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### **Carrageen molecular marker database (CaMM-Db): A comprehensive database for Carrageen (*Chondrus crispus*) molecular markers**

**Jyotika Bhati, Tanmaya Kumar Sahu and Pankaj Kumar Pandey**  
Indian Agricultural Statistics Research Institute, India

CaMM-Db has been developed to manage the molecular marker information on *Chondrus crispus* (carrageen) and to make it accessible to the biological community. The database contains derived micro satellites and SNPs (Single Nucleotide Polymorphisms) from carrageen genomic sequences. The purpose for which carrageen is used is also achieved by other Indian red seaweeds like *Gracilaria* and *Hypnea* species. Except carrageen, the genome sequences of none of the red seaweeds are available in public domain. Thus, an insight into carrageen genome will help enable the biotechnologists to work on carrageen and the other red seaweeds. Keeping the above in view, CaMM-Db was developed using the carrageen genomic sequences from the databases of National Center for Biotechnology Information (NCBI) for micro satellite determination and SNP discovery. Till date, no SNPs for *Chondrus crispus* are submitted to NCBI, thus, here an attempt has been made to discover SNPs from carrageen genomic sequences. This database provides information on different types motifs categorized based on different properties. The database is further integrated with Primer3 to facilitate the generation of suitable primers of interest for wet lab experimentation. As it is the first database on the molecular markers in carrageen genome, it can be used as a valuable resource for the scholars indulged in genetic research on carrageen and other Indian seaweeds.

[singh.jyotika@gmail.com](mailto:singh.jyotika@gmail.com)

### **A study on resistance pattern of ESBLs producing bacterial inhabitants of Delhi stretch of river Yamuna**

**Kehkashan Siddiqui, Mohammad Tahir Siddiqui and Qazi Mohd Rizwanul Haq**  
Jamia Millia Islamia, India

Antibiotic resistance thwarts the treatment of infectious diseases leading to high rate of mortality worldwide. The heightened use/misuse of antimicrobials has worsened the situation by selection and dissemination of resistant isolates and in turn resistance determinants. Extended-spectrum  $\beta$ -lactamases (ESBLs) turn out to be a helping hand that impedes the treatment of infections caused by *Enterobacteriaceae*. Polluted water environments are hotspot for the acquisition and dissemination of resistance genes where exchange of genetic elements (i.e., plasmids, transposons and integrons) between distant related bacteria occurs. The present study was performed to access the antibiotic resistance pattern among the inhabitant bacterial isolates of Delhi stretch of river Yamuna and also to determine the prevalence of ESBL genes among isolates conferring resistance. Out of 231 isolates obtained from ten different sites receiving domestic and industrial sewage, 118 were resistant to cefotaxime. 68 isolates positive for ESBL production via PDCT were also found to confer resistance towards other antibiotics with different mode of action. High level resistance to ertapenem left carbapenems in vein that are widely regarded as the drugs of choice for treatment of severe infections caused by ESBL producing *Enterobacteriaceae*. When accessed for ESBL genes these isolates marked the presence of blaTEM, blaSHV and blaCTX-M individually and in combinations. The identification of highly resistant ESBLs-producing bacteria in polluted river water raises alarming concern to the increasing resistance that would lead humanity in a situation worse than pre-antibiotic era, hence, putting forth an urgent need to devise strategies for preventing emergence and dissemination of resistance.

[kehkashansiddiqui7@gmail.com](mailto:kehkashansiddiqui7@gmail.com)