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ACKNOWLEDGEMENT. Travel grant for attending the conference was provided by Indian Statistical Institute, Department of Science and Technology and Council for Scientific and Industrial Research.

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MEETING REPORT

Quantitative genetics on the rise*

The science of genetics owes its origin to the rediscovery of Mendel's Laws of Inheritance in the year 1900. Earlier, the discovery of these laws was possible due to selection of discrete traits, each of which was apparently controlled by a single gene. Much before the rediscovery of Mendel's Laws, however, Francis Galton and Karl Pearson demonstrated that many traits in humans exhibited continuous heritable variation, which could not be explained by Mendel's Laws. Thus, soon after the rediscovery of Mendel's Laws, two main groups of geneticists emerged: the Mendelians, who believed that all heritable differences were qualitative and discontinuous, and the Biometricians, who proposed that all heritable variation was quantitative and continuous. Subsequently it was shown by Ronald Fisher and others that inheritance of quantitative variation could also be explained on the basis of Mendelian inheritance, if a trait is assumed to be controlled by many genes (polygenes) and further, if it is assumed that the expression of these polygenes is influenced by the environment. This also led to a distinction between simple and complex quantitative traits (QTs), and laid the foundation of quantitative genetics (QG).

Initially the inheritance of simple QTs (e.g. skin colour in humans, kernel colour in wheat or corolla length in *Nico-*

tiana) was studied using Mendelian methods. Later it was realized that most QTs are complex traits and their inheritance cannot be studied by Mendelian methods. Therefore, a biometrical approach was proposed that was popular during the 1960s and 70s. Though this approach allowed partitioning of genetic variances and estimation of genetic effects for individual QTs, it did not allow identification of individual loci contributing to the inheritance of a QT. The recent emergence of molecular markers and extensive use of statistics in the study of the inheritance of complex QTs allowed identification of the so-called quantitative trait loci (QTLs), which could be cloned and characterized to study the details of genetic control and biochemistry of QTs. The study of QTs could also be used in population genetics (PG) and evolutionary biology, which made this area of research most promising.

During the later half of the last century, QG had its ups and downs. For instance, at the First International Conference on Quantitative Genetics (ICQG1) held in Iowa State University, USA in 1976, there was a feeling of pessimism¹, which was largely overcome by the time the Second International Conference on Quantitative Genetics (ICQG2) was held in 1987 in North Carolina State University (NCSU), USA^{2,3}. Since then, during the last two decades, significant progress in the field of QG has been made first, due to the availability of molecular markers and genome sequences, and secondly, due

to the development of statistical tools for genetic dissection of quantitative traits. This was amply demonstrated in the presentations made at the Third International Conference on Quantitative Genetics (ICQG3) recently held in China.

The conference began on the first day (19 August) with registration, reception and a full-day workshop on 'Population genetics, QTL mapping and association mapping' for Chinese participants. Participation was truly international in nature with representatives from as many as 28 countries (including China) from all over the globe, signifying the interest of the international community in QG.

The academic programme started on the second day with opening remarks by William Hill (Edinburgh) and a special lecture by Bruce Walsh (Arizona), who outlined the progress made since ICQG2, and future prospects in the field of QG. This was followed by several invited lectures and selected contributed papers each day. In all, there were 11 sessions (including two poster sessions) comprising 23 invited lectures, 27 contributed oral presentations, and 72 posters (although all posters were not available for display). The presentations included papers that either involved discussions of general principles or methodology, or presentation of experimental results involving animal or plant systems. Use of both molecular markers and genomic sequences in the detection of QTLs was adequately covered; to some extent their use in population genetics and evolutionary biology

*A report on the Third International Conference on Quantitative Genetics held in Hangzhou, China during 19–24 August 2007.

was also addressed. The conference was largely dominated by statistical genetics and examples of quantitative traits in animals (including humans), although some excellent presentations on plant systems were also made by Qifa Zhang (on heterosis), Ed Buckler (on association mapping) and Fred Hospital (on marker-assisted selection). It was also interesting to learn that methods of QG (including QTL analysis and association mapping) can be applied to the study of behavioural traits, genome imprinting (epigenetics), copy number variants (CNVs) and cis-SNPs and heterosis-environment interactions. The organizers plan to make the videos and presentations of the lectures available on the web.

