In this issue of Mobile Genetic Elements

Elaine L. Ellerton
Landes Bioscience; Austin, TX USA

Research Papers: MITEs Make All the Difference, pp. 127–32

Hunting for miniature inverted-repeat transposable elements (MITEs) in plant and animal genomes has become easier with the advent of two new programs, MITE-hunter and RSPB. Chen et al. make use of these programs to search for MITEs in the rice (O. sativa) cultivar Nipponbare. They were able to determine that the majority of these MITEs originated and amplified after the divergence of the rice relative, B. distachyon. The authors speculate that the large phenotypic and genotypic diversity seen in O. sativa may arise from a high amount of presence/absence (P/A) polymorphisms of MITEs.

Comparing MGE Distributions in Primates, pp. 133–41

About 50% of human genomes are composed of transposable elements, but what about our near cousin, the Macaca mulatta, or rhesus macaque? In this research paper, Rawal et al. endeavor to find out. The group identified and studied Alu and L1 retrotransposons throughout the genome of M. mulatta and compared this distribution with other primate genomes. They also looked at the physiochemical properties of the surrounding DNA around the transposon insertion sites. The authors found similar distribution patterns in humans and M. mulatta, suggesting a common mechanism for mobile genetic element distribution throughout primate genomes.

Mini-Review: Silencing Better than Out-Crossing, pp. 142–4

One way to remove deleterious mutations garnered from transposable elements (TEs) is by using an outcrossing breeding system vs. self-fertilization. Interestingly, the highly outcrossed plant species A. lyrata tend to retain the same amount of transposition variants as compared with its inbred cousin A. thaliana. In fact, although outbred, A. lyrata has a bloated, TE full genome, much larger than A. thaliana. Juliette de Meaux and Ales Pecinka look at this from the viewpoint of transcriptional control of TEs. The authors suggest that gene-silencing mechanisms may have quite a lot power in controlling genome size and in contributing to the evolution of transposition rate.

Commentaries: P. acnes: A Spotty History, pp. 145–8

With a name like Propionibacterium acnes, it wouldn’t be a surprise to find that it was associated with acne vulgaris, or simply what we call acne. However, a clear-cut association has not been discovered between this Gram-positive bacterium and the bane of most teenagers, as P. acnes is also found on healthy skin. In this commentary, Brüggemann et al. review their recent research indicating that different phenotypes of P. acnes may be due to the invasion of mobile genetic elements. Further study should help to unravel distinctions between the mutualistic and parasitic properties of this bacterium.

You Got Your Ubiquitin in my Prokaryote!, pp. 149–51

The many microbes that inhabit our GI tract are important for many reasons. They aid in the development of our immune system and they aid in the breakdown of hard to digest plant materials. In this commentary, Patrick and Blakely focus on a specific GI resident, Bacteroides fragilis. During annotation of this bacterial genome, the authors identified a gene encoding a specifically eukaryotic protein, ubiquitin. Most likely acquired via horizontal transfer, the authors discuss potential roles that this bacterial ubiquitin may have in health and disease.

Researching Rumen Plasmids, pp. 152–3

Eating a diet consisting mostly of grass would probably not do humans any favors and possibly cause a lot of gastrointestinal stress. Thankfully, ruminants, animals that primarily eat plant-based foods, do quite well as they have extra digestive compartments that can breakdown these foods into easily digestible components. The rumen compartment is chock-full of microbiota, making it a good place to research plasmids. These replicating genetic elements act as a powerful evolutionary force by introducing new traits into bacteria and in this commentary, Itzhak Mizrahi discusses recent research that turns to the rumen niche to uncover the traits and identities in this particular plasmidome.

< Insert Retroelement Here >, pp. 154–7

Retroelements make up a significant amount of our genomes, but whether they are able to exact any effect relies, in part, on whether they end up in inter or intragenic regions. Alus and L1s are examples of highly abundant retroelements, making up about 33% of our genomes, and are interspersed equally between these two distinct genomic regions. These retroelements do take part in altering the expression of our genes, especially when inserted into an intron. In this commentary, Kaer and Speek discuss three ways that intronic Alus and L1s can affect transcription:

*Correspondence to: Elaine L. Ellerton; Email: elaine@landesbioscience.com
Submitted: 06/13/12; Accepted: 06/20/12
http://dx.doi.org/10.4161/mge.21519
intron retention, cryptic polyadenylation and forced exonization. The authors also speak of other possible types of transcriptional interference.

**Evolving Sex Chromosomes Marked by Retroposons, pp. 158–62**

Successfully classifying species of organisms into their correct groups is an arduous and controversial affair. Luckily, looking at retroposon insertions is tremendously helpful for inferring phylogeny. The method of looking at retroposons as markers has been especially useful when looking at the evolution of gametologs. In this commentary, Alexander Suh discusses both the advantages and limitations of using this method to understand the evolution of sex chromosomes when it comes to birds. His findings reveal the complexity of the evolutionary history of avian sex chromosomes.

**Gene Transfer on a Global-Scale, pp. 163–7**

Gene transfer between bacteria has quite an effect on the global architecture of their genomes. These transfer events can cause an increase in size and distribution of functional gene categories within the genome. This commentary, written by Grassi, Grilli and Lagomarsino, comments on their recent contributions to this field and also discusses possible future directions their findings may take them.