Two major features of PSLV – the number of new technologies which were developed for the PSLV and the continuous improvement resulting in 50% improvement in the payload performance have been highlighted by the authors. The versatility of PSLV in doing geosynchronous and deep space missions finds appropriate mention. While discussing the peculiarity of the GSLV configuration and the range constraints, the authors could have also mentioned the alternate configurations studied and the perceived development difficulties. One alternate configuration had a liquid core of L-110 and employed solid strap-ons. This would have been an elegant configuration and incidentally L-110 was subsequently developed for the GSLV-Mk III. The authors have detailed in the endnote, the effort towards the indigenous cryogenic engine development. The development story could have included the efforts of a core group under Gowariker in the early 1970s, which started cryogenic engine technology development and one more pilot study done by Namboodiry on the liquid hydrogen availability for such development after the successful flight of SLV-3. All the earlier efforts were stalled for non-technical reasons and could have helped in maturing the technology faster.

The profiles in technology development of the various subsystems of the launch vehicle are included and give a glimpse of the diversity of processes and performance requirements. The authors have condensed and abridged the details without losing the essence of the development stream within the constraints of space. Averments like 'grains for large motors are not made as a single piece (monolithic). It is both unsafe and difficult to do so' (p. 196) are out of place and not correct. Some dates and the reasoning behind decisions like that concerning the RATO motor (p. 216) are not correctly reflected. These are minor and in no way reduce the importance or the essence of development being portrayed.

Women scientists have played important leadership and supportive roles and their contribution could have merited some mention. The lay person may have some difficulty in appreciating the book, especially the later sections. The authors in their attempt to maintain the 'semi-popular' style of the book have not been able to do complete justice to the profiles in technology development. A few drawings and sketches would have rendered the material more understandable.

The chapter on 'The quartet' makes fascinating reading and the reader is provided with rare vignettes of the personalities of the great men behind the space programme. Bhabha, Sarabhai, Dhawan and Brahm Prakash stewarded the space programme with conviction and nobility of leadership – qualities which emboldened the ISRO community to delve into uncharted territory with confidence. The leadership was open to the fact, that while mastering technology mistakes will occur and the solution lay in understanding the issues, analysing them in depth and correcting them. These leaders were not risk-averse, but could take decisions based on reasoned thinking. In turn, they groomed good leaders.

The book is a useful contribution to the five decades of rocket development efforts at ISRO.

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Annual Review of Genetics, 2011. Bonnie L. Bassler *et al*. (eds). Annual Reviews, 4139 El Camino Way, Palo Alto, CA 94303-0139, USA. Vol. 45. ix + 469 pp. Price: US$ 86.

It is difficult to sum up all the developments of a research area in a year in one book, especially when the task is to cover all the major developments in the area of genetics. However, the *Annual Review of Genetics* (*ARG*) 2011, as before, has attempted to cover the developments in the last few years in a wide range of topics in genetics from bacteria, fungi and nematodes to plants and animals.

The volume starts with a well-documented review by Sommer and Streit, on comparative genomics of nematode species. The comparison of genetic processes between *Caenorhabditis elegans* and its close relatives *Caenorhabditis briggsae* and *Pristionchus pacificus* reveals a high number of diverse control mechanisms, and alerts the research community that sequence conservation and gene function(s) are totally unrelated issues. All the seven sequenced nematode genomes indicate a relatively high number of novel genes, which have no apparent orthologs in other organisms. The authors finally conclude that an emerging principle of comparative genomics of nematode parasites is the absence of a general mechanism of parasitism.

As in eukaryotes, the regulation of cell growth and cell death is also important for bacteria under various stress conditions. Almost all bacteria contain a gene that codes for toxins, which may inhibit cell growth. These toxins are co-expressed with their antitoxins from an operon called the toxin–antitoxin (TA) operon. The chapter on TA systems explains how, under stress conditions, stress-induced proteases digest less stable antitoxins to free the toxins in the cells, which interact with various cellular targets to cause cell death. The released toxins help in survival during adverse conditions, e.g. they cause cells to enter persistence or quasi-dormant state in which they are completely resistant to antibiotics and may also play a vital role in eliminating the damaged cells from their populations.

