of high cytoplasmic AR expression in tumour cells and CD3 T-cells predicts poor outcome for patients diagnosed with PCa.

http://dx.doi.org/10.1016/j.pbj.2017.07.017

PS165
ALDHs as potential biomarkers in myeloid neoplasms – Preliminary study
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Aim: The aim of the study is to evaluate the expression of aldehyde dehydrogenase (ALDH) in patients with myelodysplastic syndromes (MDS) and acute myeloid leukemia (AML) to verify their potential as a marker for the diagnosis and/or prognosis of these diseases.

Introduction: ALDH superfamily is a group of 19 enzymes critical to the protection against toxic aldehydes, and have been associated with multiple diseases, namely in cancer. MDS are characterized by ineffective hematopoiesis associated with progressive peripheral blood cytopenias, and a predisposition toward leukemic transformation. MDS pathophysiology is a complex multistep process that involves genetic and epigenetic abnormalities in genes associated with differentiation, cellular proliferation, and apoptosis. Since ALDHs are involved in some of these biological processes, the deregulation of these enzymes may influence MDS and AML development.

Methods: To this end, we analyzed the expression levels of 8 ALDH isoforms, ALDH1A1, ALDH1A2, ALDH1B1, ALDH1L1, ALDH1L2, ALDH3A2, ALDH4A1, and ALDH16A1, in 31 patients (16 MDS and 15 LMA) and 19 healthy controls. ALDH expression levels were analyzed using RT-PCR and differentially expressed genes were quantified by qPCR. The statistical analysis was carried out by variance analysis and $\chi^2$ test. Survival were analyzed by Kaplan Meier curves ($p < 0.05$).

Results: Preliminary results indicate that all MDS patients express ALDH16A1 isofrom whereas only 67% of controls ($p < 0.05$) show expression of this isofrom. Moreover, AML patients have lower ALDH1A2 expression levels than MDS and controls and only 20% of AML patients express this isofrom (MDS = 54% and controls = 55%). The ALDH1L2 is only expressed in chronic myelomonocytic leukemia subtype of MDS. Furthermore, our original genome-wide approach highlighted putative novel molecular mechanisms in cell cycle biology. Given the cancer-specificity of these abnormalities, the identified compounds will inspire the development of drugs to selectively target cells with higher incidence of centriole abnormalities.

Conclusion: This work provides the first single-centriole-level portrait of centriole abnormalities in cancer and contributes to the understanding of their molecular origins, namely by revealing novel molecular mechanisms in cell cycle biology. Given the cancer-specificity of these abnormalities, the identified compounds will inspire the development of drugs to selectively target cancer cells.

Acknowledgements: This work is supported by an EMBO Installation Grant to NLBM.

References

http://dx.doi.org/10.1016/j.pbj.2017.07.019