

## In this issue

### A wisp of the exotic

The arthropods make silk to protect growing young ones, to use in foraging and even restraining the female during mating. The weaver ant uses its larvae as bobbins to weave its nest from silk the larvae secrete. Although silk is produced by a large number of insects, spiders and relatives of centipedes, 'sensuous silk, soft as a sigh, luxurious and romantic' is only the one given by *Bombyx mori*. The Chinese discovered it five thousand years ago and now supply fifty tons of it to half the world. They have domesticated and now keep more than five hundred varieties of silk-producing *Bombyx* moths. Most research in silk is reported from Japan in the last several decades. India, the third largest producer perhaps consumes even more.

We have from antiquity fancied silk. Technologically, although we have cloned the silk fibroin, it is unlikely that we will be able to spin it into a yarn of such great exquisiteness that the cuticular spigots of the silkworm achieve. No one seems to have improved on the inventions of legendary empress Xi Ling Shi who in 2640 BC discovered after dropping a cocoon into hot water the only practical way to unwind the glistening mass of yarn from pupae. Silks are made of essentially only three amino acids – glycine, alanine and serine. The polypeptides form either alpha helical, cross beta or parallel beta structures providing the necessary strength and flexibility. Insects in general make silk only of one protein and it may be a large fraction of all proteins they make. Thus silk is good biotechnology material and certainly genetic and molecular genetic methods could be of great value to the silk industry. The moth could with its abundance of production of a singular protein be of great utility for biotechnologists as some have amply demonstrated.

J. Nagaraju in a review article (page 151) puts down in one place attempts at molecular genetic work

with the silk moth *Bombyx mori*. The author says this will further widen the scope of genetic analysis of the organism. May be. The moth could be intrinsically interesting in many ways and a model for all silk producers. Silkworm is a good model system for studying silk production and the entire machinery although biologically, the spider in fact may be a more sophisticated spinner. I do not see the silkworm as a genetic resource nor see the point in genomics of this organism for any purpose other than improving the quality of silk or in using the worm to spin proteins of interest in large amounts. Do we need to have another genome project for this? In any case the *Current Science* reader will find this review informative.

K. S. Krishnan

### In search of QTLs

There is an interesting tale of a king who was very keen on the details of the entire human history and hence appointed a huge team of able experts to document it in detail. The team did a commendable job and came out with a 100-volume write up in ten years and submitted it proudly to the king. But the king was by then so much engaged in his administration, accounting and other state management that he hardly had any time to read this monumental work. But being still keenly interested, he ordered a condensation of the 100 volumes to a readable size. The team happily accepted the challenge and extracted the contents to ten volumes in about five years. But by then the king was too weak and unable to read such a vast material and ordered them to condense it to one small volume. The team again attempted this and by the time it almost did the job the king was on the deathbed. Unable to control his curiosity to 'know' the human history he summoned the team to summarize the findings. The leader who

had some insight into the details rushed to the king and summarized the entire human history in one line: 'They were born, they suffered and then died'. The king died happy.

Too frequently the plant breeders are in a state similar to that of the king. They are keen to understand the entire physiological basis of yield and other traits, genetic mechanism regulating these traits, the arrangement of genes regulating them on the chromosomes, etc. with the hope that by knowing it all, they could be more efficient in creating (breeding) the new varieties. Historically, physiologists, molecular biologists and recently the neo-geneticists have been promising exactly these to the practising plant breeders. But unfortunately, history has shown that like the king, the breeders eventually have been attaining their 'end' results even before they are treated with the full treatises they wished to. The reason is simple: as with the king, the breeders are always busy and 'running out of time' in meeting their immediate deadlines of addressing the problems of increasing yield of, or building disease resistance into, their varieties. They hardly have time to incorporate the details they wish to while breeding but they are breeding the superior plant types successfully.

Fortunately however, the concern for feeding the breeder with the requisite information continues and there are unstinting efforts to generate information required by him. One such recent addition to the list is the generation of chromosome maps showing the loci controlling the quantitative traits. Familiarly known as QTL maps, they are being generated for a wide range of major crops such as maize, tomato, rice, etc. and there are international teams working towards generating these maps in as much detail as possible using a range of molecular techniques available. In rice for instance, as in several crops, networks of teams have been established such that they all work towards a common

goal of building these maps. It is hoped that availability of these maps would assist in molecular based selection of the complex traits such as resistance to biotic and abiotic stresses that cannot otherwise be measured easily. The paper by Raghavendra Prasad and his colleagues (page 162) is one inline with such continued efforts to prepare the maps of the QTLs in rice.

