

Development and application of novel cloning strategies for analysis of genes controlling embryo development

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'Development and Application of Novel Cloning Strategies for Analysis of Genes Controlling Embryo Development.'

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ABSTRACT

Initially, we aimed to identify novel genes regulating vertebrate neurogenesis and somitogenesis by screening cDNAs derived from gastrulation/neurulation stage zebrafish embryos for clones revealing corresponding genes with expression patterns suggestive of roles in these processes. The lack of suitable cDNA libraries prompted us to devise a simplified method for producing randomly-primed, directionally cloned cDNA libraries from small amounts of embryonic tissue. To achieve this, several techniques were combined, including cDNA synthesis on a solid carrier, random priming of 1st cDNA strand synthesis, non-specific priming of 2nd cDNA strand synthesis and amplification of initially small amounts of cDNAs by suppression-PCR.

A pilot-scale *in situ* screen using a cDNA library produced by the above method identified a gene, *spadetail*, that is expressed in presomitic mesoderm and in unidentified, apparently irregularly distributed cells of the spinal cord. *spt* functions in mesodermal development, yet its role in neural tissue remains unknown. Analysis of the *spadetail*-expressing neural cells' gene co-expression profile and dorsoventral location implied that they are Dorsal Longitudinal Ascending interneurons. Quantitative analysis of these cells' rostrocaudal distribution showed that there is a tendency to higher cell numbers in rostral spinal segments. The observation that *spadetail*-expressing neurons are frequently juxtaposed to somitic cells expressing neurons may be 'inefficiently' patterned by *spadetail*-expressing somitic cells or that the expression of *spadetail* in both tissues is induced by a common positional cue.

The strategy for non-specific priming was then extended to develop a simple technique for cloning unknown DNA sequences flanking known DNA. An initial non-specific PCR amplification was performed with a single primer that binds specifically within known sequence and non-specifically in the unknown DNA region. In a second reaction, the sequences of interest were amplified from the primary reaction mixture (that also contains undesired sequences) with nested PCR using a primer that had been extended further downstream from the primer used in the initial PCR. This enabled isolation of a 0.5 kb region of amphioxus *Notch* cDNA, that, in turn, contributed to the subsequent analysis of the evolution of vertebrate *Notch* genes.