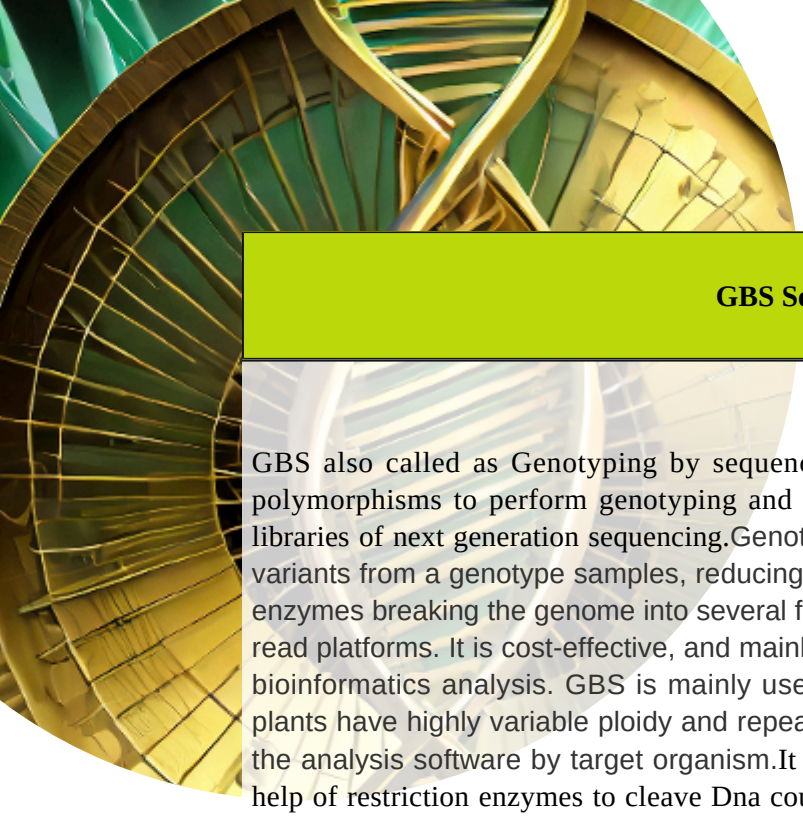

GBS Sequencing

GBS also called as Genotyping by sequencing is used to discover the single nucleotide polymorphisms to perform genotyping and wide association studies and for preparing the libraries of next generation sequencing.Genotyping-by-sequencing (GBS), identifies genetic variants from a genotype samples, reducing genome complexity with the help of restriction enzymes breaking the genome into several fragments whose ends are sequenced on short-read platforms. It is cost-effective, and mainly produces missing data and needs a complex bioinformatics analysis. GBS is mainly used on crop plant genomes, and because crop plants have highly variable ploidy and repeated content.The performance usually varies in the analysis software by target organism.It largely reduces the genome complexity with the help of restriction enzymes to cleave Dna coupled with Dna barcode adaptors. It can provide high SNP coverage in gene rich regions in cost effective manner and it also increase the number of tags in the essays which is missing and requires complex bioinformatics analysis. Because of its highly ploidy and repeat content, it is used on crop plant genomes and performance of GB analysis vary by target analysis.

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