

2R or not 2R is not the question anymore

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In his comments on our Opinion article (The evolutionary significance of ancient genome duplications. *Nature Rev. Genet.* **10**, 725–732 (2009))¹ Amir Ali Abbasi (Piecemeal or big bangs: correlating the vertebrate evolution with proposed models of gene expansion events. *Nature Rev. Genet.* 6 Jan 2010 (doi:10.1038/nrg2600-c1))² argues that it is not justified to speculate about the evolutionary consequences of two rounds of whole-genomic duplication (WGD) in vertebrates, given that strong evidence is lacking that such duplications occurred during the evolution of this group.

The evidence for WGDs and the recognition of their profound effects on the evolution of phenotypic novelty and biological diversification more generally has been rising steadily with the advent of genomics. Empirical support for the hypothesis of two rounds of WGD (termed the 2R hypothesis) during the evolution of chordates/vertebrates was initially based only on a limited number of gene families (mostly *Hox* genes)^{3,4,5}. Until about 5 years ago it was occasionally still debated as to whether the presence of four *Hox* clusters, and other duplicated genes, was due to a large number of independent duplication events or a single WGD⁶. This is no longer the case⁷: the collection of more genomic data, the addition of synteny information, the finding of widespread paralogous chromosomal regions and, more recently, the comparative analyses of entire genomic sequences^{8,9} support the hypothesis of WGD during the evolution of chordates⁷. The empirical evidence for the chordate 2R and the teleost fish-specific genome (FSGD) duplications is now so strong that it is universally accepted in the scientific community; this issue was therefore only covered

in passing in our recent review on WGDs and their significance for evolution in *Nature Reviews Genetics*¹.

Abbasi², however, questions the support for the 2R hypothesis, claiming that it still remains debated today. He points out correctly that evidence for the 2R hypothesis was based initially on data from only a small number of genes and vertebrate and non-representative invertebrate genomes. Abbasi² argues that conclusions from this limited evidence produced a distorted picture of the evolution of the vertebrate genome. Recent genomic sequences from a larger number of invertebrates show that even phenotypically simple organisms, such as the sea anemone *Nematostella vectensis*, can possess many genes and gene networks that were initially thought to be vertebrate-specific¹⁰. We might therefore be able to trace the origins of a set of components from the vertebrate genetic tool kit to the deuterostome genome or even to the common ‘urbilaterian’ ancestor. Although we agree with Abbasi that these are exceedingly interesting findings, and also agree that there is no simple and predictable relationship between gene number and organismal complexity, we fail to see how these new genomic data should challenge the evidence for two rounds of genome duplication during chordate evolution.

Genomes show surprising conservation on the one hand, but on the other hand they also display rather dynamic aspects in which tandem duplications of genes commonly occur and local and even chromosomal segmental duplications abound. How (and indeed whether) genomic architecture is related to phenotypic diversification or how it is related to the

origin of evolutionary novelties are highly interesting questions, but they remain largely unsolved¹¹. However, evidence for the two rounds of genome duplication during chordate evolution is very strong, and it would seem safe to say that the debate over 2R is settled and is no longer an open question¹². As we point out in our Opinion article¹, it is only the evolutionary effects of events such as WGDs on evolution that are debated¹¹, and no longer whether or not two rounds of WGD occurred during the evolution of chordates.

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