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IN BRIEF

NON-CODING RNA

Small RNA determines silkworm sex

A single female-specific PIWI-interacting RNA (piRNA) determines sex in the WZ sex determination system of the silkworm *Bombyx mori*, in which males have two Z sex chromosomes and females have one Z and one W sex chromosome. This W-chromosome-encoded piRNA is produced from a precursor termed *Fem*. In female embryos, the inhibition of signalling by *Fem*-derived piRNA induced the production of male-specific splice variants of *Bmdsx*, the RNA products of which act further downstream in silkworm sex development. The researchers identified a target gene of *Fem*-derived piRNA on the Z chromosome, which they called *Masc*. Silencing of *Masc* is needed for the production of female-specific isoforms of *Bmdsx* in female embryos, whereas in male embryos the Masc protein regulates dosage compensation and masculinization.

ORIGINAL RESEARCH PAPER Kiuchi, T. *et al.* A single female-specific piRNA is the primary determiner of sex in the silkworm. *Nature* **509**, 633–636 (2014).

PATHOGEN GENETICS

Single-cell analysis of intra-host variation

A new method has been developed to analyse intra-host genetic diversity of malaria infections from patient blood. Malaria infections are often comprised of a complex assortment of parasite lineages — also known as multiple-genotype infections. In this study, cell sorting was followed by whole-genome amplification to generate sufficient DNA from infected red blood cells for subsequent genotyping and sequencing analyses. Better understanding the impact of various combinations of intra-host drug resistance and virulence haplotypes could facilitate more directed treatment strategies in the future.

ORIGINAL RESEARCH PAPER Nair, S. *et al.* Single-cell genomics for dissection of complex malaria infections. *Genome Res.* http://dx.doi.org/10.1101/gr.168286.113 (2014)

DISEASE GENETICS

Incidental medical findings in genetic research

Human genome sequencing studies can uncover genetic variants that have potential medical implications for the donor participants (known as incidental findings). In these cases, there is debate about whether the affected participants should be informed, as such knowledge can cause distress but can also enable beneficial early medical intervention. Lawrence *et al.* assessed the likely frequency of incidental findings by carrying out exome sequencing of 543 individuals (from 159 families) and analysing the set of 56 genes that the American College of Medical Genetics and Genomics (ACMG) recommends for reporting pathogenic variants to participants. Reportable variants were identified in 5.0% of individuals (8.8% of families) — a higher value than that found in two previous studies (~1.0–3.4% of individuals) — although the authors highlighted experimental and bioinformatic sources of variability in the calling of pathogenic variants. In a separate study, Bollinger *et al.* used an online survey of ~1,500 people to determine public preferences for receiving incidental findings; 78% said that they would be interested in receiving incidental findings if they were participants in a hypothetical genetic research study. The respondents prioritized receiving results that concern risk of serious or treatable diseases, and at no financial cost.

ORIGINAL RESEARCH PAPERS Lawrence, L. *et al.* The implications of familial incidental findings from exome sequencing: the NIH Undiagnosed Diseases Program experience. *Genet. Med.* http://dx.doi.org/10.1038/gim.2014.29 (2014) | Bollinger, J. M. *et al.* Public preferences for the return of research results in genetic research: a conjoint analysis. *Genet. Med.* http://dx.doi.org/10.1038/gim.2014.50 (2014)