

existed in different eras of ancient and medieval India. In particular, appendices highlight the history of the value of  $\pi$  in ancient and medieval India and an interesting note on the Kuttaka procedure of linear solution of equations of Aryabhata I and Bhaskara I; indeterminate equations of second and higher degree; zeros and decimal system. Interestingly, one of the appendices contains a computer program in C language using the Cakravala method, which shows, how advanced mathematics was in early and medieval India.

Chapter 8 provides a brief history of physics existing in India in the periods covered. Very early India saw the development of measurement of length, time and mass and the units used. The concepts of atomism, motion, sound, heat and light as well as the atmosphere, in particular, the prediction of monsoon rains, existing in the ancient and medieval India have been covered.

Chapter 9 is the largest chapter and rightly so, dwelling on the vast and diverse literature existing in India from ancient days. In this chapter the richness of India's literature has been highlighted in full glory. Pali, Prakrit, Buddhist hybrid Sanskrit, Sanskrit and Tamil literature are described in detail quoting verses, prose and drama. The author quotes that the earliest known literature exists in Vedas. Hymns from *Rig Veda* are quoted as examples of literature with passion and boldness. An interesting point noted is that much of the classical Indian literature is based on eroticism or adult content, but packaged in 'description which is distant, impersonal and formal and yet enjoyable'. The main body of the chapter starts with Jataka tales of Pali literature and the parallels with the *Ramayana*. The author then highlights the parallels with the *Mahabharata* and shows that the Jataka tales have more similarity with *Mahabharata*. Similarly, the parallels of these tales with other stories are also mentioned. Subsequently, Prakrit literature, Buddhist Hybrid Sanskrit, Sanskrit and Tamil literature are covered. Quite understandably, the Sanskrit literature gets a broader and more in-depth coverage. Poetry, drama, prose and epics from Sanskrit literature are covered well. Many verses have been quoted in the book. Works of the famous writers Asvaghosha, Kalidasa, Kalhana, Sudraka, Banabhatta and others are quoted. Of course, it is only natural that *Ramayana*

and *Mahabharata*, the great epics of India, have been described in detail with the debate on the dates in which these are written. Different versions of *Ramayana* and the inconsistencies have been highlighted. An interesting point of *Ramayana* being inspired by *Iliad* may be debatable. *Mahabharata* has been covered at depth as well. The encyclopedic nature of *Mahabharata*, including knowledge from *Vedas* and *Puranas*, instructions of ethical and religious nature, stories, myths and legends. An interesting subsection deals with a comparison between Sita and Draupadi. Some similarities between these epics have been highlighted. The end of this chapter has an overview of Tamil literature and is mainly based on available translations of early and middle period Tamil literature. A sub-section on the influence of Indian literature on western countries is interesting.

The final chapter 10 deals with classical Indian art. In the beginning of this chapter, the author admits to the difficulty of defining art in a concise manner and how art depends on response. History of ancient and medieval Indian art has been covered quite well. Monumental architecture of Indus Valley Civilization, Stupas and temples can be mentioned in a special way as symbols of Indian art. The chapter also deals with art forms in different regions of the country and in particular north and south India. At the end, the author brings out connection from the past to present, by referring to the art form of Satyajit Ray, some of his art forms are reflection of ancient and medieval art. The author returns to the main theme of the book, how science, literature and art are entangled with particular reference to ancient and medieval India.

Each chapter contains a lot of facts, citations and documents in the diverse areas, which are hard to find in a single book. Several appendices presented in the book have shown the detailed collections by the author and would be extremely valuable. The objective of the book is to interconnect the areas of science, art and literature and provide insights into understanding how one could have been inspired by the other. The author makes some comments on these from the point of view of a scientist, but mainly concentrates on presenting facts and implies such connections. Anyone reading the book will be able to make one's own

conclusions on such interconnections from the vast documents presented. The task of presenting ancient and medieval India in such vast areas of knowledge is a big challenge and I thank the author for taking up this challenge and doing a wonderful job. I am unaware of any such exercise done before by any author, whose own knowledge of civilization has clearly come out so well in this book.

