Applications of next-generation sequencing in Lotus, blueberries and spiders.

PhD defense, Friday 24 October 2014. Vikas Gupta.

During his studies, Vikas Gupta has utlized next generation sequencing (NGS) to analyze the genomes of Lotus, blueberries and spiders. The need for analyzing the large and increasing amount of sequencing data has increased the demand for efficient, user friendly, and broadly applicable computational tools. During his PhD studies, Vikas Gupta has developed two tools, *shortran* and *GABox*, for small RNA data analysis and genome annotation, respectively.

Vikas Gupta has generated genomics and transcriptomics resources to facilitate the research on three species at a genomic scale. In Lotus, a specific miRNA was found to be involved in the plant-microbe symbiosis, where a parallel approach of the small RNA sequencing and the degradome sequencing was used. In blueberry, anthocyanin encoding genes were found to be enriched in ripe fruit and several other genes were identified to go through developmentally regulated alternative splicing. In spiders, proteomics-supported genome annotation was used to study the silk- and venom-related genes.

These findings contribute to the understanding of Lotus, blueberry and spider at the molecular level, and resources and tools presented in the study, should be valuable to scientific research communities pursuing related work.

The PhD degree was completed at the Bioinformatics Research Center (BiRC) and Department of Molecular Biology and Genetics, Science and Technology, Aarhus University.

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Title of dissertation: Applied bioinformatics: Genome annotation and transcriptome analysis

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Language: The PhD dissertation will be defended in English.

The defence is public.

The dissertation is available for reading at the Graduate School of Science and Technology/GSST, Ny Munkegade 120, building 1521, room 112, 8000 Aarhus C.