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Modeling the proteome of a Marek's disease transformed cell line: a natural animal model for CD30 overexpressing lymphomas

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Abstract

Marek's disease (MD) in the chicken, caused by the highly infectious MD α-herpesvirus (MDV), is both commercially important and a unique, naturally occurring model for human T-cell lymphomas overexpressing the Hodgkin's disease antigen, CD30. Here, we used proteomics as a basis for modeling the molecular functions and biological processes involved in MDV-induced lymphomagenesis. Proteins were extracted from an MDV-transformed cell line and were then identified using 2-D LC-ESI-MS/MS. From the resulting 3870 cellular and 21 MDV proteins we confirm the existence of 3150 “predicted” and 12 “hypothetical” chicken proteins. The UA-01 proteome is proliferative, differentiated, angiogenic, pro-metastatic and pro-immune-escape but anti-programmed cell death, -anergy, -quiescence and -senescence and is consistent with a cancer phenotype. In particular, the pro-metastatic integrin signaling pathway and the ERK/MAPK signaling pathways were the two predominant signaling pathways represented. The cytokines, cytokine receptors, and their related proteins suggest that UA-01 has a regulatory T-cell phenotype.