In summary, this book may be recommended to students and teachers of Universities and can be a basis for a course on history of science. In fact, as the author wrote in the preface, the inspiration to write this book grew out of a course taught by the author. This is an excellent book on a rare subject. The author has taken up this challenge and written an excellent book, which can be kept as a valuable collection.

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**Annual Review of Genetics, 2014.** Bonnie L. Bassler, Michael Lichten and Gertrud Schüpbach (eds). Annual Reviews, 4139 El Camino Way, P.O. Box 10139, Palo Alto, CA 94303-0139, USA. Vol. 48. vii + 611 pp. Price: US\$ 96.

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If we look at the new technologies that have driven genetics research in the recent past, two of them are particularly highlighted. First, development of a better gene editing technology CRISPR/Cas9, and second, advent of third-generation sequencing technology. Till recently, knocking out a gene was a difficult task. That too, it was standardized in a few model organisms. Development of clustered regularly interspaced short palindromic repeats (CRISPR/Cas9) for use in gene knockout has changed this significantly. Researchers are now trying to knockout genes in non-model organisms. What is fascinating in this technology is its portability. It has been tried in so many different organisms; it seems the technology works in most of the organisms. Third-generation sequencing technology addressed two

important bottlenecks in sequencing – longer sequence length and sequence quality. Newer applications of these technologies in genetics are being developed. We are witnessing publications of many such applications in different journals. These applications are quickly being adapted by researchers to address many problems in genetics. This volume contains a compilation of recent developments in genetics using such technologies and also touches on other important areas of genetics, including different aspects of *Drosophila* biology, transposable elements, RNA biology, plant and microbial genetics, cell division, DNA function, epigenetics and human diseases.

The fruit fly *Drosophila melanogaster* has contributed significantly to the field of genetics in the last 100 years and the present volume dwells on some important aspects related to *Drosophila* biology. Jeffrey and O'Farrell emphasize on genetic and molecular studies done in *D. melanogaster* to decipher changes in cell division during its early embryogenesis. Early development of embryo exhibits a period of fast cell division, which is possible due to changes in mechanism of cell division with an unusually quick S phase and lack of gap phases (G phase). This phenomenon changes late in embryo development (prior to gastrulation) with longer S phase and introduction of post-replicative gap phase (G2 phase) to slow the cell cycle. Results obtained in *Xenopus* and *Drosophila* provided evidence that changing ratio of nucleus to cytoplasm (N : C ratio) is crucial in slowing down the cell cycle, which is achieved by inhibition of *Cdk1*. In another chapter, Pocha and Montell describe the importance of single and collective cell migrations during *Drosophila* development. The migration of cells plays an important role in development of organisms and any defects in the process leads to many diseases. By comparing the cellular and molecular mechanisms for single and collective migrations, the authors predict that there is a common theme upon which evolution has built different variations and in this the role of Rho family GTPases is crucial along with cadherins and integrins for adhesion in all cellular movements. In another interesting report on *Drosophila* biology, Charlesworth and Campos review evolutionary consequences of recombination with special

emphasis on rates of recombination and patterns of DNA sequence variation and evolution in different regions of the *Drosophila* genome. Genetic recombination is pivotal for efficiency of selection as natural selection acting at one site affects evolutionary processes at linked sites.

Transposable elements are found in almost all eukaryotes and form an important component of genotypic variation and evolutionary selection. Richardson *et al.* review the available evidences for long interspersed element 1 (LINE-1 or L1) in the brain and also signify the mechanism for generating somatic mosaicism in mammalian and *Drosophila* brain. The presence of methyl binding protein MeCP2 and key cell cycle regulator ATM is known to limit transposon activity in mammalian brain and limitations of these factors will lead to neuronal retrotransposition and neurological diseases. Addressing a key aspect of transposable elements, Fricker and Peters review the molecular mechanism involved in the replication of mobile elements. In a majority of the cases, the lagging strand template is targeted using a variety of features specific to this strand. The authors also address the idea that, in order to protect the vulnerable lagging strand the hosts may have evolved systems to protect it.