The only criticism which the author has about the recent developments in the area of QG and the presentations made at ICQG3 is the widening gap between animal/plant breeders (including molecular breeders) and the geneticists on the one hand, and the statisticians on the other. There are only few practising animal or plant breeders, who understand statistics underlying the genetic analysis of QTs, and still fewer statistical geneticists, who ever practice animal and plant breeding. Therefore, there is a need to develop hu-

man resource with training in both genetics and statistics to address the complex problems of genetic dissection of complex QTs.

There appears to be a lack of activity in this area of research in India, where we have not been able to keep pace with the recent developments in the field of QG. There is hardly any school of statistical genetics with workstations having powerful supercomputers for QG research. The centres of bioinformatics established so far are more oriented towards genomics research rather than QG. Consequently, no statistical tools for research in the area of QG are being developed in India. Also, application of the latest statistical tools for genetic dissection of QTs (developed elsewhere) in animal/plant systems is being practised at few centres and that too rather superficially. The funding agencies in India (ICAR, ICMR, CSIR, DST, DBT, etc.) need to take notice of this poor state of the science of QG in our country and take remedial measures to improve the situation. We can certainly learn a lesson from research activity in our neighbour country, China, where not only high-quality research in QG is underway in different laboratories, but national and international conferences with participa-

tion from around the world are regularly organized to help Chinese scientists interact and collaborate with those from other parts of the world. A major effort in India is needed to develop centres of statistical genetics with emphasis on QG, both in animal and plant systems.

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ACKNOWLEDGEMENTS. I thank Indian National Science Academy, New Delhi for nominating me to visit China under CAS-INSIA Bilateral Exchange Programme to participate in ICQG3.

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MEETING REPORT

Promising achievements and new challenges in agriculture biotechnology*

By understanding global trends and national and regional needs, most of the countries in Asia have been visible in articulating their support for agribiotechnology as a new engine for economic growth. To place Malaysia in an advantageous position in the rapidly growing

national, regional and global agribiotechnology market, there has to be a policy in place. The Malaysian Government had launched the National Biotechnology Policy in 2005, and advancement of agribiotechnology is a part of it. The 4th Asia Pacific Conference on Plant Tissue Culture and Agribiotechnology 2007 (APaCPA-2007) was held recently in Malaysia to look at the current agribiotechnology trends and scenario in Asia, to showcase what has been achieved so far and review the challenges and opportunities in agribiotechnology. The theme of the conference was 'Biotechnology for better food, health and quality living'. There were 12 plenary talks, seven concurrent sessions, and an embedded trade

exhibition, business forum, and a one-day 'orchid symposium'. About 430 registered participants and 103 speakers from different institutions belonging to 28 countries participated in this five-day event.

M. G. K. Jones (Murdoch University, Perth, Australia) in his opening plenary lecture spoke on the current status of agribiotechnology in the Asia region, and presented examples of success and discussed future prospects for development. He highlighted that the world population will increase by about 3 billion from the current value to about 9 billion by 2050, and a large proportion of this increase will be in the Asia-Pacific region. He projected providing enough food for the ex-

*A report on the 'Asia Pacific Conference on Plant Tissue Culture and Agribiotechnology 2007', held at PWTC, Kuala Lumpur, Malaysia during 17-21 June 2007, and organized and sponsored by AIMST University, Ministry of Agriculture and Agro-based Industry, and State Government of Kedah Darul Aman in collaboration with 11 institutions and under the auspices of 'Asia Pacific Association of Plant Tissue Culture and Agribiotechnology'.