Commentary and Review

*Perspective*

Gene-balanced duplications, like tetraploidy, provide predictable drive to increase morphological complexity

Michael Freeling and Brian C. Thomas

**Research**

*Articles*

Genomic organization of the sex-determining and adjacent regions of the sex chromosomes of medaka


Amplification generates modular diversity at an avirulence locus in the pathogen *Phytophthora*

Rays H.Y. Jiang, Rob Weide, Peter J.I. van de Vondervoort, and Francine Govers

A systems view of haloarchaeal strategies to withstand stress from transition metals

Amardeep Kaur, Min Pan, Megan Meislin, Marc T. Facciotti, Raafat El-Gewely, and Nitin S. Baliga

**Letters**

Close sequence comparisons are sufficient to identify human cis-regulatory elements

Shyam Prabhakar, Francis Poulin, Malak Shoukry, Veena Afzal, Edward M. Rubin, Olivier Couronne, and Len A. Pennacchio

Functional noncoding sequences derived from SINEs in the mammalian genome

Hidenori Nishihara, Arian F.A. Smit, and Norihiro Okada

Ubiquitous selective constraints in the *Drosophila* genome revealed by a genome-wide interspecies comparison

Daniel L. Halligan and Peter D. Keightley

Thousands of corresponding human and mouse genomic regions unalignable in primary sequence contain common RNA structure

Elfar Torarinsson, Milena Sawera, Jakob H. Havgaaard, Merete Fredholm, and Jan Gorodkin

Suz12 binds to silenced regions of the genome in a cell-type-specific manner


(continued)
Identification of clustered YY1 binding sites in imprinting control regions
Jeong Do Kim, Angela K. Hinz, Anne Bergmann, Jennifer M. Huang, Ivan Ovcharenko, Lisa Stubbs, and Joomyeong Kim

Genomic localization of RNA binding proteins reveals links between pre-mRNA processing and transcription
Ian A. Swinburne, Clifford A. Meyer, X. Shirley Liu, Pamela A. Silver, and Alexander S. Brodsky

Evidence for variation in abundance of antisense transcripts between multicellular animals but no relationship between antisense transcription and organismic complexity
Miao Sun, Laurence D. Hurst, Gordon G. Carmichael, and Jianjun Chen

Following tetraploidy in an Arabidopsis ancestor, genes were removed preferentially from one homeolog leaving clusters enriched in dose-sensitive genes
Brian C. Thomas, Brent Pedersen, and Michael Freeling

Errata

Open Access paper.

Cover A fossil of Cooksonia pertoni, one of the earliest land plants, was found in Shropshire, England. Although Cooksonia were only a few centimeters tall and did not have leaves, flowers, or seeds, its dichotomously branching stems tipped in sporangia made it one of the most morphologically complex land plants during the Upper Silurian, ~410–420 million years ago. This illustrates that the maximums of plant morphological complexity—represented by present-day Angiosperms such as daisies and orchids—have certainly increased over time. In this issue, Freeling and Thomas show that repeated tetraploidies along the plant lineage help to explain this rising trend in morphological complexity. By analyzing the consequences of the most recent tetraploidy in the Arabidopsis lineage, Thomas et al. supply some details on how tetraploidy naturally leads to chromosomal clusters of dose-sensitive genes. (Photo and fossil: Hans Steur, The Netherlands. [For details, see Freeling and Thomas, pp. 805–814 and Thomas et al., pp. 934–946.])