PROTEIN PROFILE IN CHRONIC MYELOPROLIFERATIVE NEOPLASMS (MPN).

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AIMS: Perform a genomic and proteomic analysis in myeloproliferative neoplasms (MPN), essential thrombocythemia (ET) and Polycythemia Vera (PV) that can determine the origin and divergence physiopathogenic of both diseases.

MATERIALS AND METHODS: Studies consisted of 68 samples in total, including 52 patients, 26 ET JAK2V617F positive and 26 PV and the remaining 16, healthy donors. Peripheral blood neutrophils (SP) were used in all experiments. cDNA was used for quantitative PCR of the gene MMP14. PCR results were validated by flow cytometry using anti-MMP14 and anti-CD45 antibodies. We used the cytosolic protein fractions of these cells for a screening by 2D-DIGE gels and subsequent mass spectrometry. Statistical analysis of the results of quantitative PCR was performed using the Wilcoxon test (p-value <0.05). DeCyder v 7.0 software was used (GE) for the analysis of 2D-DIGE gels and Mascot for MS.

RESULTS: MMP14 showed a differential expression between PV and ET populations (over-expressed in PV) regardless of treatment (p-value: 0.001). Preliminary analysis by flow cytometry suggest aberrant expression of MMP14 in PV and ET neutrophils compared with healthy donors. 2D-DIGE gels and mass spectrometry revealed the MMP9 protein overexpressed in ET compared to the PV positive. Other differentially expressed proteins were found in both populations, like HSPA8 and HSPA1A chaperones.

CONCLUSIONS: Along with other metalloproteases, MMP14 and MMP9 may be involved in phenotypic divergence of PV and ET as well as in the pathogenesis of NMP-philadelphia negative.