High-throughput immunophenotyping of 43 ferret lymphomas using tissue microarray technology

To validate the use of the tissue microarray (TMA) method for immunophenotyping of ferret lymphomas, a TMA was constructed containing duplicate 1-mm cores sampled from 112 paraffin-embedded lymphoma tissue specimens obtained from 43 ferret lymphoma cases. Immunohistochemical (IHC) expression of CD3, CD79 alpha, and Ki-67 (MIB-1) was determined by TMA and whole mount (WM) staining of each individual case for result comparison. There was a high correlation between CD79 alpha and CD3 results comparing ferret TMA and WM sections (kappa statistic 0.71-0.73 for single-core TMA and 0.79-0.95 for duplicate-core TMA) and between continuous data from Ki-67 staining of ferret TMA sections and WM sections (concordance correlation coefficients 0.77 for single cores and 0.87 for duplicate cores). Subsequently, a panel of commercially available antibodies was applied to the TMA for the analysis of expression in ferret lymphomas. The results of this study confirmed previously published results suggesting specific cross-reactivity of the applied IHC markers (CD3, CD79 alpha, Ki67) with ferret lymphoma tissue. Other IHC markers (CD45Ro, bcl2, bcl10, MUM1, CD30, vimentin) were also expressed in subsets of the included ferret lymphomas. Further studies are necessary to determine the usefulness of these markers for diagnostic and prognostic evaluation of ferret lymphomas. In conclusion, the TMA technology was useful for rapid and accurate analysis of protein expression in large archival cohorts of ferret lymphoma cases.

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