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Proteomic profiling of anti-transferrin pull-down in patients with underlying oxidative stress

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Human serum tansferrin (hsTf) is a major circulatory protein crucial for the transport/metabolism of Fe^{3+} ions. By sequestering and delivering ferric ions to target tissues/cells hsTf maintains redox homeostasis. Oxidative stress (OS), one of the hallmarks of (patho)physiological conditions, alters protein structure and function. The main role of hsTf hinges on specific interaction with cellular Tf receptor (TfR) while other interactions contribute to diverse functions. The aim of this study was to profile interacting partners of hsTf in the samples of serum coming from patients diagnosed with a wide range of pathological conditions with underlying OS status. Anti-hsTf pull-down samples were analysed using mass spectrometry. Data went through analysis by appropriate bioinformatic tools. Results reveal differences in expression of hsTf interacting proteins in sample groups of patients suffering from kidney insufficiency subjected to dialysis treatment (peritoneal-PD or hemo-HD) also with patients with gestational diabetes compared to respective healthy sample groups. Colorectal cancer stage T3 versus T2 stage shows an inverse distribution of expression profiles in comparison to healthy samples. Most prominent differences are seen in hsTf interacting partners involved in the complement and coagulation cascades and cholesterol metabolic pathways, suggesting a multifaceted role of hsTf in these processes throughout the course of the disease.

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