Two articles discuss about plant genetics. The first one by Klee and Giovannoni deals with genetics and control of tomato ripening. The tomato fruit development and ripening is considered as a classic model system to elucidate the important developmental processes in plants since it is being regulated by network of genes, especially different transcriptional factors. This review provides a detailed description of effects of ethylene as well as transcriptional factors in controlling the fruit ripening process. The legume and rhizobial symbiosis, a beneficial association of a plant and bacterium that results in conversion of atmospheric nitrogen into biologically active nitrate and ammonia forms, is one of the key issues to be elucidated in agriculture in view of rising fertilizer prices especially nitrogen. Comprising two key developmental processes, i.e. nodule organogenesis and bacterial infection, the association or the so called 'symbiosis' of legumes and rhizobium bacteria is

a complex phenomenon to understand and also to extend this knowledge to cereal crops on which more than half of the world's population is dependent upon. The second review by Oldroyd *et al.*, has elegantly brought out this important aspect right from infection of the bacteria to synthesis of nitrate and ammonia compounds in the soil from atmospheric nitrogen. Although the association is beneficial to both organisms, plants seem to have set up certain criteria/ rules for the bacteria to cause infection and formation of nodules. The review discusses a series of events such as polarized root-hair tip growth, process of bacterial infection and promotion of cell division in the cortex that lead to nodule formation and thereby fixation of atmosphere nitrogen. Understanding the biology of this coordination of nodule formation and bacterial infection is likely to open up new avenues to develop nitrogen-fixing varieties in cereal crops.

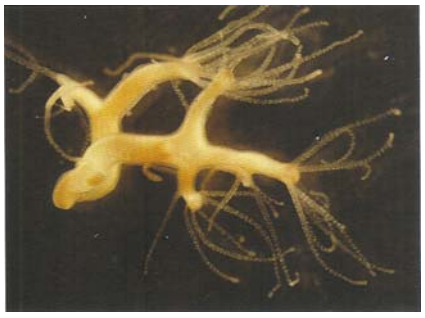
Hybrid incompatibility is an important event in speciation. Maheshwari and Barbash review the genetics of hybrid incompatibility and conclude that hybrid incompatibilities result as a consequence of the interactions between genetic divergences that have occurred within the hybridizing species.

Genetics does not end without the mention of one important cellular regulator, RNA. In this volume, there are three chapters on small RNAs. Similar to RNAi in eukaryotes, a recently discovered adaptive immune mechanism in bacteria called CRISPR (clustered regulatory interspaced short palindromic repeats)–Cas (CRISPR-associated proteins), is well-documented in the review by Bhaya *et al*. The CRISPR–Cas system utilizes exposure to foreign nucleic acids to subsequently target and destroy incoming related viruses and plasmids. This review provides the required leads for future research in this area and catalogues most of the previous publications in this nascent field of research. Understanding the biogenesis and functions of mitochondrial (mt) tRNAs is important for insights into molecular pathogenesis of mitochondrial diseases. Suzuki *et al.* discuss the biogenesis, function and structural aspects of human mt tRNAs and the diseases caused by mutations. The genes encoding these tRNAs are highly susceptible to point mutations, which are the primary cause of mitochondrial dysfunction. The review also discusses the pathogenic mutations of nuclear factors that are involved in the biogenesis and function of mt tRNAs, indicating the functional importance of these tRNAs in mitochondrial activity. Totipotency of the germline and pluripotency of the stem cells must be sharing common mechanisms. Piwi proteins are thought to be involved in one of such shared mechanisms. Piwi proteins bind to piwi-interacting RNAs (piRNAs) that are generally 26–31 nucleotides long. A chapter by Juliano *et al*. is devoted to these developments. Piwi proteins and piRNAs are shown to be most abundantly expressed in germline cells. Moreover, recent studies suggest that the piRNA pathway mediates epigenetic programming and post-transcriptional regulation, indicating their specific function or role in the germline.

Myxobacteria are Gram-negative soil inhabitants having complex lifecycles like swarming, fruiting body formation and sporulation. As they lack flagella, they are unable to swim in the liquid culture and exhibit gliding mobility on solid surfaces usually in coordinated groups or as isolated individuals. About 40 genes of *Myxococcus xanthus* were shown to be involved in this gliding mobility. Protein-labelling studies infer the involvement of large multiprotein structural complexes, regulatory proteins and cytoskeletal filaments in the gliding mobility. Nan and Zusman, in their review, summarize recent endeavours that provide exhaustive information on motility of *M. xanthus*.

