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IN BRIEF

GENOME INSTABILTY

Mechanisms of HPV integration

This study used whole-genome sequencing and molecular approaches to identify human papilloma virus (HPV) integration sites in human cancers. Five HPV-positive and five HPV-negative cell lines that were derived from cervical cancers and from head and neck cancers were studied. The authors found that HPV integrates at sites of host genome instability, such as sites of amplifications and rearrangements — a finding that was confirmed in primary cancers. The discovery that these sites are flanked and bridged by HPV has led the authors to propose a model of 'looping', in which integration by HPV results in viral–host concatemers and in oncogene disruption.

ORIGINAL RESEARCH PAPER Akagi, K. *et al.* Genome-wide analysis of HPV integration in human cancers reveals recurrent, focal genomic instability. *Genome Res.* http://dx.doi.org/10.1101/gr.164806.113 (2013)

GENOME EDITING

TALENs for microRNAs

Techniques for knocking out microRNAs (miRNAs) to assess their functions are limited by off-target effects. Kim *et al.* have developed 540 transcription activator-like effector nuclease (TALEN) pairs to target 274 miRNA loci in humans. The authors show that these 'genome editors' are specific and provide general design strategies for generating the equivalent TALENs in other species. To demonstrate the use of their approach, they showed that related miRNAs suppress different targets despite their similarities.

ORIGINAL RESEARCH PAPER Kim, Y.-K. *et al.* TALEN-based knockout library for human microRNAs. *Nature Struct. Mol. Biol.* http://dx.doi.org/10.1038/nsmb.2701 (2013)

POPULATION GENOMICS

Triallelic sites and demographic history

An important summary statistic in population genetic studies is the site-frequency spectrum, which describes the distribution of allele frequencies in the population. Theoretical work has generally assumed that one mutation at most has occurred at each site, but this is unlikely to hold for large populations. These authors model the frequency spectrum for a triallelic site, at which two mutations have occurred. They show that such sites are more useful than biallelic sites for detecting the influence of demographic history.

ORIGINAL RESEARCH PAPER Jenkins, P. A., Mueller, J. W. & Song, Y. S. General triallelic frequency spectrum under demographic models with variable population size. *Genetics* http://dx.doi.org/10.1534/genetics.113.158584 (2013)

DEVELOPMENT

A mechanical route to robustness

Robustness is important during development to avoid defects that result from internal and external perturbations, and networks of genes and signalling pathways have been shown to promote this property. This study shows that mechanical cellular mechanisms can also be involved. Working in *Drosophila melanogaster*, the authors identify two new actin-regulating proteins: the zygotically expressed Serendipity-α (Sry-α) and the maternally provided Spitting image (Spt). In optimal conditions, Spt is sufficient for embryonic cellularization, whereas both Spt and Sry-α are required at high temperatures or when actin assembly is genetically perturbed.

ORIGINAL RESEARCH PAPER Zheng, L. *et al.* The maternal-to-zygotic transition targets actin to promote robustness during morphogenesis. *PLoS Genet.* http://dx.doi.org/10.1371/journal.pgen.1003901 (2013)

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