The past decade has indicated growing evidence suggesting a much wider role for non-coding RNAs (ncRNAs) in biology and this volume covers some important topics. Bonasio and Shiekhatar in their review have elucidated the large and complex category of long non-coding RNAs (lncRNAs) as well as their role in regulating gene expression. The discovery of RNA interference (RNAi) and its role in post-transcriptional gene silencing in the 1990s has made a prominence of regulatory functions of ncRNAs. The authors state that there is a need for better understanding of functional roles of ncRNAs before a complete picture of the scope of ncRNA catalogue in higher eukaryotes emerges. Taking the RNA biology topic further, Hui *et al.* review the importance of mRNA degradation in differential gene expression in bacterial cells. This also highlights mRNA turnover and various pathways by which the messages are degraded, affecting the lifetimes of individual transcripts.

Plant genetic research holds a significant place in today's world as it

addresses concerns related to bioenergy, food security and climate change. This volume describes the importance of plant research in a few chapters. Lane *et al.* emphasize on the need and importance of the presence of a comparative epigenomic plant resource – plant ENCODE, similar to that of ENCODE project existing for humans, flies, worm and mice. These ENCODE projects help in generating genome wide maps of sequence variation, protein–DNA interactions and inter- or intra-chromosomal interactions, and data related to coding RNAs and ncRNAs. The next review by Zuo and Li highlights an important question in the field of plant genetics concerning the grain size of rice and genetic factors affecting its growth. Several quantitative trait loci for grain size have been validated by molecular tools and many of them are known to act in different genetic pathways along with genes involved in cell proliferation and elongation.

Studies describing genetics of bacteria are also well represented in this volume. The review dwelling on structure and regulation of flagella in *Bacillus subtilis* by Mukherjee and Kearns describes recent advances in the field. The large number of flagella and absence of periplasm makes *B. subtilis* a valuable model organism for studying initial events of flagella morphogenesis. Recent investigations demonstrate that *B. subtilis* also serves as an important organism in studying functional regulators that control flagellar rotation, wherein bifunctional glycosyltransferase/clutch EpsE detaches the rotar from the stators to depower rotation. Rotman and Seifert review two related *Neisseria* species which cause serious infections in humans. They describe in detail the genomic organization of *Neisseria* and also talk about horizontal gene transfer. Finally, the genetic factors which allowed *Neisseria* to be a successful pathogen are also described.

Meiosis is a special cell division leading to formation of gametes in all sexually reproducing organisms and also provides a source of genetic variation between the generations, which has been exploited by both plant and animal breeders. Higgins *et al.* summarize the important factors which are crucial for restricted crossover (CO) localization in barley during meiosis. In barley, CO is limited to the distal region of the chromosome, thereby presenting a potential

barrier for plant breeders. Application of moderate temperature pulse during meiosis alters chiasma distribution and provides a potential route for breeders to manipulate recombination. In another review, Keeney *et al.* explain how chromosome breakage is incorporated with meiotic progression and the precise role of feedback mechanism in creating double-stranded breaks. A review compiled by Bloom, sheds light on physical properties of DNA to get more insights into organization of centromere and its role in chromosome segregation. Centromeres are special domains of heterochromatin, which is distinguished by various histone modifications and by enrichment of cohesin, condensin and topoisomerase II proteins. The review points out the role of several components that play a role in building a functional centromere, viz. Skl1, Ndc80 and complexes like CCAN and CENP-A.

