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A review on relishing the difference between SSR markers & RAPD markers in bread wheat (*Triticum aestivum* sp.)

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Abstract
There are many molecular markers that are used to analyse or evaluate particular characters in Bread Wheat (*Triticum aestivum* sp.). As, Wheat is considered as one of the major cereals that is used as the staple food across the world, many researches have been made to develop many markers such as SSR, RAPD etc. As a recent Pangenome-based assembly, the wheat genome has 140,500 ± 102 genes, with a total of 81,070 ± 1,631 genes. SSR markers indicate a higher degree of polymorphism than other genetic markers. Their additional advantages are their automatic power and their inheritance in a dominant way compared to other types of cell markers. RAPD markers can be used to analyse genetic diversity and determine genetic relationships among cultivars, which is an important aspect of germplasm research.

Keywords: Relishing, SSR, RAPD, bread, *Triticum aestivum*

Introduction
Wheat has been cultivated in many countries for centuries (Olugbemi *et al*., 1979; Ohiagu *et al*., 1987) [2, 4]. There is ample evidence that wheat has been grown in many countries since 200BC, although the varieties currently grown are a recent introduction (Olabanji *et al*., 2004). However, domestic wheat production in Nigeria remains very low despite the growing demand for the crop. Barriers to wheat cultivation in many wheat growing areas in other countries include climate requirements, appropriate agricultural practices and preference for vegetable cultivation (Ohiagu *et al*., 1987) [4].

The development of improved agricultural practices with regard to the land preparation, planting, nutrition, water management, crop protection, harvesting and post- harvest technology have become major areas for researchers to focus on their efforts. The Global harvest, which takes about 237 million hectares per year, making a total of 420 million tons (Isitor *et al*., 1990; Langer and Hill, 1991; Olabanji *et al*., 2004) [6, 7], and at least one-fifth of a person's calorie intake (Ohiagu *et al*., 1987) [4].

Wheat is an annual grass that grows to ½,1 ¼ m in height, with a long stem that cuts through a sturdy bundle of dense cores covered with bearded bristly pegs (Smith *et al*., 2010) [8]. It is grown worldwide for its nutritious and nutritious grain, as one of the top three most productive crops, as well as corn and rice. It is used in the production of bread, biscuits, feeds, confectionary, among many, consumption. This plant, cultivated for more than 10,000 years, originates in the Fretile Crescent, along with other basic plants. However, the ancestral wheat may have looked very different from what we have today, with very little grain. Early wheat farmers apparently preferred to grow crops with larger grains, as more nutrients could be extracted from each stalk.

As a recent Pangenome-based assembly, the wheat genome has 140,500 ± 102 genes, with a total of 81,070 ± 1,631 genes. This latest conference has an average of 128,656 genes in all 18 wheat varieties, which has improved Chinese spring observations (Montenegro *et al*., 2017) [9]. The available de novo wheat genome of the International Wheat Genome Sequencing Consortium (Consortium, 2014) can be used as an important tool for simple sequential repeatable marking (SSR) tags that are distributed throughout the genome. SSRs are the preferred genetic markers, link map, organization studies, and tag-assisted selection due to their high reproduction, high allelic environment, co-operative heritage, robust expansion, automated / throughput genotyping through multiplexing (Li *et al*., 2009).

All of these traits can accelerate the process of cell reproduction. Genetics associated with a variety of factors such as productivity, quality, biotic stress and abiotic stress can be used in a breeding program using markers of their separate SSR region with diagnostic allele i.e., size differences in parent lines (Twyford and Ennos, 2012).

SSR Markers

Molecular markers can not only add to this test (in different "allelic" variations) which further enhances accuracy, but can sometimes play an important role in resolving legal disputes as well. The diversity situation can be assessed in a shorter period of time than in a two-generation trial with evolutionary uncertainty. Apart from this, the other two remaining components of DUS i.e., the similarity and stability of the earlier mentioned can also be assessed by the horizontal and vertical distribution profile of the alleles, respectively (Kwon *et al*., 2005). All of these methods require a robust set of polymorphic SSR signals from each chromosome that has / makes a unique "signature" profile in relation to other existing / controversial species.

