Genome

The genome is the genetic material of an organism. It is encoded either in DNA or, for RNA viruses, in RNA. The genome includes both the genes and Non-coding DNA/RNA.

The complete set of DNA within a single cell of an organism.

The proteome is the entire set of proteins expressed by a genome.

To analyze a specific genome region using next-generation sequencing technologies, the enrichment of DNA libraries with targeted capture methods has been standardized. For enrichment of mitochondrial genome, a previous study developed an original targeted capture method that use baits constructed from long-range polymerase chain reaction (PCR) amplicons, common laboratory reagents, and equipment.

Koganebuchi et al.,report a new targeted capture method of bacterial artificial chromosome (BAC) double capture (BDC), modifying the previous method, but using BAC libraries as baits for sequencing a relatively large gene. They applied the BDC approach for the 214 kb autosomal region, ring finger protein 213, which is the susceptibility gene of moyamoya disease (MMD). To evaluate the reliability of BDC, cost and data quality were compared with those of a commercial kit. While the ratio of duplicate reads was higher, the cost was less than that of the commercial kit. The data quality was sufficiently the same as that of the kit. Thus, BDC can be an easy, low-cost, and useful method for analyzing individual genome regions with substantial length 1).

In genetics, a mutation is a permanent change of the nucleotide sequence of the genome of an organism, virus, or extrachromosomal genetic element. Mutations result from unrepaired damage to DNA or to RNA genomes (typically caused by radiation or chemical mutagens), errors in the process of replication, or from the insertion or deletion of segments of DNA by mobile genetic elements.

The genomes of many animals, plants and fungi are tagged by methylation of DNA cytosine. To understand the biological significance of this epigenetic mark it is essential to know where in the genome it is located. New techniques are making it easier to map DNA methylation patterns on a large scale and the results have already provided surprises. In particular, the conventional view that DNA methylation functions predominantly to irreversibly silence transcription is being challenged. Not only is promoter methylation often highly dynamic during development, but many organisms also seem to target DNA methylation specifically to the bodies of active genes 2).

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Koganebuchi K, Gakuhari T, Takeshima H, Sato K, Fujii K, Kumabe T, Kasagi S, Sato T, Tajima A, Shibata H, Ogawa M, Oota H. A new targeted capture method using bacterial artificial chromosome

(BAC) libraries as baits for sequencing relatively large genes. PLoS One. 2018 Jul 12;13(7):e0200170. doi: 10.1371/journal.pone.0200170. eCollection 2018. PubMed PMID: 30001370.

[2] Suzuki MM, Bird A. DNA methylation landscapes: provocative insights from epigenomics. Nat Rev Genet. 2008 Jun;9(6):465-76. doi: 10.1038/nrg2341. Review. PubMed PMID: 18463664.

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