Replication of DNA forms a vital aspect of the central dogma of life. A review by Kelman and Kelman emphasizes on DNA replication in Archaea. Work on Archaeal systems with respect to bioinformatic, biochemical, structural and genetic studies has illustrated that the mechanisms and the proteins involved are almost similar to what is observed in eukaryotic DNA replication, as opposed to what is seen in bacteria. This review suggests that future studies should focus upon the poorly understood aspects of Archaeal replication process, like mechanisms regulating the initiation process, coordination between initiation and other cell cycle.

Integrity of genome is understood to rely on replication, repair and recombination; however, transcription is undermined and can actually result in compromising DNA integrity of organisms. The review by Robertson and Bhagawat focuses on the role of transcription in maintaining stability of DNA template and also possible evolutionary implications of transcriptional-associated mutagenesis. The review also indicates how comparative analysis of the genome will enhance understanding of how transcription modifies the outlook about mutation in both prokaryotes and eukaryotes evolutionarily.

The crucial step of transcription leads to the process of translation, which relies on an efficient machinery to decode message on mRNA to generate a functional protein without incorporating any errors.

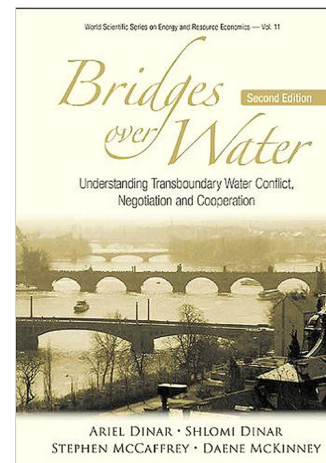
The review by Bullwinkle *et al.* focuses on incorporation of amino acids that are not directed by the genetic code. How non-proteinogenic amino acids would naturally accumulate into the system and the role of translation control machinery to avoid such accumulation are discussed.

Reviews describing various aspects of human diseases are well compiled in this volume as evident in the review by Emily *et al.* which provides an elaborate view on epigenetic mechanisms such as DNA methylation, histone modification and chromatin remodelling in causing diseases. The authors are of the opinion that identification of methylation profiles and epigenetic modifications may efficiently help in curing cancer and other syndromes related to epigenetic mechanisms. Another interesting review describing evolution of a human disease by Gerlinger *et al.*, discusses branched evolution of cancer with low-frequency driver events present in subpopulation of cells, which provide escape mechanisms for targeted therapeutic approach. This review suggests a possible genetic and epigenetic heterogeneity among cells within the same tumour, which adapt to changing environment during progression and therapy.

The recent findings from the field of genetics have been well encapsulated in this volume, providing an excellent resource for researchers working in different branches of genetics. Sincere efforts were made to cover various sub-fields of genetics, ranging from bacterial to plant genetics, and from *Drosophila* to humans, covering important metabolic processes of cells required for development and disease. This volume provides some valuable clues towards understanding some long standing questions from different sub-fields of genetics and also indicates future challenges in understanding molecular mechanism of disease-causing genes and in drug discovery.

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Water is the elixir of life and billion people worldwide suffer due to its scarcity<sup>1,2</sup>. Four out of five persons rely on renewable freshwater resources, which primarily originate in mountains and forests. Unplanned developmental projects coupled with burgeoning population, rapid urbanization and globalization have led to deforestation and water quality deterioration. This has affected the availability of water for human use and ecological needs. Hydrologic regime in the river basins is sensitive to changes in climatic conditions and land use land cover (LULC) changes<sup>3-5</sup>. About 40-45% of the world population resides in drainage basins, which account for 60% of global river flows and are a part of the territory of 145 countries. Anthropogenic-induced climatic changes are expected to significantly affect the water cycle. The available freshwater is declining rapidly, exacerbating the problems of sectorial allocation. The stakes have also been increasing with increase in number of riparian states, and unilateral developments by some riparian states are giving way to precarious situations with conflicts. Parallel developments in international river basin modelling, application of game theory, optimization of water and benefits allocation in the context of imminent climate changes have also aided in conflict resolution.