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Mapping Genetic Markers

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Abstract: *meeting the needs of people in quick and convenient ways in a rapidly developing era of Science and technology is one of the pressing problems of today. It is no secret that every year the number of akholi of the Earth is increasing with great speed. This in turn causes food, clothing, medicine and other requirements. In overcoming such problems, the science of Molecular Genetics, with its discoveries, has entered our lives to satisfy the needs of humanity in millions.*

Selection and use of Dnkmarkers in research and genealogy still remains a problem for plant selectionists. A selector must take into account a number of factors when choosing one or more types of molecular markers. The breeder must make the right choice that best suits the requirements in accordance with the existing conditions and sources for the breeding program. In this article, we will talk about the selection of plants of the map of genetic markers, in particular, the methods used in the creation of lines in which the chromasoma of the Acorn is exchanged.

Keywords: *Marker, map, sequence, Acorn, polymorphism, inbred line.*

Introduction:

It is known that genetic linkage maps determine chromasome dependence and the relative position of genetic markers relative to each other. Or in simple terms: mapping is the determination of the position of a gene or mutation in a chromasome. The term has now come into use in a broader interpretation. This applies not only to the gene, but also to any marker, which means a gene, mutation, a DNA sigmoid with an ambiguous function, a point of DNA breakdown with restriction enzymes. Thus a marker is any hereditary trait that can be identified in one way or another. Installing the localization of any marker allows you to use it to determine the position of another marker. In practice, genetic linkage maps and only they allow the localization of complex genetic markers (such as those associated with disease markers)in the first stages of the study and their subsequent training.

Molecular mapping helps determine the adhesion of a particular marker within the genome. For the analysis of genetic material, it is possible to draw up 2 different maps: the First different map is a physical map, this map helps to determine where we are in the chromasome and which chromasome we are in. Second, there is a linkage map that determines how specific genes are associated with other genes in the chromasome. Ush can determine the distance from other genes by using (sM) centi Morgans as the unit of measurement of this linkage map.

Co-dominant marker mapping can be used to identify specific locations within the genome and may reflect differences in phenotype. Marker limestones help identify specific polymorphisms within the genome. Ush indicates changes within the genome where these polymorphisms can replace or alter the sequence of the nucliotide. When developing maps, it is useful to identify several polymorphic differences between two types, as well as to identify two types of similar sequence.

Molecular markers are considered effective because they determine the abundance of genetic linkage between identifiable sites within the chromasome and are able to replicate for examination. They allow the separation of characters and identity that distinguish the type of maps in a mapping population. Finally, they determine how many alleles an organism has for a given sign(bi allelic or polyallelic). When using molecular markers to study the genetics of a particular crop, it should be remembered that markers have limitations. First of all, it is necessary to assess what Hereditary variability is within the organism under study. It is necessary to analyze what specific genomic sequence can be detected near or within candidate genes.

The first genetic concomitant map was compiled by Sturtevent in 1913. Later in 1923, Kerl Sachs combined quantitative markers with morphological markers. In 1975, Gelderman came up with the term quantitative trait locus, which meant “a fragment of a genome associated with the effects of quantitative traits”.

Following the discovery of DNA sturucture by Watson and Crick in 1953, a series of discoveries in Molecular Biology led to the compilation of genes and genetic maps. Markers based on new DNA: markers such as RELP, RAPD, AFLP, SSR, and SNP are used to conduct genetic attachment analyses and often QTL studies. Initially, f2avlod and bacross (BC)populations were used extensively in the study of quantitative character loci (MBL/QTL). However, since the genetic construction of such populations has a characteristic heterozygous nature, QTL is inconvenient to carve out. To overcome these barriers, biological recombinant inbred lines (RILs), beckross inbred lines (BILs), double-haploid lines (DH)are widely used today. Recombinant inbrd lines (RILs/RIL)QTL Analyses obtained from repeated reproduction of single seeds of F2 Generation individuals obtained from hybridization of two different homozygous plants that differ from each other between these sources are most often used.

Introns are non-protein coding DNA sequences that interrupt interoperability. the uncertainty of the sequences encoding proteins. Ests are a sequence created by DNA. A sequence of several hundred nucleotides is performed from the 50 or 30 ends of the DNA to form 50 EST or 30 EST, respectively (Huang et al. , 2017). 50 EST originates from exons. Exons are known to generally persist across species and are kept at the same level as the Constitution of the sequence in the gene family. On the other hand 30 EST hand, more non-protein coding is associated with introns or untranslated regions (UTR). Relatively, introns or UTRs are conserved across species rather than shown in a less coding sequence. The barriers to gene identification from major genomic sequences depend on the types of organisms involved, the size and complexity of the genome, and the frequency of occurrence of introns (Huang et al. , 2017). Ests are sourced from pro-DNA libraries. Currently, there are several million EST from different organisms that exist in many databases.

Ests are valuable information about gene function that is highly informative in gene identification. Ests helped design gene function research into DNA micromassives and related probes. Side - by - side, many highly valuable EST-based molecular markers have been achieved, such as Re-persistence Fragment length polymorphism, Single Nucleotide Polymorphism, Inter Simple Sequence Repeats and Cleaved Amplified polymorphic sequences (Xiao et al. , 2020). est has proven that single or low-copy RFLP applications obtained are very useful for generating high-density genetic and physical maps (Xia et al. , 2007). Ests also allow SNP and SSR markers to be produced silica (Bhardwaj et al. , 2016). SNPs are primarily developed from 30-hole ests - translated regions of cDNA clones (UTR) for un-optimization. the probability of detecting nucleotide changes associated with existing genetics is the variety of species of organisms. In this approach, the primer pairs bind together. Additions to EST sequences have been developed. PCR amplification is obtained from several genotypes with corresponding regions and sequentially. Then a sequence comparison is made by genotypes to open SNPs. Alternatively, potential SNPs can be calculated. comparison using a set of ests from different varieties and smoothing sequences (Bhardwaj et al. , 2016). EST-based SSRS are identified using pattern-finding computer programs. parts applications. Primer pairs have been developed from an existing sequence of data to determine the variation in length polymorphism between varieties of interest. Ests have been found to be a very useful resource for SSR marker

development, as typically, in different plant species, a size SSR marker can be examined from At least 20 bps ests suitable for development.

Conserved and transcribed regions as opposed to non-transcribed regions (Bushakra et al. , 2015) and is therefore assumed to be easier to transfer between the closely related generation. SSRS derived from est are more functionally differentiated.

in comparison with the SSR of non-coding genomic origin, the encial gene expression has an important place in the construction of physical maps with genetic maps ready-made sequences as well as in the positional cloning of genes, and as a result, the entire genome is sequenced. The pit contains a tetraploid (AADD)2N=4x=52 chromasome Nabor, with a genome size of approximately 2, 200-3, 000mb (a million pairs of bases) and it is 5, 200cm in total, and 26 chromasomes with an average of 400kb of centimorgan.

For such a huge genome, a large amount ofdnkmarker is required when creating a map consisting of markers that stand close to the wanted gene. This means that every 1cm requires an aging 3000 marker to cover wished.

However, markers associated with markings on acorns compared to other plant species including rice, tomatoes, rye, and wheat are very rare

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