Annual Review of Genetics, 2005. Allen Cambell *et al.* (eds). Annual Reviews Inc., 4139, El Camino Way, Palo Alto, CA, USA. Vol. 39.

Ever since the Annual Reviews introduced the series on 'Genomics and Human Genetics' a few years ago (undoubtedly, a necessary and valued addition), the *Annual Review of Genetics* (although since deprived of key developments in human genetics) has found more space and opportunity to expose readers to the genetics of lesser-known systems. As genetics moves beyond the well-known model systems to the lesser-known ones, many of these are turning out to be rather excellent models for unique features not capturable in the better-known systems. This argues strongly for delving into newer systems (that are genetically tractable) despite the difficulties and lag-times that result from working out their molecular genetics. The criticism that it leads to only a lateral increase in knowledge seems unjustified, since in many cases one observes the abilities of these systems to reveal deeper insights even into known processes. In 'Sex determination in the teleost medakka, *Oryzias latipes*', for example, Masura Matsuda reviews how the medakka (a lesser-known fish than the zebra fish and the fugu fish) is an organism where the first sex-determining genes among non-mammalian vertebrates have been determined. DMY (DM domain on the Y chromosome) was shown to be the master gene for male determination, and the possible functions of DMY are speculated upon in this review. (In contrast, the sex-determining genes in the zebra fish and the fugu fish are still unclear.) This observation, the smaller genome size of medakka as compared to zebra fish, and the added ability in medakka to generate F1 progeny from a large interstrain diversity in an inbred population makes this a viable genetic system worthy of study. Speaking of fish, this volume has three reviews on different aspects of zebra fish genetics: the genetics of hearing and balance, axis formation and another on hemotopoiesis, and perhaps reflects the coming of age of this model organism. The review on 'The moss, *Physcomitrella patens*' by David Cove, makes a lucid introduction to yet another genetically relatively unknown, but otherwise familiar, organism, the ubiquitous moss. *P. patens* is a moss, relatively widespread in temperate climates that has a predominantly haploid gametophyte phase in its life cycle permitting it to be genetically amenable to analysis (more so than ferns and seed plants). The author describes the recent developments that include the development of transformation procedures and homologous recombination, and the ability to carry out tagged mutagenesis and RNAi studies in this moss. Not surprisingly, *P. patens* is one of the two non-flowering plants (along with *Selaginella moellendorfii*) whose genome is currently being sequenced. And like mosses are wont, this one seems to be rapidly becoming an excellent model for investigations.

Among the few articles where concepts of genetics are seen through the lens of genomics, was the article by Koonin entitled 'Orthologs, paralogs and evolutionary genomics'. The author describes how the concepts of homologs, orthologs and paralogs have evolved through history, and how orthologs and paralogs, though in the literature since 1970, have only shot into prominence after the genome sequences started being released (some journal consensus is needed however on the spelling of these words: either the 'American' orthologs, etc. or the 'British' orthologues, etc.). Presenting arguments that the terms orthologs and paralogs are not 'just terms that complicate a scientific narrative while contributing nothing', Koonin lucidly and elegantly presents the case not only for the importance of these terms in understanding and interpreting genomes, but conceptually explains other new terms too that are already on the horizon. As researchers just begin to warm up to understanding homologs as having evolved either through vertical descent from a single ancestral gene (orthologs) and by duplication (paralogs), the need to further define these terms has also been convincingly presented. Thus inparalogs (symparalogs) and outparalogs (alloparalogs) result from a lineage-specific duplication subsequent to, or preceding a speciation event, respectively. Similarly, pseudoorthologs refers to genes that are paralogs but appear to be orthologs owing to a differential, lineage-specific gene loss, while coorthologs refers to two or more genes in a lineage that are orthologous to one or more genes in a another lineage, owing to a lineage-specific duplication. An interesting issue discussed by the author is that although these concepts have been generally gene-centric, the presence of multi-domain proteins (each domain having a possibly different inheritance) suggest that the notion of orthology could be applied to domains, and similarly,' to any stretch of nucleotides, down to a single nucleotide' – the latter would perhaps be realistic only for very closely organisms. On the other scale, orthology could also refer to strings or blocks of genes rather than a single gene. A second review in the area of evolutionary genomics was the article by Nei and Rooney on 'Concerted and birth and death evolution of multigene families'. Genes evolve through divergent evolution, and has been the pattern of evolution by the globin multigene family that has members dispersed across the genome with widely varying functions. However, the evolution of the tandemly repeated rDNA multigenic family in eukaryotes was found to occur through a different process involving gene conversion, in a model referred to as 'concerted evolution'. This explained how the repeat units were similar within species than across species. However analysis of other multigenic families like the histones and immunoglobins and the MHC families led to a third model of evolution of multigene families called 'the birth and death evolution' model. The authors succinctly describe these models and its background and should be interesting reading for those interested in gene duplication as being an important evolutionary process.

An insightful and exhaustive review by Douglas Wallace entitled 'A mitochondrial paradigm of metabolic and degenerative diseases, aging and cancer: a dawn for evolutionary medicine' was one that interested me greatly, and should be of interest to a large number of researchers working in these different diseases, as it builds a strong case for mitochondrial dysfunction playing an important role not only in age-related disorders, but also in cancers. The author explains how the delayed onset of age-related disorders and even cancer is a consequence of the accumulation of somatic mutations in the mitochondrial genome, that alters the reactive oxygen species tackling capabilities, leading to ultimate manifestation of the diseases. The tissue specificity, calorie intake and diet, and the individual and regional predisposition to diseases are quite convincingly built into this model.

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