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Review

An overview on genome organization of marine organisms

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ABSTRACT

In this review we will concentrate on some general genome features of marine organisms and their evolution, ranging from vertebrate to invertebrates until unicellular organisms. Before genome sequencing, the ultracentrifugation in CsCl led to high resolution of mammalian DNA (without seeing at the sequence). The analytical profile of human DNA showed that the vertebrate genome is a mosaic of isochores, typically megabase-size DNA segments that belong in a small number of families characterized by different GC levels. The recent availability of a number of fully sequenced genomes allowed mapping very precisely the isochores, based on DNA sequences. Since isochores are tightly linked to biological properties such as gene density, replication timing and recombination, the new level of detail provided by the isochore map helped the understanding of genome structure, function and evolution. This led the current level of knowledge and to further insights.

Contents

1. Introduction

Well before genome sequencing, ultracentrifugation in Cs_2SO_4 density gradients in the presence of sequence-specific DNA ligands (e.g., Ag+) was shown to lead to a high resolution of mammalian DNAs according to base composition (Corneo et al., 1968). These findings opened a new inroad in the study of the organization of eukaryotic genomes, superseding DNA reassociation kinetics (Britten and Kohne, 1968), which was based on the separation of single- and double-stranded DNAs on hydroxyapatite (Bernardi, 1965). According to the new density gradient approach the genomes of warm-blooded vertebrates were characterized by a striking long-range compositional heterogeneity (neglecting satellite DNAs; Filipski et al., 1973; Macaya et al., 1976; Thiery et al., 1976). Indeed, these genomes are mosaics of isochores, long (major than 300 kb), compositionally fairly homogeneous regions that belong to a small number of families characterized by different average GC levels (Macaya et al., 1976). A quarter of a century after the original studies that had defined the approximate sizes and compositions of isochores as well as the compositions and relative amounts of isochore families, it was reported that isochores could not be identified in the draft sequence of the human genome (Lander et al., 2001), starting a debate that is still ongoing. The different computational approaches used to disprove or redefine isochores (Eyre-Walker and Hurst, 2001; Häring and Kypr, 2001; Lander et al., 2001; Nekrutenko and Li, 2001; Cohen et al., 2005) were, however, shown to be inadequate (Bernardi, 2001; Clay and Bernardi, 2001a,b, 2005; Li, 2002; Oliver et al., 2002, 2004; Li et al., 2003), even if some of them led to a partial identification of isochores. This debate prompted us to map the isochores, as originally defined (Macaya et al., 1976), in the finished sequence of the human genome (International Human Genome Sequencing Consortium, 2004). Average GC levels were, therefore, assessed over long DNA stretches (>200 kb), while GC variation was estimated by measuring standard deviations of GC over such stretches using a 100-kb moving window (Costantini et al., 2006). In fact, we demonstrated that if one scans the GC profiles of human

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