

The evolutionary processes underlying the emergence of the α -actinin gene family

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Abstract

The aim of this study was to use recently sequenced invertebrate genomes of early deuterostomes – *S. purpuratus* (Sea urchin), *C. savignyi* (Sea squirt) and *B. floridae* (Lancelet), to identify the evolutionary footprints that bridge the gap between ancient invertebrate and modern vertebrate α -actinins. Using the α -actinin gene family as a case study, we have provided evidence to support the current proposed framework for gene evolution to generate functional diversity within a gene family.

Keywords: gene duplication, gene family

1 Introduction

The α -actinins are an ancient family of actin binding proteins with homologues in all three domains of life. Vertebrates possess four α -actinin genes postulated to arise from a single invertebrate ancestral gene. All members of the α -actinin family share a distinct domain topology consisting of an actin binding domain, a central rod domain and a C-terminal EF hand domain. Among the features which distinguish the vertebrate from the invertebrate α -actinins are the alternative splicing of the EF-hand domain to create distinct functional forms, and the partitioning of the gene itself into more intron/exon blocks.

2 Method and Results

The aim of this study was to use recently sequenced invertebrate genomes of early deuterostomes – *S. purpuratus* (Sea urchin), *C. savignyi* (Sea squirt) and *B. floridae* (Lancelet), to identify the evolutionary footprints that bridge the gap between ancient invertebrate and modern vertebrate α -actinins.

In this study, we successfully identified orthologues of α -actinin in all three invertebrate species. The most primitive of these, the sea urchin, had an α -actinin gene structure similar to all invertebrates identified in previous studies. We then performed gene structure analysis of the sea squirt α -actinin, and identified an increase in intron/exon blocks; these are uncharacteristic of invertebrates, thus marking the sea squirt as the earliest species identified to date with vertebrate-like α -actinin gene structure. The retention of this newly acquired feature was observed in the lancelet, in which two α -actinins were also identified. In addition, both lancelet α -actinins identified contained a duplication of an exon encoding part of the EF hand domain.

3 Discussions

Together, these evolutionary markers provide insight into the sequence of evolutionary events responsible for the emergence of two α -actinin genes from a single ancestral gene. We now plan to acquire/perform gene sequencing of key species between lancelet and fish to further elucidate the hypothesised mechanism of gene duplication responsible for transitioning the two intermediary α -actinins to the four present day α -actinins in this vertebrate gene family. Using the α -actinin gene family as a case study, we have provided evidence to support the current proposed framework for gene evolution to generate functional diversity within a gene family.

References