Z3 13 **Expression patterns and functional studies of *Xenopus trithorax* genes: *XMll*, *XBrm*, and *XBrg1***

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The *trithorax* group (trxG) of activators and *Polycomb* group (PcG) of repressors are believed to control the expression of several key developmental regulators by changing the structure of chromatin. One of the main strategies by which cells alleviate chromatin-mediated repression is through the action of ATP-dependent chromatin remodeling complexes. Chromatin remodeling complexes mediate a change in chromatin structure, assisted by sequence-specific DNA binding trxG proteins such as Mll and GAGA, and perhaps by recruiting histone deacetylases to stably induce a hyperacetylated active state. Furthermore, the vertebrate SWI/SNF cmplexes is an evolutionarily conserved, multi-subunit machine, involved in chromatin remodeling during transcriptional activation. Within this complex, the Brm and Brg1 proteins are mutually exclusive subunits that are believed to affect chromatin structures using the energy of ATP hydrolysis. We isolated partial cDNA sequences of *Xenopus Mll, Brm,* and *Brg1* (*XMll, XBrm,* and *XBrg1*) and examined expression patterns of these genes during the developmental processes. All three genes were expressed both maternally and zygotically throughout Xenopus development. *In situ* hybridization was performed to study in more detail the spatial expression pattern on these genes. The first attractable signals were observed in the neural fold of early neurula. At the tailbud, the signals concentrated in cells of the developing head, neural tube and somites. To investigate the functional significance of trxG proteins, we studied the role of the XMll, XBrm, and XBrg1 in embryogenesis.

Key Words : trithorax group, SWI/SNF complex, *Mll, Brm, Brg1, Xenopus.*