CD Review

Organic Cultivation of Rice – Seed and Harvest. CDs produced by Centre for Indian Knowledge Systems, 30 Gandhi Mandapam Road, Kotturpuram, Chennai 600 085.

Perhaps no other crop plant is cultivated more widely in the world than rice. Rice is cultivated in more than 113 countries and provides for livelihoods of nearly 250 million people. It is the staple food for over half of the world's population and provides 27% of the dietary energy supply and 20% of the dietary protein intake in the developing world. India is the second largest producer of rice in the world after China and is a staple food of 65% of the Indian population. Rice accounts for nearly 46 and 42% of the cereal and total food grain production respectively, in India. Along with the other staple crop wheat, rice has been one of the few crops that have contributed to the staggering intensification of agricultural practices, including the use of artificial fertilizers and pesticides and more recently in the use of genetically modified (GM) crops. With the intensification unlikely to abate due to increased demand by a growing population, there has been an increasing concern of the impacts, including loss of soil fertility, diminishing soil biodiversity and of course, the lack of sustainability in the entire process. Challenged by these concerns there have been attempts, world over, to develop alternate methods of farming which are environment-friendly and economically feasible. In the context of poor farmers from India and other developing countries, sustainable and organic agriculture methods based on locally-available resources, could contribute to agricultural production without causing further environmental damage.

Of late, due to a greater awareness among the public, the market for organically produced foods is on the rise. In India, organic farming was practised on only about 4800 ha in 2003 with a net export value of Rs 89 crores. This accounts for only 0.8% of the current global organic produce market. Some of the major organically produced agricultural crops in India include plantation crops, spices, pulses, fruits, vegetables and oil seeds (www.fao.org). In recent years, increased interest in organic farming methods has been evidenced by both farmers and the government. A number of research institutions, NGOs and other bodies have helped promote sustainable methods of farming.

The Centre for Indian Knowledge System (CIKS) at Chennai, has recently developed a film series on the 'Organic Cultivation of Rice'. This is a timely and welcome contribution to not only the farming community, but also for all those interested in agriculture at large. The CD compiles information on the traditional organic cultivation methods used by farmers based on several years of research and interaction with farming communities.

The first film in the series provides an overview of organic rice cultivation from sowing to harvest. It provides in detail the step-wise process involving seed selection, nursery, planting, pest attack and harvest. At every step, the authors encourage the use of locally available materials in and around the farms. For example, *Pongamia* and neem, which are the source of green manure and biopesticides respectively, are encouraged to be used at one or the other stage during farming. The second film provides details of organic soil enrichment using plant and animal products such as cow dung, legume plants, etc. Several methods of compositing, including farm composting, vermicompost and heap compost have been dealt in detail.

The third film deals with the management of common pests of paddy. The most commonly used vegetables such as garlic, green chilies and ginger are shown to be effective in controlling several pests of paddy. The simple rope technique for the effective control of lepidopteran pests such as skipper has been elegantly demonstrated. The fourth and final film highlights the important diseases affecting paddy and their control measures.

The total duration of these four films is 110 minutes in English and 99 minutes in Tamil. These films are available in both DVD and VCD formats and reasonably priced at Rs 250. Considering the extent of information presented on the indigenous knowledge and organic cultivation of rice, the CDs form an invaluable contribution. However, like any product, there is some scope for improvement to make it even more valuable to users. With a little more editing, redundant and repetitive information could be avoided. Further, some sharp editing can make the CD crisper and shorter (75 minutes). The small booklet issued with the CD is well produced and provides a snippet of the information contained in the CD. But these comments should not detract the good job done by CIKS. I only wish that CIKS produces the CD in other local languages.

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Annual Review of Genomics and Human Genetics 2005. Aravinda Chakravarti and Eric Green (eds). Annual Reviews, 4139 El Camino Way, Palo Alto, CA 94303, USA. Vol. 6. 462 pp. Price not mentioned.

The *Annual Review of Genomics and Human Genetics 2005* edition covers a wide range of topics relating to genetics of various human diseases and behaviour, X-chromosome inactivation in mammals, human evolution and natural variation in human genes and genomic archeology and genomic prospecting of wild cats.

At the beginning, Alfred Kudson gives a personal account of the last 60 years of the 'Golden Age' in genetics and medicine. His review deals with the discovery of retinoblastoma as a tumour suppressor gene and as a key regulator of the cell cycle.

