Identification of biomarkers in patients with ulcerative colitis in a comparative proteomic study of colon biopsies

[1]Nina A. Poulsen, [1]Hanne Søndergaard Møller, [2]Vibeke Andersen, [3]Stig Purup & [1]Lotte Bach Larsen
[1]Department of Food Science, Faculty of Agricultural Sciences, Aarhus University, Tjele, Denmark
[2]Medical Department, Viborg Regional Hospital, Viborg, Denmark
[3]Department of Animal Health and Bioscience, Faculty of Agricultural Sciences, Aarhus University, Tjele, Denmark

Ulcerative colitis is a chronic –inflammatory disease of the colon affecting young persons with a lifelong course and severe impact on the life quality of the affected persons and the community in terms of disease leaves and health care expenses. The incidence of 10 per 100.000 inhabitants per year is rising in the Western World. Thus, identification of relevant biomarkers is essential for improved early diagnostic and treatment. Proteomic analysis can be useful for this purpose and we applied a comparative approach to characterize potential biomarkers associated with inflamed colon mucosa. Biopsies from both inflamed mucosa in rectum and from a non-inflamed epithelium from left colonic flexur were sampled in twenty colitis patients. This experimental design assures an affected as well as a control sample within the same patient. The proteomic profiles were characterized using 2D-gel electrophoresis (2D-GE). A total of 797 spots were annotated by image analysis. Differentially expressed proteins were subsequently identified using multivariate statistics, which is appropriate for long and lean data sets with numerous variables and few samples. Principal component analysis clearly grouped control samples separately from the colitis samples and partial least squares discriminant analysis was applied to identify markers responsible for this grouping. The results indicate that the proteomic signature of the different colon mucosas is strong and increase the potential for finding new biomarkers for early colitis diagnostics. In order to identify those spots being significantly correlated with the inflammatory disorder, we will combine univariate and multivariate statistics and in near future selected proteins will be further analyzed applying peptide mass fingerprinting using MALDI TOF-TOF mass spectrometry.