

Comparative Proteomical Analysis Of Human Plasma From Patients With Laryngeal Cancer

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Laryngeal cancer is a significant disease worldwide of increasing incidence, especially due to tobacco and alcohol consumption, which have a synergistic effect. Two contrasting ideas of immune system role during cancer development are commonly accepted: first that it fights against tumor cells, and second that it aids tumor progression. Thus, there is no clear understanding about the immune response in laryngeal cancer. In this study, plasmas, where most components of the immune system are present, from patients with laryngeal cancer and from healthy smokers (control group) were evaluated by 2D gel electrophoresis followed by MS protein identification. Twelve gels were obtained and compared against each other using the software BioNumerics. Samples from patients without cancer showed 34 well defined spots, while the ones from samples with cancer showed 45 distinguished spots. Proteins were detected on every gel around pH 4-10 from molecular weight of 10-60 kDa. Few differences were found among the cancer and control patients. However, three different spots appeared exclusively in gels from patients with cancer. These three differential proteins correspond to Ig gamma-3 chain C region, complement component C4 and Ig kappa chain C region. Moreover ten more spots were also identified in both gels. In summary, this study reinforces the importance of the immune response as target in the understanding and treatment of laryngeal cancer.

Key Words: Immune system, Laryngeal cancer, Proteomics.