BOOK REVIEWS



Transgenic insertion of the gene responsible for the production of green fluorescent protein (GFP) results in mice that fluoresce when exposed to ultraviolet light. The GFP gene has been successfully expressed in bacteria, fungi, plants, insects, and mammalian cells.

The twelfth chapter covers one of the most important issues in drug discovery – IP rights and patents. Finer nuances of what is patentable, obviousness, inventorship, assignment and ownership, patent application contents and classification are covered in this chapter.

Case studies in drug discovery are covered in the final chapter. Tamiflu, HDAC inhibitors, HIV protease inhibitors, nitrofurantoin, terbinafine, loratidine, MPTP, bupropion and COX-2 inhibitors are covered in this chapter. Details of how changes in the structure of the molecule impact their activity are provided. The chapter covers issues related to safety of the drug molecule, identification of the role of metabolite and challenges in finding selective COX-2 inhibitors.

The book is well written and is recommended for libraries or individuals who are interested or are working in the area of drug discovery. The readers will benefit if early discovery concepts such as 'biology-oriented synthesis', 'fragment-based drug discovery' or 'diversity-oriented synthesis' are included. Hopefully, the author will incorporate these in future editions.

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Landforms of the World with *Google Earth*: Understanding our Environment. Anja M. Scheffers, Simon M. May and Dieter H. Kelletat. Springer, Dordrecht, The Netherlands. 2015. 391 pp. Price: US\$ 129.00. ISBN 978-94-017-9712-2.

Google Earth's reach extends from the layman who pins his home to the Earth, to the professional scientific journals asking for KML files of study areas. A revolution to the power of ten would have been witnessed by mankind if Google Earth was available during the era of Alexander the Great or Charles Darwin. The popularity and utilization achieved by Google Earth since inception into the cyber world in 2004 is simply marvellous. This all embracing coverage of Google Earth, which has elevated the status of maps and images from esoteric collections housed in dusty libraries to cutting edge technology is brought out well in this book. The authors bring to life the agility of Google Earth, especially as related to the needs of the geoscientific community seeking to understand our environment through landforms. This book with a sparse, yet crisp narration and beautiful illustrations stands out in all aspects. At places, an oblique angle view of Google Earth images provides a digital elevation model which helps the reader to internalize the terrain. Google Earth's bird's-eye perspective images are also supported by classical terrestrial photographs by these authors. The Google Earth image of Joshua Tree National Park, California, USA and its corresponding terrestrial photograph (p. 68, figures 3.9 c and d respectively) are identical and prove the veracity of the high-resolution images.

Landforms on the Earth's surface are neither identical nor static – from the

majestic peaks of the mighty Himalayas to the deepest Mariana Trench and the spectacular Devils Tower to deep impact craters of Chicxulub - but are dynamic. Earth abhors static, its dynamism is what drives and sustains life, and this sense of fluidity in a solid Earth is elucidated well in this book with Google Earth efficiently capturing our planet in its brilliant hues. The book also provides a virtual field tour for both the professional as well as amateur geologists. It is split into four parts based on the geomorphic processes that carved out a particular landform. Abstract for each chapter, which is unusual in textbooks other than edited volumes, gives a glimpse of the tale that the chapter tells.

This highly illustrated textbook will be an asset to any geologist, and should be on the book shelves of geology libraries of all colleges and universities in India. This book will also help a geologist to rove over in the *Google Earth* platform to enjoy the spectacular landforms and identify them. It was Henry Hudson, the great English navigator and sea explorer who said, 'This land may be profitable to those that adventure it'. And this book leads you on a semi-adventure, if not on an adventure, all in itself.

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Annual Review of Genetics, 2015. Bonnie L. Bassler, Michael Lichten and Gerturd Schüpbach (eds). Annual Reviews, 4139 El Camino Way, Palo Alto, CA 94303-0139, USA. Vol. 49. ix + 718 pp. Price: US\$ 99.

'HIGHLY ESTEEMED SIR:

The acknowledged pre-eminence your honour enjoys in the detection and classification of wild-growing plant hybrids makes it my agreeable duty to submit for your kind consideration the description of some experiments in artificial fertilization.'

Thus began the first of a series of letters addressed to the renowned Swiss botanist Carl Nägeli during 1866–1873. These

letters were from a Moravian monk Gregor Mendel, 'Monastery capitular and teacher in the high school'¹. Mendel started his correspondence with Nägeli a year after he had read in front of the Brünn Natural History Society, Mendel's own paper containing results of his hybridization experiments with the garden pea, Pisum². He was writing to Nägeli regarding his failure to repeat in other plants, Mendel's own observations from garden pea. Nägeli actively replied to Mendel's letters and it was Mendel who finally broke the correspondence, leaving Nägeli unconvinced about the validity of his discoveries³. The world had to wait more than three decades for Mendel's principles of inheritance to be 'rediscovered⁴.

The year 2015 marked 150 years since Mendel made his results public. The lukewarm reception of this occasion, compared to the frenzy of activity and jamboree that accompanied the Origin sesquicentenary in 2009, is typical of biologists and historians of science alike^{5,6}. Compared to the profusion of literature on Darwin's or even Wallace's life and works, both scholarly as well as popular that are regularly produced, the same for Mendel, in spite of much effort, would hardly take the fingers of one hand to count. To be exact, Vítězslav Orel's masterly work was the only scholarly analysis of Mendel's life and work⁷ until, fortunately, Jan Klein took upon himself the daunting task of writing an updated and by far the most extensive biography of the scientist monk till date⁸. Quite characteristically, Klein's book was reviewed in none of the mainstream genetics or heredity journals.

