

subsequent editions of the book. The author has dedicated a full chapter describing various applications of mass spectrometry to protein science. Mapping of intact protein isoforms using top-down approach by multidimensional separation techniques followed by mass spectrometric analyses of peptides and fragments analysed with the help of proteome database has become a versatile technique today. Combination of this technique with differential mass spectrometric analyses has been used to achieve label-free detection and quantification of even low-abundance proteins and peptides. High-throughput mass fingerprinting is one of the major breakthroughs in mass spectrometric applications in proteomics. Rapid analyses of human plasma proteome by exploiting multidimensional ion mobility mass spectrometry have revolutionized the capabilities of this versatile technique. Combining electrospray ionization travelling wave ion mobility spectrometry with tandem mass analyses has been shown to yield information on topology along with the mass of the large macromolecular systems. These are some of the frontier developments in the area where the mass spectrometric studies are used to determine structural properties of the biomolecular complexes. The author has provided a lucid discussion on such developments citing suitable examples and also highlighted laser-based high-speed mass spectrometric techniques (e.g. MALDI, LAESI) which have been developed to image biological materials such as tissue samples. Some of these techniques can provide high-throughput imaging methods for potential clinical and pathological applications. The author has also briefly described developments of bioinformatics tools for analyses and interpretation of mass spectrometric results. Several software have been developed to identify the tandem mass spectral signatures of peptides using protein or genomic databases using different models of fragmentation pathways of peptide ions. These bioinformatic tools have enabled fast analyses of a large number of samples with significant accuracy. Some of the software also interface with the instrument for suitable data-dependent acquisition of MS/MS spectra, leading to substantial reduction in the time of experiment.

Overall, this is a well-written textbook highlighting recent developments and

challenges in protein mass spectrometry. The organization of the chapters in the book has been thoughtful and is meant for a non-expert and beginner in the area. The author has also described some of the most difficult methods and latest developments in the area, making the book an important source of information even for experts and practitioners of protein mass spectrometry. It would indeed be a priced collection for any science library and would serve as a useful reference to the latest developments in the subject.

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Annual Review of Genetics, 2016.

Nancy M. Bonini, Michael Lichten and Gerturd Schüpbach (eds). *Annual Reviews*, 4139 El Camino Way, Palo Alto, CA 94303-0139, USA. Vol. 50. vii + 618 pp. Price: US\$ 102.

Since the last *Annual Review of Genetics* was published, the world saw the launch of the *Human Cell Atlas* – a multi-institute, multi-country endeavour to create a profile of all the different kinds of cells in a human body in terms of their gene expression and other molecules¹. This has been possible due to the unprecedented advances made in the field of sequencing single DNA/RNA molecules. On the other hand, discovery of ancient remains of both *Homo sapiens* and other hominins continues to revolutionize our understanding of human evolution²⁻⁴. Recent findings have pushed the history of *H. sapiens* at least 100,000 years further back than that considered earlier^{5,6} and have thrown light on the food habits of the Neanderthals⁷. Genetics, as it has since its inception, retains its position at the helm of biological research.

This volume opens with an article by James Haber, in which he summarizes his life's work on double-strand break (DSB) repair. For the last 40 years Haber has been studying the role of homolo-

gous recombination (HR) and other processes in the repair of such potentially lethal DNA damages using the model, budding yeast *Saccharomyces cerevisiae*. A couple of other articles in this volume also deal with HR. Gray and Cohen discuss the role of HR in meiotic crossover. During prophase I, the number of DSBs introduced in the chromosomes, is at least an order of magnitude larger than the final number of crossovers. The process of selection of these DSBs is known as designation. Gray and Cohen discuss the mechanism of DSB formation and designation, and also the proteins involved in the process. On the other hand, McVey *et al.* take a detailed look at the role of eukaryotic DNA polymerases in HR across diverse taxa. As has been mentioned above, HR is involved in DNA repair in a variety of contexts such as in meiosis and DSB repair. This review gives a detailed description of the different DNA polymerases and how they mediate such processes.

It is a delight to notice that in this volume the idea of evolution forms a common thread in majority of the reviews, including those mentioned above. Both McVey *et al.* as well as Gray and Cohen take a comparative approach in their respective reviews. A detailed comparison of meiosis across different eukaryotes is the focus of a review by Loidl. It also provides some interesting insights about the origin and diversification of the meiotic process. Loidl argues that although meiosis has had a single origin in the common ancestor of all eukaryotes, there are substantial differences in its detail across taxa. Moreover, he notes that the synaptonemal complex is absent in several scattered taxa across distant lineages, suggesting its later origin. Loidl emphasizes the lack of detailed study on meiosis in non-model organisms. The life cycle of several multicellular eukaryotes such as many plants and fungi alternates between haploid and diploid states, a phenomenon termed alternation of generations (AOGs). The proportion of an organism's life cycle spent as haploid and diploid is also extremely variable across lineages. The genetic basis of the origin and maintenance of AOGs in land plants is discussed in the review by Bowman *et al.* The authors provide a detailed description of the genes involved in this process across different major plant groups such as bryophytes, angiosperms, etc. The role of two homeobox

genes emerges as pivotal in haploid to diploid transition.

