Abstract:

Abstract Background A global proteomic strategy was used to identify proteins, which are differentially expressed in the murine model of severe malaria in the hope of facilitating future development of novel diagnostic, disease monitoring and treatment strategies. Methods Mice (4-week-old CD1 male mice) were infected with Plasmodium berghei ANKA strain, and infection allowed to establish until a parasitaemia of 30% was attained. Total plasma and albumin depleted plasma samples from infected and control (non-infected) mice were separated by two-dimensional gel electrophoresis (2-DE). After staining, the gels were imaged and differential protein expression patterns were interrogated using image analysis software. Spots of interest were then digested using trypsin and the proteins identified using matrix-assisted laser desorption and ionization-time of flight (MALDI-TOF) mass spectrometry (MS) and peptide mass fingerprinting software. Results Master gels of control and infected mice, and the corresponding albumin depleted fractions exhibited distinctly different 2D patterns comparing control and infected plasma, respectively. A wide range of proteins demonstrated altered expression including; acute inflammatory proteins, transporters, binding proteins, protease inhibitors, enzymes, cytokines, hormones, and channel/receptor-derived proteins. Conclusions Malaria-infection in mice results in a wide perturbation of the host serum proteome involving a range of proteins and functions. Of particular interest is the increased secretion of anti-inflammatory and anti apoptotic proteins.