This volume of the Annual Review of Genetics has been published in this Mendel sesquicentenary year. As the number of the volume suggests, for 49 years now, the editors of this series have been bringing out in-depth reviews about the most pressing contemporary topics in genetics. Almost every area in the vast arena of research termed 'genetics' now, from molecular genetics to biotechnology, from neurobiology to cancer biology, and evolutionary, population and quantitative genetics, even historical aspects of this field, have been covered. This series stands as a testament to the huge advancement made in this field in the past 50 years.

This volume combines a judicious mix of both basic as well as applied genetics.

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Gene editing techniques such as TALENS and CRISPR-Cas9 system have enabled geneticists to manipulate genes and study their consequences with extreme precision. Not surprisingly then, two of the articles in this volume directly deal with these technologies, while several others at least allude to their application in various contexts. Hotta and Yamanaka discuss how such techniques can advance the most obvious, but yet to be fully achieved case of gene therapy. Whereas Douam et al. discuss how such techniques could help understand the genetic basis of host tropism of human pathogens. As it is difficult to have animal models for pathogens that can infect only humans, or humans and a few primates, 'genetically humanized' animals can be created using methods like TALENS and CRISPR-Cas9 systems along with gene knockdowns/knockins, aiding the study of the biology of such parasites.

The relative paucity of the number of protein-coding genes, given the large genome sizes in organisms gave rise to the notion that most of the genome must be useless 'junk DNA'. With advances in their understanding, however, geneticists have come to realize that very little of the genome (not even repetitive sequences) is devoid of any function. Apart from stretches of DNA acting as enhancers, several other stretches of DNA are transcribed, but not translated. During the past 20 years or so, such non-coding RNAs have been observed to play an essential role in fine regulation of gene expression. In fact, the technique of RNA-interference (RNAi) is based on the principle, that RNAs can modulate the expression of other RNAs. In this volume, Fromm et al. review our current knowledge of vertebrate microRNAs (miRNAs). They explore the loss and gain of miRNA genes and families in different lineages through comparative analysis of the miRNAome from various vertebrate taxa. They also discuss the huge number of human RNAs included as miRNAs in miRBase that are not miRNAs and propose a novel method for human miRNA annotation. In order to ameliorate this situation, the authors have created a separate database MirGeneDB containing miRNA genes reannotated using their method. On the other hand, Barquist and Vogel review one of the dominant bacterial regulatory RNAs, i.e. small RNA (sRNA). Their emphasis is to elucidate how high-throughput sequencing technologies (RNA-seq) in combination with functional genomics can accelerate the discovery of this abundant non-coding RNA in the bacterial transcriptome, and also aid in the understanding of their function.

Genetics and its application is one of the dominant securers of public funding, and one would expect genetics to play a major part in the endeavour to ensure food security to all. Elizabeth Kellog discusses the usefulness of the cereal Brachypodium distachyon as a plant model for studying genetics. Unlike the present major plant genetic system Arabidopsis thaliana, this plant is closely related to wheat and barley. Therefore, emergence of this species as a model can provide important insights into the biology of major crops. On the other hand, Han et al. provide a convincing case on how increase in nitrogen use efficiency (NUE) can increase crop productivity. They advocate the use of classical methods of quantitative genetics, QTL mapping and selection of candidate genes in enhancing NUE. They also discuss the challenges behind the design and execution of such studies.

Next generation sequencing (NGS) technologies, just like other areas of genetics, have revolutionized the different branches of evolutionary and quantitative genetics. Weigel and Nordborg discuss how these recent advancements can expedite the study of adaptation in wild plant species. Reviewing the discoveries made in A. thaliana, they elucidate the modus operandi of conducting such a study. They emphasize how plants have been studied very little to understand adaptation, but at the same time discuss the limiting factor of having access to isogenic lines to carry out the required experiments. Finally, they posit how gene-editing technologies can be used to create such lines. Complex language is a mode of communication limited only to humans among extant organisms. Graham and Fisher review our current understanding of the genetics of language using heritable language-related disorders. They discuss how methods such as NGS technologies, genome wide association studies (GWAS), studying molecular networks, finding a suitable animal model and neuroimaging can aid in finding and elucidating the function of genes related to language, speech and reading abilities.

Hughes and Page review our current understanding of the evolution and function of the mammalian Y-chromosome. They emphasize that although the role of Y-chromosome in testis determination and spermatogenesis has been well studied, recent research suggests that there are genes on the Y-chromosome with functions unrelated to reproductive biology, such as disease risk. However, this third aspect of Y-chromosome function is only beginning to be understood. Although each nucleotide is thought to have an equal probability to be mutated, recent discoveries have revealed mutations to occur in clusters. Clan and Gordein review the current understanding of the occurrence of this phenomenon with special emphasis on its mechanism.

This volume contains 30 reviews in all, and the ones discussed above are only a few highlights of this volume. Additional topics covered in this volume include centromere association during meiosis, association of the bacterial cell membrane in transcription and translation, mismatch repair during replication in eukaryotes, meiotic silencing and so on. A detailed review of all the topics included is beyond the scope of this review and the competence of the reviewers involved. However, this much is assured: researchers from any area of genetics will find something of interest in this volume.

Mendel became the abbot of St. Thomas Abbey, Brünn in 1868, following which his scientific work more or less ceased. He died on 6 January 1884, both he and his discoveries unknown to, and unappreciated by, the scientific community⁹. No one, not even Mendel, had he received his due recognition and an opportunity to become part of mainstream academia, could have imagined how his insights into the particulate nature of the genetic material would lead to such a colossal enterprise in just 150 years.

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