

Activity1: Analysis of bisulfite sequenced data of hybrids and their parental lines

Objective: Heterosis is the phenomenon of increased vigor in F_1 s in comparison to their parents. However, the molecular mechanism underlying the heterosis is still under debate. The role of epigenetic mechanism in the heterosis has been recently pointed out, and it is observed that changes in DNA methylation level appear to be related to heterosis. Therefore, global methylC-seq of hybrids and their parental lines will provide information to understand the role of epigenetic variation in terms of DNA methylation to correlate with the hybrid performance.

Materials and methods: Bisulfite sequencing of two hybrids, ICPH 2671 and ICPH 2740 and their parental lines, ICPA 2043, ICPR 2671 and ICPA 2047, ICPR 2740 respectively was performed for whole genome DNA methylation profiling.

Results and discussion: To understand the potential role of DNA methylation in heterosis, whole genome bisulfite sequencing and a comparative analysis of leading pigeonpea hybrid, ICPH 2740 and its parental lines ICPA 2047 and ICPR 2740 were accomplished. Results showed an increased level of DNA methylation in hybrid as compared to parents, mostly in transposable elements and up- and downstream region of genes, followed by CDS and intronic regions. Predominantly increased methylation level in the regions that were differentially methylated in the two parents and covered by small RNAs, reflecting the involvement of RNA-directed DNA methylation (RdDM) pathway in the hybrid.

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Next step: Differentially methylated gene will be validated using qRT-PCR for expression variation in hybrids compared to the parental lines.