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IN BRIEF

EVOLUTIONARY GENETICS

Selective inheritance of mitochondrial DNA

Two studies in *Drosophila melanogaster* provide insights into the mechanisms that prevent the transmission of harmful mutations in mitochondrial DNA (mtDNA). By disrupting mitochondrial function using RNA interference, Hill *et al.* show that mtDNA replication in the germ line depends on organelle fitness. Using heteroplasmic flies, which contain both wild-type and mutant mitochondrial genomes, they then found that the transmission of the deleterious genome — containing a temperature-sensitive lethal mtDNA allele — was gradually purged over several generations at the restrictive temperature. This finding indicates that selection against the mutant mtDNA occurs to ensure the inheritance of healthy mitochondria to successive generations. The authors propose that mitochondria with a high proportion of wild-type mtDNA replicate faster than those containing more mutations, which leads to "a decrease in the proportion of mutant mtDNA through oogenesis," as the authors state. In the second study, Ma *et al.* show that purifying selection results from competition between mitochondrial genomes within an organism without any effect on organismal survival or fertility. In addition, the researchers show that selection can stabilize the transmission over multiple generations of harmful variants that complement each other. For as long as they are selected at stable ratios, the complementing mutations are not deleterious.

ORIGINAL RESEARCH PAPERS Hill, J. H., Chen, Z. & Xu. H. Selective propagation of functional mitochondrial DNA during oogenesis restricts the transmission of a deleterious mitochondrial variant. *Nature Genet.* **46**, 389–392 (2014) | Ma, H., Xu, H. & O'Farrell, P. H. Transmission of mitochondrial mutations and action of purifying selection in *Drosophila melanogaster*. *Nature Genet.* **46**, 393–397 (2014)

RNA

easiRNAs — guardians of the plant genome

A new small RNA pathway has been described, in which microRNAs trigger the biogenesis of epigenetically activated small interfering RNAs (easiRNAs) from reactivated transposable elements in *Arabidopsis thaliana*. During reprogramming of the germ line, when epigenetic marks are erased and the plant genome is most vulnerable to activated transposons, these easiRNAs specifically target transposon transcripts. This plant transposon defense mechanism resembles the PIWI-interacting RNA pathway in animal germ lines, which also acts as a fail-safe mechanism to prevent transposon activation during reprogramming.

ORIGINAL RESEARCH PAPER Creasey, K. M. *et al.* miRNAs trigger widespread epigenetically activated siRNAs from transposons in *Arabidopsis*. *Nature* http://dx.doi.org/10.1038/nature13069 (2014)

HUMAN GENETICS

In your face — predicting facial features from DNA

Researchers have identified 24 single-nucleotide polymorphisms in 20 genes that are significantly associated with facial features and used this data to develop a program that can predict 3D facial structure on the basis of these markers. High-resolution facial images of ~600 participants from 3 West African–European admixed populations were used to form detailed 3D images. Claes *et al.* then jointly modelled face shape, sex and genomic ancestry with genetic markers in candidate craniofacial genes to analyse the independent effects of genetic variants on facial features. Although more research is needed before this method might be applicable — for example, in forensics — this proof-of-principle study indicates the plausibility of such an approach.

ORIGINAL RESEARCH PAPER Claes, P. *et al.* Modeling 3D facial shape from DNA. *PLoS Genet.* **10**, e1004224 (2014)