Towards a comprehensive proteome of normal and malignant human colon tissue by 2-D-LC-ESI-MS and 2-DE proteomics and identification of S100A12 as potential cancer biomarker

The aim of this study was to characterize the proteome of normal and malignant colonic tissue. We previously studied the colon proteome using 2-DE and MALDI-MS and identified 734 proteins (RoeBer, M., Rollinger, W., Palme S., Hagmann, M., et al., Clin. Cancer Res. 2005, 11, 6550-6557). Here we report the identification of additional colon proteins from the same set of tissue samples using a complementary nano-flow 2-D-LC-ESI-MS. In total, 484 proteins were identified in colon. Of these, 252 had also been identified by the 2-DE/MALDI-MS approach, whereas 232 proteins were unique to the 2-D-LC-ESI-MS analysis. Comparing protein expression in neoplastic and normal colon tissue indicated elevated expression of several proteins in colorectal cancer, among them the well established tumor marker carcinoembryonic antigen, as well as calnexin, 40S ribosomal protein S15a, serpin H1, and S100A12. Overexpression of these proteins was confirmed by immunoblotting. Serum levels of S100A12 were determined by ELISA and were found to be strongly elevated in colorectal cancer patients compared to healthy individuals. We...
conclude, that 2-D-LC-ESI-MS is a powerful approach to identify and compare protein profiles of tissue samples, that it is complementary to 2-DE/MALDI-MS approaches and has the potential to identify novel biomarkers.