It has been shown that epigenetic mechanisms provide an additional layer of transcriptional control that regulates gene expression. These mechanisms are critical components in the normal development and growth of cells. The rapidly evolving field of epigenetics offers exciting new opportunities for the diagnosis and treatment of complex clinical disorders. There are two reviews in this volume that deal with this field. Intellectual disability (ID) refers to a condition of significant limitations both in intellectual functioning and in adaptive behaviour. A wide variety of chromosomal aberrations and a number of gene mutations are reported to cause ID. Bokhoven evaluates several of these causes and suggests that even though quite a number of mutations related to ID have been identified, the increasing power of sequencing allows further elucidation of a large number of mutations that were previously unknown. The author provides a few examples which offer proof of concept that improvement of symptoms is not impossible for some forms of ID and therefore raise hope to improve the quality of life for the afflicted individuals. This chapter also deals with epigenetic link to ID, as the epigenetic control of neuronal gene expression is also commonly affected in ID. The number of transcription factors and epigenetic regulators associated with normal and impaired intelligence is rapidly growing. These developments promise the possible therapy for ID. Another chapter on epigenetics is about genomic imprinting by Barlow. This is a genetic phenomenon by which certain genes are expressed in a parental-specific manner. This chapter compiles recent developments in the understanding of how imprinted protein-coding genes are silenced. In particular, this review focuses on the role of non-coding RNAs that have broad relevance as yet another layer of regulatory information in the mammalian genome.

Starting from a fertilized egg to a grown-up individual, each cellular process is regulated by genes. Developmental genetics is a branch that studies the regulation of cell growth, differentiation and morphogenesis. A review by Tschopp and Duboul discusses how changes in transcriptional regulation can diversify gene function and thereby fuel the morphological evolution. Different genetic strategies that have been developed to tackle the intricate relationship between genomic topography and the transcriptional activities of the *Hox* gene family are discussed. Previous reports suggest that maternal factors actively promote both dorsal and ventral cell fate specification in embryonic dorsoventral axis



A two- to three-week-old β-catenin transgenic hydra with several secondary body columns and heads.

formation. A review by Langdon and Mullins throws more light on molecular factors and mechanisms that establish and pattern the dorsoventral axis of the zebrafish embryo. Another well-collated review is on developmental events leading to axis formation in hydra by Bode.

Previously, most of the biological experiments were performed on groups of cells or tissues presuming that all cells of a particular type are identical. However, recent single-cell analysis experiments show that this assumption is not correct. Individual cells within the same population may differ dramatically. Reviewing the genomics at the single-cell level, Kalisky *et al.* discuss a variety of approaches to single-cell genome analysis. They conclude that most information derived from future studies will link the genomic and transcriptomic data from single cells to their microscopic physical and biological context.

V(D)J recombination or somatic recombination is a mechanism of genetic recombination in the early evolving stages of immunoglobulin genes and T-cell receptors production of the immune system. Schatz and Swanson discuss the mechanisms of initiation of V(D)J recombination. Copy number variation is functionally significant, but has yet to be fully ascertained. These variations are widespread in the human genome and play an important role in human diseases and population diversity. A review article by Girirajan *et al.* explores recent advances in the study of rare and common copy number variants in normal human populations in relation to human diseases.

DNA double-strand breaks is one of the major cytotoxic forms of DNA damage, and their repair is important for cell survival and maintenance of integrity of the genomes. Symington and Gautier review the components of the end resection machinery, the role of resection in DNA damage signalling, and the regulation of these activities during cell division in budding yeast.

A few species alter their genomes during development. In ciliated protozoa, the whole genome reorganization occurs universally during differentiation of the somatic macronucleus. Chalker and Yao, in their review, describe with different models how this process takes place. Besides, they also talk about the importance of the epigenetic mechanism and homologous RNAs in guiding the genome rearrangements.

Genetics comprises a vast area from viruses to animals. This volume has something to offer to every geneticist working on myriad topics. It is also of general interest as it encompasses all the major developments in sub-disciplines of genetics such as epigenetics, developmental genetics, bacterial genetics, etc. After going through the volume, the one topic that I missed was a review on classical genetics. Most of the reviews have a box item on future perspectives, which is important, as these are carefully drawn out future steps by pioneers in the field.

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