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Identification of a Novel Phenotype of Myeloid Cells in Classical Hodgkin Lymphoma

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Classical Hodgkin lymphoma (cHL) characteristically shows few malignant cells in a microenvironment comprised of inflammatory cells. Although cHL is associated with a high cure rate, recent studies have associated poor prognosis with increased macrophages in involved lymph nodes (LN). It was recently reported that in cHL patients with relapsed disease post-allotransplant, tumor-infiltrating macrophages are derived from circulating monocytes and not resident macrophages. Thus, the role of monocytic infiltration and differentiation in cHL may be more relevant to defining prognosis in cHL patients and potentially have therapeutic implications. Most studies identify tumor associated macrophages using markers (e.g., CD68) that detect the entire myeloid lineage. In contrast to other myeloid markers, SR-A is expressed by tissue macrophages but not monocytic precursors. In this study, we examined expression of the Class A Scavenger Receptor (SR-A/CD204) in cHL LNs. We confirmed a high prevalence of cells that stained with the myeloid markers CD68, CD163, and CD14 in cHL LNs. However, SR-A protein expression determined by immunohistochemistry was limited to macrophages localized in sclerotic bands characteristic of nodular sclerosing cHL. In contrast, SR-A protein was readily detectable in solid tumor metastasis to LNs and in resident macrophages in control tissue (spleen, lung, liver). The results of SR-A protein expression paralleled the expression of SR-A message determined by quantitative RT-PCR indicating [illegible] expression and/or SR-A lineage determ[illegible]e phenotype, perhaps reflecting altered transcriptional regulation of SR-A expression. These data provide evidence for a unique macrophag[illegible] differentiation of myeloid cells, in LNs of cHL patients.