ANALYSIS OF THE EXPRESSION AND REGULATION OF *XENOPUS* FRIZZLED7

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Abstract

The *Xenopus laevis* frizzled7 (Xfz7) gene shows a very dynamic and complex gene expression pattern during embryogenesis. Xfz7 is also known to be involved in the three different pathways of Wnt signalling. The overall aim of this project was to study the expression and regulation of Xfz7. Within this context we wished to focus on investigating the expression of Xfz7 at stages 35 and above, locate its transcription start site, clone its full promoter and define the various promoter elements that drive tissue specific activation of Xfz7 gene expression.

We have shown, by *in situ* hybridisation, a novel dorsal line expression pattern of Xfz7 at later stages of *Xenopus* development, which we consider to be a developing lymph vessel. We also have shown by *in situ* hybridisation that two other genes Xblimp1 and Xesr1 co-localise at the dorsal line.

We have cloned 7.5 kb of sequence upstream of the translation start site. We have identified by using BLAST, a region of the Xfz7 upstream sequence which shows identity to the *Xenopus* laevis SCL gene promoter. We have also shown by multiple alignment of various Frizzled7 genomic sequences that there is not much significant conservation in their 5' upstream sequences except for between *Xenopus laevis* and *Xenopus tropicalis* and between human and mice. By utilizing *Xenopus* transgenics and deletion analysis of this 7.5 kb upstream sequence, we have shown a 233 base pair region in the immediate proximal promoter to be responsible for some aspects of Xfz7 expression, most notably dorsal neuro-ectoderm expression during gastrulation and the expression in the eye, heart and the novel dorsal line, at later tadpole stages (stages 38-40).

We have shown that the immediate upstream region including this 233 bp region shows a high degree of conservation between *Xenopus laevis* and *Xenopus tropicalis* and have identified some core promoter elements and putative transcription factor binding sites within this 233 bp region that we presume might play a role in driving gene expression. We speculate that the 3' sequence of Xfz7 might also contain regulatory sequences, which might play an important role in defining the complete endogenous pattern of Xfz7 expression during *Xenopus laevis* development.