Painful crises are the major sickle-cell disease (SCD) clinical manifestation probably due to significant increase in dense red blood cells (RBC) and reduction of their ability to pass through capillaries. Using proteomic strategies (see figure below), we aimed to discover novel SCD prognosis biomarkers as early predictors of the transition from steady-state to vaso-occlusive crises thus, allowing a prompt and specific therapeutic intervention.

In RBC-soluble fraction 2DIGE maps, more than 900 spots per gel were resolved and a total of 226 spots differentially expressed spots were recognized, corresponding a 134 proteins by MS analysis (see figures 1-5).

Molecular functions and associated pathways revealed enrichment in proteins involved in haematological disease, cytoskeleton rearrangements, signal transduction or response to reactive oxygen species, altered mechanisms with implications in SCD vaso-occlusive episodes. Further complete characterization and validation of differently expressed proteins in both RBC and plasma may constitute a specific biosignature of steady-state to crisis transition in SCD.

Conclusion

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