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*Myc*in chicks

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   Overexpression of the c-*myc* oncogene induces multistaged neoplastic progression leading to B-cell lymphomas in the bursa of Fabricius. In the May 22 Proceedings of the National Academy of Sciences, Neiman *et al*. describe the use of microarray analysis to define the genetic networks important for *myc*-induced lymphomagenesis (*Proc Natl Acad Sci* USA 2001, **98:**6378-6383). The authors created a customized cDNA microarray containing over 2,200 genes associated with the immune system - details can be found on the Chick Website. They compared gene expression profiles of several stages of normal embryonic bursal development, *myc*-induced pre-neoplasic transformed follicles, metastatic lymphomas and the DT-40 lymphoma cell line. They found that a small subset of genes was differentially regulated during bursal differentiation, whereas hundreds of genes were influenced by c-*myc* expression. The best correlation between *myc* expression levels and gene induction was observed in pre-neoplastic follicles. *Myc*-induced genes include those involved with cell growth and energy control. The authors suggest that high levels of *myc* overexpression are more important for early lymphoma induction than for late-stage metastasis.

References

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