In many countries, such an SSR profile is a prerequisite for the official "Germplasm Bank" as an integral part of germplasm ownership and protection. Globally there are many varieties and the classification of such varieties requires a complete genome scanning of SSRs to obtain polymorphic markers. Cell markers are required to test the purity of wheat seeds and to separate hybrids (Wang *et al*., 2014a). Molecular Markers can provide a complete picture of genetic information. Markers give a precise measure of genetic diversity. Microsatellite is a simple sequential repeat (SSR) of about 1-6 nucleotide. They are widely distributed throughout the genome.

SSR markers indicate a higher degree of polymorphism than other genetic markers. Their additional advantages are their automatic power and their inheritance in a dominant way compared to other types of cell markers. These features, coupled with their easy availability and SSR signals, cover all 21 wheat chromosomes. SSR tags have been used in seed bank collections to promote wheat germplasm and to show genetic diversity in wild relatives.

SSR Markers found near targeted genes can be transferred to the wheat variety development program (Leonova *et al*., 2011). Limited Simple Sequence Repeats were used in Genome Wide Association Studies (GWAS) in 14 different aspects using a single locus single trait (SLST), a multi-locus model (MLMM), and a multi-dimensional model (MTMM) model, to obtain fewer QTLs wheat (Jaiswal *et al*., 2016). Therefore, mass excavation of SSR mines from each chromosome is required, which can be used in additional QTL (Quantitative trait locus) and genetic discovery by the construction of a link map with a high-density sign. SSR tags can be used in various classifications and product tracking of products and products (Fujita *et al*., 2009).

RAPD Markers

Random Amplified Polymorphic DNA (RAPD) tags are widely used in genetic studies, DNA fingerprinting, map design and link analysis between wheat genotypes. Marking organization research has been done, which not only allows genetic modification / QTL (QTL, plural trait loci) high levels of confidence, but also allows genetic / QTL detection, which can facilitate discovery in communication-based studies. molecular signals that are not under the influence of nature are considered superior to morphological markers. Different cell signals are currently available for genome mapping and to mark different useful features in the breeding process assisted by the wheat marker in stressful situations.

The use of random amplified polymorphic DNA (RAPD) as a genetic marker system in wheat was evaluated. With carefully chosen primers and meticulously calibrated reaction conditions, reproducible amplification results were generated from varietal, homozygous single chromosome recombinant line and wheat/alien addition line genomic DNA. DNA concentration, Mg2+ concentration, polymerase concentration, and denaturing temperature are all factors that influence RAPD patterns. In wheat, RAPD products' non-homoeologous, non- dose responsive, and dominant behaviour devalues their utility as genetic markers for linkage map creation, and the high likelihood that the amplified fragments arise from repetitive DNA limits their use as a source of traditional RFLP probes. RAPD markers, on the other hand, will almost probably find a wide range of uses in genotype analysis where single chromosomes or segments of chromosomes are involved.

RAPD markers can be used to analyse genetic diversity and determine genetic relationships among cultivars, which is an important aspect of germplasm research. conservation and characterization DNA fingerprints based on RAPD Seed varieties that are in the process of being certified can be valuable. Plant breeders, traders, growers, and seed producers and the certifying organisations can have an examination of a greater number of genotypes in the parents. The use of a RAPD marker can help with fast genetic diversity forecast among their crosses (Abd-El Haleem) (2009); *et al*., 2009).

Conclusion

SSR markers are the repetitive sequences that help in the easy detection and identification of the gene of interest of particular characters on the chromosomes. Microsatellites, also known as Simple Sequence Repeats (SSR's) or Short Tandem Repeats (STRs), are 2-5 base set DNA repeating sequences. It's similar to a Tandem Repeat with Variable Numbers (VNTR). Microsatellites are frequently found together. SSR markers have a number of advantages over other types of markers. The first benefit is their great repeatability, which is particularly valuable in genetic analysis. It also does not necessitate ultra-pure template DNA. The polymorphic genetic information content of the SSR marker system is the technology's second advantage. The Random Amplified Polymorphic DNA (RAPD) technique may be used in molecular ecology to determine taxonomic identity, assess family links, analyse mixed genome samples, and build particular probes as an expansion to the range of existing techniques using polymorphic DNA markers.

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