B 4

Assessment of genetic homogenization in *Wolbachia* infested arthropod species

Fathimath Nishana, N. Reshma, A.A. Sabana, Ann Rose Bright, R. Pikankatta[1] and Tony Grace

Department of Genomic Science, Central University of Kerala, Padanakkad, Kasaragod

[1] Department of Biochemistry, Central University of Kerala, Padanakkad, Kasaragod

Wolbachia are intracellular, gram negative, alpha proteobacteria which infects a wide range of arthropods and some nematode species. These bacteria can cause a number of reproductive modifications in their hosts, including cytoplasmic incompatibility between strains and related species, parthenogenesis induction, male killing and feminization of genetic males. It is estimated that at least 20% of arthropods and some nematode species are infected with this bacterium. *Wolbachia* have the ability to sweep through a population. So it carries the maternally transmitted factors during the sweep. Here we investigated whether mitochondrial homogenization has happened in the *Wolbachia* infected insect species in comparison to uninfected insects. For this the mitochondrial COI gene was amplified from *Wolbachia* infected and uninfected insect species. DNA sequences of 10 *Wolbachia* infected and uninfected insect species revealed that the mean evolutionary diversity between subpopulation and overall population is very low. Phylogenetic analysis revealed that *Wolbachia* infected and uninfected insect species are clustered together as a group which indicates no significant difference in mitochondrial variation within or between species infected with Wolbachia. The results from this study suggest that mitochondrial homogenization has not occurred in the insect species used for the study.

B 5

Homology modeling deduced 3-D structure of adenylation domain of *Pseudomonas fluorescens* Pf-5 non-ribosomal peptide synthetases (NRPS)

T.P. Jamshinath, N. Philip Job, M.K. Rajesh, Murali Gopal and George V. Thomas

Bioinformatics Centre, Central Plantation Crops Research Institute, Kasaragod

Pyoverdines are group of structurally related siderophores produced by *P. fluorescens*. The present work attempts to predict the three dimensional structure of *P. fluorescens* Pf-5 Non Ribosomal Peptide Synthetases (NRPS), a class of peptide secondary metabolites that are produced by *Pseudomons fluorescens* which is involved in the biosynthesis of pyoverdine biosynthetic pathway. The 3-D structure of adenylation domain of *P. fluorescens* Pf-5 NRPS was predicted using MODELLER 9.10. based on templates showing similar identity to the target protein [2AMQ (*Brevibacillus brevis*), 2VSQ (*Bacillus subtilis*), 3E7W (*Bacillus subtilis*) and 3DHV (*Bacillus cereus*)]. We generated five models and the model with the discrete optimized potential energy (DOPE) score was chosen. Loop refinement was performed to increase the

quality of the model with the best DOPE score. The secondary structure of the protein was determined by using PORTER, SOPMA, GOR, NetsurfP. STRIDE was used to calculate the secondary structure of NRPS protein. Evaluation and verification of the model was done using Procheck via Ramachandran plot which showed that 86.4% of the residues were in most favorable region and around 9.4% of the residues were in additional allowed regions. Based on the PROMOTIF program, it was found that the percentage of â-strand was 14.7%, percentage of 3,10 helix was 2.6 % and percentage of á-helix was 31.9 %.

B 6

Genetic variation among populations of snakeweed grasshopper *Hesperotettix viridis*

A.A. Sabana, Fathimath Nishana, N. Reshma, Ann Rose Bright and Tony Grace
Central University of Kerala, Padanakkad, Kasaragod

Among the herbivores insects, grasshoppers are highly polyphagous. *Hesperotettix viridis* (Thomas) is an oligophagous grasshopper native to North America. They mainly feed on composites either *Guteirrezia sarothrae* or *Solidago mollis*. We used mitochondrial CO1 region and four microsatellite markers to evaluate the genetic variation among the population of two host races from Montana and Wyoming in US. From mitochondrial DNA data, neighbor joining analysis revealed two distinct host associated clusters. Genetic distance analysis revealed high genetic variation among host variants and lower genetic variation within the same host form irrespective of geographic distance between sampling locations. However microsatellite data reveals significant genetic variation among all populations. Genetic differentiation among sub-population as estimated by F_{ST} value was 0.311 revealing significant genetic differentiation among the populations.

B 7

Effects of genotypes and growth regulator combination in *in vitro* culture of rice

S. Jyothileksmi, Dijee Bastian, Rose Mary Francis
College of Horticulture, Vellanikara 680656

Rice is a very important cereal crop globally. Production of callus and the prime step in crop plant to be manipulated by biotechnological mean. The success of cell and tissue culture research depends upon reliable callus culture and plant regeneration in tissue culture of rice is influenced by many factors such as culture medium composition, explants source, genotype and environment. The study was conducted to find out the best media composition for callus induction and to identify the best responding variety to *in vitro* culture in rice. The source of explants for *in vitro* studies was dehulled seeds of two popular rice varieties in Kerala- Swarna Prabha and Vaishak. Surface sterilization of seeds was carried out with 70% ethanol (2 minute) followed by treating it