Libby *et al.* address the issues of endogenous genetic susceptibility and multifactorial complexity glaucoma. The review emphasizes upon the importance of genetic factors affecting susceptibility to intraocular pressure elevation and those affecting retinal ganglion cells and optic nerve susceptibility in glaucoma pathogenesis. Mutations in various genes contributing to primary open-angle glaucoma, developmental glaucoma and pigmentary glaucoma are described. The authors suggest that large-scale epidemiologic studies in conjunction with new sophisticated data analysis techniques for complex genetic and environmental interactions could help in deciphering the complex interactions that underlie human glau-

coma susceptibility. Furthermore, animal model systems and genomic tools could be employed to ask questions about individual cell population responses to glaucomatous insults.

Tartaglia and Gelb describe the genetics and pathogenesis of Noonan syndrome and related disorders. Mutations in the *PTPN11* gene which encodes the protein tyrosine phosphatase SHP-2 contribute to ~50% of Noonan syndrome cases. The authors have discussed the molecular heterogeneity and spectrum of molecular defects in the *PTPN11* gene contributing to Noonan syndrome and related disorders, and have reviewed the importance of increased prevalence of two childhood leukaemias (juvenile myelomonocytic leukaemia and acute lymphoblastic leukaemia) and Noonan syndrome. The effect of gain-of-function PTPN11 mutations leading to increased signal transduction through the RAS/MAP kinase cascade in disease pathogenesis is discussed. It is hoped that future work employing mouse models of Noonan syndrome would contribute to development of novel therapeutic strategies and better molecular diagnostic tools.

Chow *et al.* have presented an overview of mammalian X-chromosome silencing and the current understanding of the molecular events involved in silencing an X-chromosome. The role of the *XIST* gene, which encodes an ~17 kb untranslated RNA that coats the inactive X-chromosome present in the multifunctional domain called as X-inactivation centre of X-chromosome is discussed. They also reviewed the role of *trans*-acting factors (poly comb group proteins Ecd/Enx and Ring 1A/B, BRCA1) in X-chromosome inactivation. The authors have discussed the nature of genes which escape X-inactivation and the functional significance of such escape mechanism and dwell on the differential mechanisms that distinguish genes that escape from those that are subject to inactivation. Reviewers highlight the relevance of Lyon's repeat hypothesis, which postulates that L1 LINE elements could be the way stations or booster elements in the X-chromosome inactivation and suggest that new genomic databases, new technologies and new model systems would contribute to deciphering the importance of *cis*-and *trans*-acting factors that mediate lyonization.

Anne Bowcosk has reviewed the genetics of autoimmune disease, psoriasis and the role of Major Histocompatibility Complex in disease pathology. Dysregulation of genes or pathways controlled by the RUNX family of transcription factors (which are involved in hematopoietic cell development, development of T-cells in the thymus, chromatin remodelling and gene silencing) could contribute to autoimmunity. The author describes the various genetic approaches employed for understanding the pathogenesis of autoimmunity. The functional significance of various genes (like *CsK*, *PAG*, *PTPN22*, *PDCD1*, etc.) in autoimmune disorders is also discussed.

ATP-binding cassette (ABC) transporter superfamily of genes encode proteins involved in transport of a diverse set of substrates across membranes. Dean and Annilo have presented with elegance the role of these genes in human diseases like adrenoleukodystrophy, cystic fibrosis, retinal degeneration, hypercholesterolemia and cholestasis. The authors have discussed the conservation of ABC genes and evolution of gene families. Determination of the three-dimensional structure of ABC transporters in future would help in the better understanding of the function of the said proteins in cell physiology.

Stone *et al* review the statistical challenges in discriminating functional genomic elements from the bulk of the genome. The authors have presented a detailed account of comparative genomics literature and consider the impact of an expanding diversity of orthologous sequences to resolve functional elements. They highlight the importance of comparative sequence analyses based on multiple sequence alignments and well-characterized species phylogenies, and emphasize the impact of deep sequence alignments and mathematical modelling on the universal features of comparative methodology, viz. specificity, sensitivity and phylogenetic scope.

Maternally inherited human mitochondrial DNA (mtDNA) has been extensively used for unravelling socio-cultural effects that might have influenced human evolution, matrilocality versus patrilocality effects or the social stratification induced by the caste system. Pakendorf and Stoneking discuss the importance of mtDNA studies in combination with analyses of the Y-chromosome and nuclear DNA variation in answering questions about human population history and evolution, ancient DNA and forensic DNA applications.

Ahmad *et al.* review the current status in molecular genetic studies of humans in defining the pathogenesis of cardiomyopathies. The authors have presented with simplicity the current understanding of hypertrophic cardiomyopathy, glycogen cardiomyopathy, dilated cardiomyopathy and restrictive cardiomyopathy. It is hoped that future studies on myocyte and myocardial response to genetic variations would help in better understanding of the molecular basis of the various cardiomyopathies and help in early detection of individuals prone to arrhythmias and sudden death.