Physiologically even defining the quantitative traits such as resistance to salt is a tough task especially when one wishes to study and map the genes regulating them. Plants could exhibit resistance to increased salt levels in different stages and through different mechanisms. Most of these are least understood in most crops and this makes the task of mapping them all the more tough and challenging. Raghavendra Prasad and his colleagues have hence begun with a simple technique: to map the genes involved in resistance to salt at the stage of seed germination and seedling growth. The seeds of a dihaploid population that is being widely used for such mapping process, were germinated under normal (no salt) and 5% NaCl conditions in the petri dishes and the relative performance of different lines under salt conditions was estimated. Based on the extent of associations of different salt-resistant traits among themselves and with those already mapped markers, they located the loci controlling these traits onto the chromosomes with a defined probability (called LOD for Log of Odd Ratios). They obviously plan to build the maps of the loci that offer salt resistance for later stages of the growth of rice. This would indeed be a very challenging task. Given the complexity of traits such as salt tolerance and/or resistance one wonders if this process of loci hunting could ever end.

Turning to questions very familiar to those working with the QTLs, how reliable and useful are these

QTL markers for breeders? Obviously the usefulness could be a direct fallout of the reliability and the reliability can be evaluated only with more data being accumulated. Though this in essence is being questioned by some quantitative geneticists (Arunachalam and Shanti, *J. Genetics*, 1993, 72, 73), well-planned experiments have demonstrated that the QTLs can be used reliably (Stromberg *et al.*, *Crop Science*, 1994, 34, 1221) – as reliably at least as the conventional selection techniques. Thus there is a strong case coming up for more intensive work on molecular markers and more labs are turning to appreciate this fact. Hopefully we shall have intensely detailed and reliable maps in future. We shall also hope that the 'breeder-king' lives longer enough to harvest the efforts of these experts before he gives way to the newly emerging feudal kings – the bio-technologists.

K. N. Ganēshaiah

### A HGV alert

Inflammation of the liver caused by viruses ranks second only to diarrheal diseases in the list of leading epidemical diseases in India. The common kinds of viral hepatitis are initiated by hepatitis A virus spread through contaminated food and water or by hepatitis B virus transmitted parenterally. There are also other viruses which are called 'non-A non-B' hepatitis viruses because they are neither A nor B. Studies on non-A non-B virus hepatitis gathered considerable momentum after accurate methods of identifying the viruses became available. Several new viral types were described in due course. One of these viruses has characteristics of hepatitis A and another form is blood transmitted and thus is similar to HBV. Epide-

miological features and association of different viral types with various clinical forms of liver disease such as acute hepatitis, subacute liver failure, fulminant liver failure, chronic hepatitis, liver cirrhosis and hepatic carcinoma have been the theme of investigations of several Indian scientists, who have made significant contributions to hepatitis research. Indian researchers described for the first time the enteric non-A non-B hepatitis virus designated hepatitis E virus (HEV). P. Kar *et al.* report the results of another notable study on page 189.

Less than four years ago, an RNA virus considered a non-A-E hepatitis agent was discovered and christened as hepatitis G virus (HGV). The virus whose genomic organization is similar to hepatitis C virus (HCV) is distinct from HCV though transmitted parenterally and sexually. In serological studies the frequency of infection by HGV, in many parts of the world, is reported to be higher than infection by either HBV or HCV. Several studies, which probed the association of HGV with various forms of liver diseases, suggest that the virus may be involved in the causation of fulminant hepatic failure, a dominant reason for the death of patients with liver disease. Infection by HGV is considered to be rare in India. Kar and colleagues observe a high prevalence of HGV in Indian patients with fulminant hepatic failure, a frequency higher than that of any other type of hepatitis virus in Indians with fulminant hepatic failure. They, however caution that HGV may still not be an independent causative agent since in their study, HGV infection was mostly seen as a co-infection with other hepatitis viruses. Their findings bring forth several issues for scrutiny and would surely rejuvenate those who had imagined that HGV infection is rare in India.

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