Abstract 2217: Prognostic and predictive values of CD68+ macrophage and aberrant expression of cathepsin L, IL-12, CTL4A genes in classic Hodgkin's lymphoma

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Abdel-Rahamn Zekri · Abeer A Bahnassy · Ahmed El Bastawisy · Show all 7 authors · Hend F. Yousif

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Abstract

Background: Despite advances in the treatment of classic Hodgkin lymphoma (CHL), current therapies fail to cure 10%-15% of patients, and a similar proportion of patients may be over-treated, resulting in both short-term and long-term treatment-related complications. Current prognostic models predict the outcome of treatment with imperfect accuracy, and clinically relevant biomarkers have not been established to improve on international prognostic score.

Patients and Methods: CD 68 protein and RNA expression were assessed in 81 classic Hodgkin's lymphoma patients from Egypt by immunohistochemistry and Quantitative real time PCR (Q-RTP) respectively. Then CD 68 positive and CD 68 negative cases where profiled using the SABioscience array (Qiagen). Genetic aberrations were correlated to standard prognostic factors, patients response to the treatment, progression free and overall survival (PFS, OS) rates. Results: Increased CD68 protein and RNA expression were detected in 70.3% and 53.1% of the cases, respectively. Increased CD68 protein associated significantly with old age >40 (p = 0.035), advanced stage (p = 0.007), and poor response to treatment (DP/SD, p = 0.001). CD68 RNA expression significantly associated with age (p = 0.035), and poor response to treatment (DP/SD, p = 0.001). CD68+ positive patients, showed high expression of cathepsin L, IL-12, ATXN2L, CTL4A and...
Abstract: 2217: Prognostic and predictive values of CD68+ macrophage and aberrant expression of cathepsin L, IL-12, CTL4A and MMP11 (p<0.01)

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