

Identification of conserved C2H2 zinc-finger gene families in the Bilateria

ABSTRACT

Based on current metazoan phylogeny, the minimum complement of C2H2 zinc-finger genes in the genome of the bilaterian common ancestor is composed of these 39 groups.

INTRODUCTION

The Bilateria is a group of microorganisms that comprises mostly eukaryotes (e.g. bacteria, protists and archaea), eukaryotic cells and eukaryotic proteins. The Bilateria includes a variety of species, including some that are widely distributed in the world, some that are restricted to specific regions and some that are restricted to specific geographic regions.

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CONCLUSION

Remarkable conclusions By comparing *Drosophila* and *C. elegans* sequences with human sequence- at least 39 families of C2H2 ZNF genes have been identified (of which 17 have not been defined) and we now estimate that there are 38 definitive groups of orthologous genes, each deriving from a single gene in the common ancestor of these three organisms. Based on current metazoan phylogeny, it is clear that one of those families represented the minimum level of expression for C1H2-Z3 molecules, which indicates that they represent indicating that this condition