificity criteria required for diagnosis or prognosis disease. Pancreatic cancer is a heterogeneous disease that finding a single disease-related biomarker is like fishing for a needle in the ocean. Although CEA, CA 19-9 and CA 125 have been commonly used as biomarker in pancreatic cancer, but due to the limited sensitivity and specificity, these markers is still been hindered in the clinical applications. Considering the early diagnosis of pancreatic cancer will significantly improve the prognosis of patients. It’s urgent to find a minimally invasive and efficient method of detecting early pancreatic cancer. The purpose of this study is to identify discriminating protein patterns and find potential biomarker in serum samples by matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) MS between pre/postoperative pancreatic cancer patients and healthy controls.

Methods: We collected the serum samples of pancreatic cancer patients (preoperative and postoperative) and healthy controls from the First Affiliated Hospital of Xi’an Jiaotong University (201009–201203). 23 serum samples from PC patients (12 preoperative and 11 postoperative) and 76 from healthy controls were analyzed using matrix-assisted laser desorption and ionization time-of-flight mass spectrometry (MALDI-TOF MS) technique combined with Magnetic Beads-based weak cation-exchange chromatography (MB-WCX). ClinProTools software selected several markers that make a distinction between pre/postoperative pancreatic cancer patients and healthy controls.

Results: The serum peptidome fingerprints of all preoperative or postoperative pancreatic cancer patients and 76 healthy controls were detected in this study. 49 m/z distinctive peaks were found among the three groups, of which 33 significant peaks with a P < 0.001 were detected. Two proteins (m/z = 1866.83 and 4055.17) were both down-regulation in pancreatic cancer which screen out by software can distinguish the pre/postoperative pancreatic cancer patients and the healthy controls. About 15 proteins in postoperative group tend to return to normal group, may be potential biomarkers in assessment of pancreatic cancer resection.

Conclusion: Using a MB-MALDI-TOF MS method to generate serum peptidome profiles of pancreatic cancer will provide a new approach to identify potential biomarkers for diagnosis and prognosis of pancreatic cancer.