

<i>Perspective</i>	Commentary and Review	
	Gene-balanced duplications, like tetraploidy, provide predictable drive to increase morphological complexity Michael Freeling and Brian C. Thomas	805
<i>Articles</i>	Research	
	Genomic organization of the sex-determining and adjacent regions of the sex chromosomes of medaka Mariko Kondo, Ute Hornung, Indrajit Nanda, Shuichiro Imai, Takashi Sasaki, Atsushi Shimizu, Shuichi Asakawa, Hiroshi Hori, Michael Schmid, Nobuyoshi Shimizu, and Manfred Scharl	815
	Amplification generates modular diversity at an avirulence locus in the pathogen <i>Phytophthora</i> Rays H.Y. Jiang, Rob Weide, Peter J.I. van de Vondervoort, and Francine Govers	827
	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	841
	Close sequence comparisons are sufficient to identify human <i>cis</i> -regulatory elements Shyam Prabhakar, Francis Poulin, Malak Shoukry, Veena Afzal, Edward M. Rubin, Olivier Couronne, and Len A. Pennacchio	855
<i>Letters</i>	Functional noncoding sequences derived from SINEs in the mammalian genome Hidenori Nishihara, Arian F.A. Smit, and Norihiro Okada	864 ^{OA}
	Ubiquitous selective constraints in the <i>Drosophila</i> genome revealed by a genome-wide interspecies comparison Daniel L. Halligan and Peter D. Keightley	875
	Thousands of corresponding human and mouse genomic regions unalignable in primary sequence contain common RNA structure Elfar Torarinsson, Milena Sawera, Jakob H. Havgaard, Merete Fredholm, and Jan Gorodkin	885
	Suz12 binds to silenced regions of the genome in a cell-type-specific manner Sharon L. Squazzo, Henriette O'Geen, Vitalina M. Komashko, Sheryl R. Krig, Victor X. Jin, Sung-wook Jang, Raphael Margueron, Danny Reinberg, Roland Green, and Peggy J. Farnham	890

(continued)

Identification of clustered YY1 binding sites in imprinting control regions	901
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	912
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	922
Miao Sun, Laurence D. Hurst, Gordon G. Carmichael, and Jianjun Chen	
Following tetraploidy in an <i>Arabidopsis</i> ancestor, genes were removed preferentially from one homeolog leaving clusters enriched in dose-sensitive genes	934
Brian C. Thomas, Brent Pedersen, and Michael Freeling	
Errata	947

^{OA}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.])