Nature Reviews Genetics | Published online 15 Jul 2016

IN BRIEF

PATHOGEN GENETICS

Making male malaria mosquitoes

UK researchers have identified and characterized a master regulator of the sex determination process in the African malaria mosquito *Anopheles gambiae*. The team analysed the transcriptomes of male and female embryos and identified the gene *Yob* as a maleness-conferring Y chromosome-linked factor. *Yob* expression was observed from the onset of zygotic transcription throughout the life of males. The gene was found to encode a 56-amino-acid protein that controls the male-specific splicing of *doublesex* (*dsx*). Ectopic embryonic delivery of *Yob* mRNA was lethal for genetically female embryos, but had no effect on genetic males. By contrast, silencing of embryonic *Yob* expression resulted in male-specific lethality, suggesting a role of Yob in dosage compensation. *Yob* could be useful as a tool to produce male-only generations for transgenic approaches to control vector-borne diseases.

ORIGINAL ARTICLE Krzywinska, E. *et al.* A maleness gene in the malaria mosquito *Anopheles gambiae*. *Science* **353**, 67–69 (2016)

TECHNIQUE

Genome-wide quantification of 5hmC in single cells

A new technique enables genome-wide detection and quantification of the epigenetic mark 5-hydroxymethylcytosine (5hmC) in single cells. Based on a method for bulk 5hmC sequencing, 5hmC marks are glucosylated using the T4 phage β-glucosyltransferase, then cut by the restriction enzyme AbaSI. Digested genomic DNA is ligated to double-stranded adapters containing a 2-nucleotide random 3′ overhang, together with a cell-specific barcode, an Illumina 5′ adapter and a T7 promoter. *In vitro* transcription is used to amplify the DNA fragments linearly in a strand-specific orientation, and the amplified RNA is fragmented and undergoes directional RNA library preparation. When applied to mouse embryonic stem cells, a median of 44,000 unique 5hmC sites per cell was detected. Substantial cell-to-cell variability existed between the number of 5hmC sites on the two strands of the same chromosome. Differences in age between the strands of a chromosome could explain the 5hmC strand bias, as confirmed by a new stochastic model.

ORIGINAL ARTICLE Mooijman, D. *et al.* Single-cell 5hmC sequencing reveals chromosome-wide cell-to-cell variability and enables lineage reconstruction. *Nat. Biotechnol.* http://dx.doi.org/10.1038/nbt.3598 (2016)

CHROMATIN

Programmed R-loop formation

Using DNA–RNA immunoprecipitation followed by cDNA conversion coupled to high-throughput sequencing (DRIPc–seq), researchers have profiled the genome-wide prevalence and distribution of R loops in mouse and human cells. Mapping of R loops at near base-pair resolution and in a strand-specific manner showed that the co-transcriptional hybridization of nascent RNAs to template DNA is a conserved, prevalent and dynamic feature of mammalian chromatin that can impact gene expression. Epigenomic profiling revealed that R loops associate with specific epigenomic signatures: at promoters, R loops associate with an open, histone H3 lysine 4 (H3K4) hypermethylated and hyperacetylated state characteristic of strong CpG island promoters; at terminators, R loops associate with an enhancer- and insulator-like state; and R-loop formation seems to be a conserved hallmark of a broad class of transcription terminators.

ORIGINAL ARTICLE Sanz, L. A. *et al.* Prevalent, dynamic, and conserved R-loop structures associate with specific epigenomic signatures in mammals. *Mol. Cell* http://dx.doi.org/10.1016/j.molcel.2016.05.032 (2016)