SNP Genotyping: A Key Tool in Modern Genetics

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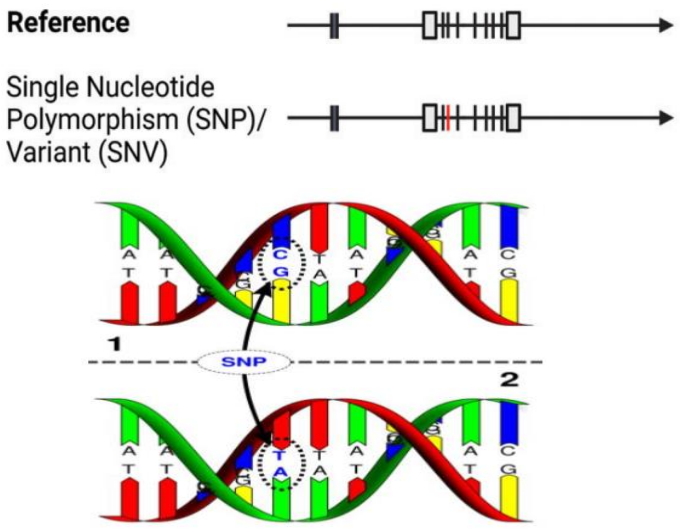
Introduction

Single Nucleotide Polymorphisms (SNPs) or single nucleotide variants (SNVs) are variations in DNA that occur at single nucleotides in the genome at a specific site and are present in a population at an appreciable level (typically >1%). These variations occur naturally, and across the whole genome. Certain SNPs can be diagnostic of conditions or certain phenotypes. Lander first presented the concept of SNPs in 1996 (Al-Samarai *et al*. 2015). Typical SNP frequencies are in the range of one SNP in every 100-300 bp. SNP genotyping is the process of identifying which specific SNPs are present in a plant's genome. Traditional plant breeding methods, which rely on phenotypic selection, are time-consuming and less precise compared to marker-assisted selection (MAS). As highly polymorphic and distributed throughout the genome, SNPs offer superior resolution in genetic mapping and genome-wide association studies (GWAS). Recent advancements in sequencing technologies, such as genotyping-by-sequencing (GBS) and next-generation sequencing (NGS), have further enhanced the efficiency of SNP discovery and genotyping in plants. Their high abundance, stable inheritance, and ease of detection make these markers indispensable in Plant genetics.