Human taste perception has been a subject of active research over the years. Dennis Drayna has extensively reviewed the literature on the genesis of five major taste classes (sweet, sour, bitter, salty and umami) which are primarily mediated by ion channels and G-protein coupled receptors. Future research in genetics of human taste perception would be directed to gain more insights into cellular and molecular aspects of the process and to study the variations in genes encoding taste-specific second messenger systems and downstream signalling components.

Cystic fibrosis (CF) is a disease condition which affects the lungs, pancreas, intestine, liver, male reproductive tract and sweat glands in humans. It is an autosomal recessive disease caused by mutations in the cystic fibrosis conductance regulator (*CFTR)* gene. Garry Cutting has reviewed the latest work on the cause–effect association of *CFTR* mutations and CF disorder. Of the 1100 disease-associated mutations in *CFTR,* one mutation AF508 accounts for around 70% of CF alleles worldwide with varied phenotypic expressions. The search for a modifier gene for CF has remained elusive so far. It was suggested that genetic and epigenetic factors near the *CFTR* locus might influence the CF disease variability. Future challenges lie in identifying the *cis*- and *trans*-factors which might affect the severity of CF disease.

Smukste and Stockwell give an excellent account of chemical genetics, an approach which employs chemical tools to study biological systems in much the same way as genetics. Innovations in high-throughput screens, development of new phenotypic assays and screening protocols in the last few years has been helpful in studying signalling pathways and other interesting cellular processes. Recent developments in the field have rendered

possible the screening of large-scale libraries of chemical compounds generated through synthetic routes. Future challenges include devising multi-pronged strategies involving genetics and biochemistry techniques aimed at understanding the 'mechanism-of-action' of these chemical compounds.

Single nucleotide polymorphisms (SNPs) are a form of genetic variation, which offer an important tool for genetic association studies with an aim to link the DNA variants contributing to an increased susceptibility to human diseases. More than 10 million SNPs discovered in human genome sequencing efforts in the last few years offer a unique opportunity to look at association studies. Crawford *et al.* describe recent trends in studying the natural genetic variation in humans and discuss efforts on the resequencing of more than 500 human candidate genes for SNP discovery. They describe in detail the research work on SNP association studies using both direct and indirect approaches to mine information useful for candidate gene association studies.

Pinkel and Albertson discuss recent trends in comparative genomic hybridization (CGH) studies, wherein the whole genomic DNA from query and reference samples are differentially labelled, hybridized and the differences in hybridization intensities are analysed which yields variations in DNA copy number. CGH analyses is employed to detect whole genome polymorphisms such as dosage abnormalities, namely chromosome aneuploidies, presence of supernumerary chromosomes, segmental duplications and deletions, and in genomic analysis of cancer. Future work in CGH analyses holds promise for medical genetics, especially in clinical applications, which would increase our understanding of cancer and other diseases.

Diez-Roux and Ballabio have analysed the current understanding and future perspectives of sulfatase gene family. Sulfatases are a highly conserved family of proteins catalyzing the hydrolysis of sulphate ester bonds from a wide variety of substrates. The authors have explained the importance of post-translational modification of sulfatases to their biological activity and the correlation between the mutations in sulfatase modifying factor (SUMF1) and multiple sulfatase deficiency (MSD) and the relation between sulfatases and genetic diseases such as metachromatic leukodystrophy, Hunter syndrome and chondrodysplasia punctata. They also describe the utility of animal models to study the role of sulfatases in human disease and the possible therapeutic interventions.

The increasing wealth of genome sequence information of various organisms is aiding in our understanding of different human diseases and in devising strategies to control them. Giallourakis *et al.* discuss the importance of computational strategies and integrative genomics for large-scale genome analyses in elucidating gene functions and discovering disease-causing genes. Integrating clinical informatics databases with genomics databases in future would help in identifying a disease-causing gene, underlying a sporadic disease simply based on the presenting symptoms in a single individual. With advances in genotyping and sequencing technologies, the future is poised for a rapid shift from candidate gene studies to genome-wide association studies for human diseases.

Studies on big cats were carried out initially with an aim of conservation of these wild animals. However, the translational benefits of studying big cat genomes have become evident only recently (in the post-genomic era). O'Brien and Johnson have reviewed the approaches of computational algorithms being applied to address biological questions that surround free-ranging species not traditionally suitable for genetic enquiry. They explain how insights into phylogenetic hierarchy, demographic contractions, geographic population substructure, behavioural ecology and infectious diseases have revealed strategies for survival and adaptation of these predators. Studies on big cat genomes offer an opportunity for genomic prospecting in a distinct, highly adapted and successful predatory lineage.

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