1. FEBS J. 2006 Apr;273(8):1637-48.

**Isochore structures in the chicken genome.**

Gao F(1), Zhang CT.

Author information:

(1)Department of Physics, Tianjin University, China.

The availability of the complete chicken genome sequence provides an unprecedented opportunity to study the global genome organization at the sequence level. Delineating compositionally homogeneous G + C domains in DNA sequences can provide much insight into the understanding of the organization and biological functions of the chicken genome. A new segmentation algorithm, which is simple and fast, has been proposed to partition a given genome or DNA sequence into compositionally distinct domains. By applying the new segmentation algorithm to the draft chicken genome sequence, the mosaic organization of the chicken genome can be confirmed at the sequence level. It is shown herein that the chicken genome is also characterized by a mosaic structure of isochores, long DNA segments that are fairly homogeneous in the G + C content. Consequently, 25 isochores longer than 2 Mb (megabases) have been identified in the chicken genome. These isochores have a fairly homogeneous G + C content and often correspond to meaningful biological units. With the aid of the technique of cumulative GC profile, we proposed an intuitive picture to display the distribution of segmentation points. The relationships between G + C content and the distributions of genes (CpG islands, and other genomic elements) were analyzed in a perceivable manner. The cumulative GC profile, equipped with the new segmentation algorithm, would be an appropriate starting point for analyzing the isochore structures of higher eukaryotic genomes.

DOI: 10.1111/j.1742-4658.2006.05178.x

PMID: 16623701 [Indexed for MEDLINE]