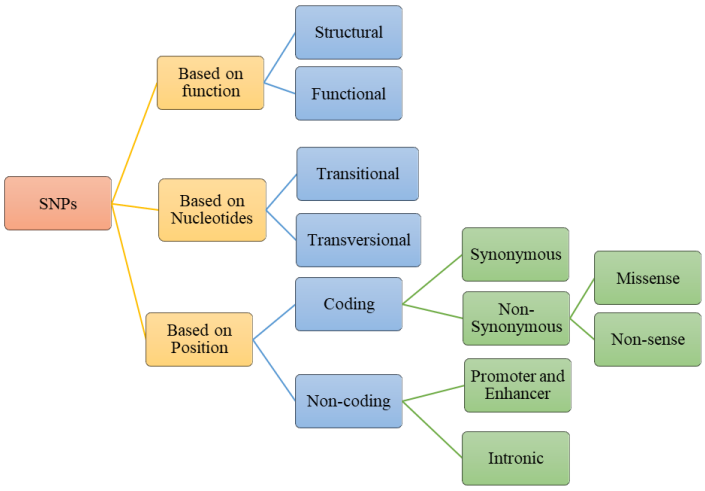


Types of SNPs

- **Coding SNPs:** These SNPs occur within the coding regions (exons) of genes and can directly affect protein function. They are further divided into:
- **Synonymous SNPs (Silent SNPs):** These do not change the amino acid sequence of the protein. Since the genetic code is degenerate (multiple codons can code for the same amino acid), some SNPs in coding regions do not alter the resulting protein. These may still have regulatory impacts, such as affecting mRNA stability or splicing.
- **Non-synonymous SNPs:** These change the amino acid sequence of the protein. Non-synonymous SNPs are further categorized into:
- **Missense SNPs:** A single nucleotide change results in the substitution of one amino acid for another in the protein sequence, potentially altering protein function.
- **Nonsense SNPs:** A single nucleotide change introduces a premature stop codon, leading to a truncated protein that is often non-functional.
- **Non-coding SNPs:** These SNPs occur in non-coding regions of the genome, such as introns, regulatory sequences, and intergenic regions. While they do not directly affect protein sequences, they can influence gene expression and regulation:
- **Promoter and Enhancer SNPs:** SNPs in promoter or enhancer regions can affect the binding affinity of transcription factors, leading to changes in gene expression levels.
- **Intronic SNPs:** SNPs within introns may impact mRNA splicing, thereby influencing the final mRNA product. In some cases, they may create or abolish splice sites, leading to altered protein structures.
- **Structural SNPs:** These SNPs affect regions of the genome involved in structural variation, such as those responsible for DNA packaging

or chromatin architecture. They may not directly influence gene function but can affect the physical organization and accessibility of the genome.

Functional SNPs



Some SNPs can be classified based on their direct influence on phenotypic traits. For example, SNPs linked to disease resistance, flowering time, or yield in plants are often called functional SNPs, as they have a clear impact on observable characteristics. Transition SNPs: A purine (A or G) is substituted for another purine, or a pyrimidine (C or T) is substituted for another pyrimidine. These are more common than transversions.

Transversion SNPs: A purine is substituted for a pyrimidine or vice versa. These are less frequent but more likely to have significant biological impacts because they cause more drastic structural changes in the DNA.

Applications of SNP Genotyping in Agriculture

Marker-Assisted Selection (MAS): SNP genotyping is widely used in marker-assisted selection (MAS), where genetic markers are used to select plants with desirable traits. By genotyping large populations for SNP markers linked to these traits, breeders can identify the best candidates for breeding programs**.** SNP markers linked to disease resistance genes have been used in crops like wheat and rice to select for resistance to pathogens such as *Puccinia triticina* (leaf rust) (Yadav *et al.* 2019) and *Magnaporthe oryzae* (rice blast).

Genome-Wide Association Studies (GWAS) SNP genotyping plays a critical role in genome-wide association studies (GWAS), which involve scanning the genomes of many individuals to identify SNPs associated with specific traits. In maize, GWAS using SNP markers has led to the identification of genomic regions associated with traits like flowering time, yield components, and nitrogen-use efficiency. (Li *et al.* 2013)

Genomic Selection (GS) Genomic selection is an advanced breeding technique where genome-wide SNP data is used to predict the genetic potential of individual plants. Unlike MAS, which uses a few markers linked to specific traits, GS uses thousands of SNPs across the entire genome to make more accurate predictions about a plant's overall performance. This approach accelerates breeding cycles and increases genetic gains, especially for complex traits influenced by multiple genes. In wheat, genomic selection using SNP genotyping has been applied to improve grain yield and resistance to Fusarium head blight, a devastating fungal disease. (Heffner *et al*. 2011)

Crop Diversity and Conservation SNP genotyping is also used to assess genetic diversity within and between crop populations. By analyzing SNP variation, researchers can determine the genetic structure of landraces, wild relatives, and modern cultivars. This information is vital for the conservation of plant genetic resources and can be used to maintain or increase genetic diversity in breeding programs. In rice, SNP genotyping has been used to characterize the genetic diversity of wild rice species and landraces, helping to identify genes that can be introgressed into modern cultivars to improve stress resistance. (McCouch *et al*. 2012)

Pyramiding of Multiple Traits SNP genotyping facilitates the process of gene pyramiding, where multiple desirable traits (such as resistance to several diseases or tolerance to multiple abiotic stresses) are combined into a single cultivar. This approach is particularly useful in developing crops that can withstand multiple environmental challenges.

