

IN BRIEF

GENOME EVOLUTIONRecent *de novo* origin of human protein-coding genes

Knowles, D. G. & McLysaght, A. *Genome Res.* **19**, 1752–1759 (2009)

Emergence of a new gene from an intergenic region

Heinen, T. J. A. J., Staubach, F., Häming, D. & Tautz, D. *Curr. Biol.* **19**, 1527–1531 (2009)

It is generally assumed that new genes arise through duplication or recombination. Two studies have now identified genes that have arisen from non-coding DNA. By comparing the human genome with syntenic regions of other primates, Knowles and McLysaght detected three protein-coding genes that are present only in humans but are non-coding in all ancestral sequences. Heinen and colleagues identified a sequence that is present only in mice and has arisen in a large intergenic region owing to 5' indel mutations. The sequence is expressed in post-meiotic cells of the testis: a functional role was suggested by a recent selective sweep in the region and by the sperm-related defects of knockout mice.

EPIGENETICS

Epigenetic resetting of a gene imprinted in plant embryos

Jahnke, S. & Scholten, S. *Curr. Biol.* 24 Sep 2009 (doi:10.1016/j.cub.2009.08.053)

Imprinting of the Polycomb group gene *MEDEA* serves as a ploidy sensor in *Arabidopsis*

Erilova, A. *et al. PLoS Genet.* **5**, e1000663 (2009)

These papers provide new insights into the functions and mechanisms of plant genomic imprinting. Jahnke and Scholten report that the imprinting of the maize *maternally expressed in embryo* gene occurs in the embryo in addition to extra-embryonic tissues and is reset across generations. Both findings show that there is greater similarity between plant and mammalian imprinting than previously thought. Erilova and colleagues give experimental support for a previously proposed function of imprinted genes as 'ploidy sensors' by showing that perturbation of the correct parent of origin-specific expression of the Polycomb gene *MEDEA* is responsible for aborted seeds in crosses between *Arabidopsis thaliana* plants of different ploidy.

EVOLUTION

A role for a neo-sex chromosome in stickleback speciation

Kitano, J. *et al. Nature* 27 Sep 2009 (doi:10.1038/nature08441)

Sexual conflict resolved by invasion of a novel sex determiner in Lake Malawi cichlid fishes

Roberts, R. B., Ser, J. R. & Kocher, T. D. *Science* 1 Oct 2009 (doi:10.1126/science.1174705)

Sexual antagonism is predicted to drive sex chromosome evolution, but does sex-chromosome divergence driven by sexual conflict promote speciation? Two papers suggest that it might: Kitano and colleagues found a neo-sex chromosome in Japanese sticklebacks that contains loci for male behavioural traits that have contributed to isolation from an ancestral population; and Roberts *et al.* found an allele for a colour pattern in cichlid fish that is beneficial to females and is tightly linked to a sex-determination locus, and suggest that such linkage might contribute to diversification and speciation.