

## ***In silico* Distribution Analysis of Chromosomal CpG Islands in Rice (*Oryza sativa* L. spp. japonica)**

MAU Karunarathne<sup>1#</sup>

<sup>1</sup>Faculty of Science, University of Colombo, Colombo 03, Sri Lanka

<sup>#</sup>amauk1411@gmail.com

### **Abstract**

CpG islands are regulatory elements in a genome with high CpG dinucleotide density, influencing gene expression and genomic stability. These regions are important to rice biology. Despite the extensive body of research on CpG islands, the understanding of their distribution and characteristics at the chromosomal level remains limited. Hence, *in silico* analysis of chromosomal CpG islands in rice (*Oryza sativa* L. spp. japonica) is a computational approach to elucidate the chromosomal distribution and distinctive features of CpG islands within the genome of this agriculturally significant plant species. Genomic data from the GenBank and EnsemblPlants databases were utilized, with contigs NC\_029256.1, NC\_029257.1, NC\_029258.1, NC\_029259.1, NC\_029260.1, NC\_029261.1, NC\_029262.1, NC\_029263.1, NC\_029254.1, NC\_029265.1, NC\_029266.1, NC\_029267.1 representing chromosomes 1 to 12, respectively. Consistent G+C percentages were observed across all chromosomes, with GpC showing a higher frequency compared to CpC, CpG, and GpG. CpG islands were identified in the chromosomes using the Gardiner-Garden and Frommer algorithm, based on a minimum 200-bp region with an observed CpG/expected CpG (O/E ratio) of 0.6 or higher and a GC content greater than 50%. The statistical analysis unveiled significant enrichment of CpG islands (O/E ratio > 0.6) across all chromosomes. Additionally, the study employed the identification of CpG islands within the genomic loci of all chromosomes, revealing that, on average a maximum of 35% of these islands were situated within gene sequences. Chromosomes 11 and 12 exhibited comparatively lower proportions of CpG islands in contrast to the remaining chromosomes. Notably, a minimum of 68% of genes spanning all chromosomes harboured CpG islands. Mostly positioned within gene promoters, CpG islands govern gene expression through methylation, impacting growth, stress response, and development in rice. Epigenetic inheritance of CpG patterns aids trait transmission. Thus, unravelling CpG complexities promises better rice crops. In conclusion, this study offers invaluable insights into the chromosomal-level characteristics of CpG islands in rice, facilitating the advancement of our understanding of CpG island research and its intricate integration with chromosomal organization.

**Keywords:** *CpG islands, Rice, Chromosomal distribution*