In soybean, SNP genotyping has enabled the pyramiding of resistance genes against several pests, such as the soybean cyst nematode and aphids. (Kim *et al*. 2011)

Hybrid Breeding SNP markers are used in hybrid breeding to ensure the selection of parental lines with optimal combining ability. This technique improves the efficiency of hybrid seed production by

enabling the selection of highly heterozygous parents, leading to hybrid vigor (heterosis). SNP genotyping has been instrumental in improving hybrid rice varieties by selecting parents with optimal genetic combinations for higher yield and stress tolerance. (Xie *et al*. 2015)

Development of Climate-Resilient Crops With the increasing impact of climate change, SNP genotyping is essential for developing crops that can withstand extreme conditions, such as heat, drought, and salinity. By identifying SNPs associated with stress tolerance, breeders can select plants that are more resilient to changing environmental conditions. In wheat, SNP genotyping has been used to identify alleles associated with heat and drought tolerance, enabling the development of cultivars that can thrive under climate stress. (Mwadzingeni *et al*. 2016)

Crop Quality Improvement SNP markers are also applied to improve the nutritional and processing quality of crops. Traits like grain protein content, oil composition, and vitamin levels can be targeted through SNP genotyping, helping to breed crops that meet consumer demands for healthier and more nutritious food. In maize, SNP genotyping has been used to select for high oil and protein content, improving both the nutritional value and the processing quality of maize products. (Li *et al*. 2014)

Conclusion

SNP genotyping is a powerful tool that is transforming plant breeding and agriculture. By identifying and exploiting genetic markers linked to important traits, making possible the development of crops that are more resilient, higher yielding, and better suited to the challenges of the future. As costs continue to decrease, the accessibility and impact of SNP genotyping will expand, benefiting a wide range of crops, including underutilized species. This technology holds immense promise for the future of sustainable agriculture. SNP genotyping will play an even greater role in ensuring a sustainable, food-secure world.

Future Thrust

The future of SNP genotyping in plant breeding is being ready to revolutionize agriculture by enabling faster, more precise crop development. Key areas of focus include genomic selection, which accelerates breeding by predicting traits based on genetic markers, and the integration of artificial intelligence to analyse large datasets more effectively. Combining SNP genotyping with genome editing technologies like CRISPR will further enhance the ability to create disease-resistant, high-yielding, and nutritionally superior crops.

References

Yadav, S., et al. (2019). SNP marker-assisted selection of leaf rust resistance in wheat. *Frontiers in Plant Science*, 10, 1186.

Li, Y., et al. (2013). Genome-wide association mapping of flowering time and grain yield traits in maize. *BMC Plant Biology*, 13, 34.

Heffner, E. L., et al. (2011). Genomic selection for crop improvement. *Crop Science*, 51(3), 1117-1131.

McCouch, S. R., et al. (2012). Genetic diversity and population structure of rice landraces in Asia. *Nature Genetics*, 44(9), 952–956.

Kim, Y., et al. (2011). SNP-based molecular markers for soybean cyst nematode resistance. *Molecular Breeding*, 28(3), 899–907.

Xie, W., et al. (2015). Hybrid rice development through genomic selection and SNP markers. *Rice*, 8, 27.

Mwadzingeni, L., et al. (2016). Genetic diversity and SNP marker-trait association for drought tolerance in wheat. *Frontiers in Plant Science*, 7, 991.

Li, X., et al. (2014). SNP discovery for maize grain quality traits. *Journal of Agricultural and Food Chemistry*, 62(6), 1410–1417.

Al-Samarai, F. R., & Al-Kazaz, A. A. (2015). Molecular markers: An introduction and applications. *European journal of molecular biotechnology*, *9*(3), 118-130.

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