Tumour tissue consists of multiple clones in different proportions with among-clone genetic differences (d) on the order of 10^{-7} to 10^{-5} per nucleotide. For reference, in natural populations d would be 10^{-1} to 10^{-3} . Wu *et al.* have applied molecular population genetic theory to understand the evolution of tumours, with a rather ambitious title for their review, 'The ecology and evolution of cancer: the ultra-microevolutionary process'. To make their case, they rely heavily on a single measure of distinguishing neutrality from positive/negative selection – the ratio between non-synonymous and synonymous mutations (K_a/K_s). They could not have been more emphatic about the interpretation of this statistic. Using a single-gene approach they show that contrary to the earlier conclusion that there is no net selection in the genes in a tumour, there is in fact considerable heterogeneity among individual genes. Although majority of genes are evolving neutrally, a substantial proportion and a small subset are indeed under negative and positive selection respectively. These proportions are more than what is expected by chance in case of negative selection and less in case of positive selection. Their inference is based on simulations assuming neutrality. However, no measure to conclude the statistical significance of their observation is provided.

The three-way interaction among *Plasmodium*, mosquitoes and humans has attracted some of the smartest minds in genetics from Francisco Ayala to Daniel Hartl. This volume contains an article by Molina-Cruz *et al.* detailing our current understanding on the origin and spread of *Plasmodium* in relation to their mosquito vectors, and Hartl is one of the authors in it. Molina-Cruz *et al.* argue that humans received *P. falciparum* from gorillas in a single host-jumping event and when humans migrated out of Africa, they carried the malaria parasite with them. However, as their mosquito host did not migrate with them, the parasite had to rely on local mosquito vectors to complete its life cycle, leading to complex local co-evolution between the parasite and its respective mosquito host(s) in that region. They also highlight the role of the parasite immune gene *Pfs47* in the avoidance of detection by the mosquito immune system.

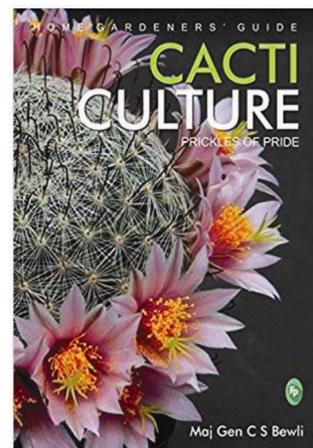
Geneticists have for long been accused of being ultra-reductionist, and two reviews in this volume by Wong *et al.*, as well as Droujinine and Perrimon, attempting a holistic approach, are welcome in this regard. The components of different genetic networks interact among themselves, and understanding them is the domain of combinatorial genetics. Wong *et al.* review the emerging technologies that are being implemented in understanding such interactions. On the other hand, Droujinine and Perrimon focus on the communication between different organs. They provide a comparative description of the different factors involved in the communication among functionally similar organs in humans and *Drosophila*. Remarkably, many of these factors are conserved between the two species.

Other highlights in this volume include articles by Bevilacqua *et al.* on the recent developments in the techniques to decipher RNA secondary structure; Quadrona and Colot on how DNA methylation profiles are inherited in plants from one generation to the next; Grath and Prsch discussing differences in gene expression between the sexes, and how and why male biased genes often evolve faster, and Naylor and Deursen on chromosomal instability and its involvement in ageing and cancer. Interested readers can access all the articles in this volume at <http://www.annualreviews.org/toc/genet/current>

1. Regev, A. *et al.*, *Human Cell Atlas*, bioRxiv, 2017.
2. Lazaridis, I. *et al.*, *Nature*, 2017.
3. Skoglund, P. *et al.*, *Nature*, 2016, **538**, 510–513.
4. Slon, V. *et al.*, *Science*, 2017, **356**, 605–608.
5. Hublin, J.-J. *et al.*, *Nature*, 2017, **546**, 289–292.
6. Richter, D. *et al.*, *Nature*, 2017, **546**, 293–296.
7. Weyrich, L. S. *et al.*, *Nature*, 2017, **544**, 357–361.

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Cacti Culture: Prickles of Pride. Maj Gen C. S. Bewli. Fingerprint Life, 113/A, Darya Ganj, New Delhi 110 002, India. Price: Rs 595, pp. 248; www.fingerprint-publishing.com.

This monograph offers critical details of culturing cacti and the prerequisites, such as soil composition, moisture and duration of light regimes in an enclosed environment. The literature documents many unique species of this xerophytic flora which have evolved with a variety of adaptations. The plant that is no longer restricted to America and is under global demand for cultivation under varied climatic conditions is imposing challenges to the growers. The book while remarkably addressing the challenges in growing cacti away from their native habitat, also reflects the great interest and experience of the author over the years.

The book addresses all challenges of cacti cultivation in the context of the Indian sub-continent. Importantly in India, the ambient temperature ranges from an excess of 47°C to a minimum of 0°C . Also, there are incessant rains during monsoon. To overcome such harsh climate regimes, cacti can be grown under controlled greenhouse conditions to take care of direct sunlight, excessive drainage and fluctuations in temperature. The author has mastered the technique of cacti propagation involving seed-cutting, grafting and tissue culture.

The book discusses the practical information required for cacti cultivation in an easy language. Mesmerizing photographs unravel the beauty of nature. The text gives a holistic view on cacti cultivation and factors that influence their growth like watering, lighting, fertilization and soil mineral composition. For