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Mini Review

Using of Molecular Markers in Plants Breeding

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Abstract

The selection of plants is very long and difficult process, which uses classic methods, such as family-group (individual) and mass selection, hybridization, mutagenesis and others. Modern varieties of agricultural plants have minimal spectrum of genetic variability. For decision this problem modern agrarian science using methods of molecular genetics, most effective is molecular marking. In this paper presents analysis of effectivity of the different molecular markers and using of them perspective in scientific work at Sumy National Agrarian University.

Keywords: Plant breeding; Selection; Molecular markers; RAPD; RFLP; AFLP; CAPS; SSR; SCAR; Winter wheat

Abbreviations: SCAR- Sequence Characterized Amplified Region; RAPD- Random Amplified Polymorphic DNA; RFLP- Restriction Fragment Length Polymorphism; AFLP- Amplified Restriction Fragment Length Polymorphism; CAPS- Cleaved Amplified Polymorphic Sequences; SSR- Simple Sequence Repeats;

Introduction

Currently, depending on the technique of execution and the characterized part of the genome, there are a large number of different DNA markers: RFLP, AFLP, RAPD, CAPS, SSR, SCAR, SNP, et al. Repeating SINE and LINE sequences can be such a genetic marker. They are retrotransposons or mobile genetic elements that are widely represented in the genomes of the entire eukaryotic kingdom and make up a large portion of genomic DNA (up to half of the plant genome). One of the earlier methods of DNA-markers getting is Restriction Fragment Length Polymorphism, also named as RFLP. One of the earlier methods of DNA-markers getting is Restriction Fragment Length Polymorphism, also named as RFLP. The principle of this method founded on detection of specific nucleotide sequences in genomic DNA, with help of "blot-hybridization". This method of analysis is in demand in our days, but in identification and differentiation of plants it has changed by methods, which basing on PCR-amplification of DNA with using of random selected primers, or primers, that compliment to known plots of genomic [1-3].

Discussion

RAPD-markers. One of the most popular types of markers in mapping of plants genomics is RAPD (Random Amplified Polymorphic DNA). The method is in amplification of DNA of object during PCR with random primer, which has length of 10–11 nucleotides. Method of detection of RAPD-markers is easy by technic execute. If the protocol has optimized, RAPD is convenient, easy and suitable for analyze of plants genomics. The method was used successfully for genome mapping of much agricultures, varieties marking and polymorphism of species. Using of RAPD-method is especially perspective for genes mapping of quantitative attributes of plants [4,5].

AFLP (Amplified Restriction Fragment Length Polymorphism) – technology of getting random molecular markers with specific primers. According to this DNA are processing with combination of 2 restriction enzymes. Specific adapters are lysing with "sticky" ends of restrictive fragments. After this fragment are amplify with using primers that complimentary to sequence of adapter and to site of restriction, and additionally bearing one or more randomly selected bases at their 3'-ends. The set of fragments obtained depends on the restriction enzymes and randomly selected nucleotides at the 3'-ends of the primers [6].

SCAR markers. SCAR (Sequence Characterized Amplified Region) or an amplified region characterized by sequencing. These

are PCR-based molecular markers derived from RAPD or ISSR fragments, which are devoid of most of the disadvantages of RAPD markers and are applicable for a variety of studies.

According to numerous observations, the data obtained using RAPD analysis using random primers are quite relative due to the sensitivity of this method to reaction conditions. Therefore, to study polymorphic RAPD fragments and create specific DNA markers based on them, it became necessary to switch to the classical PCR method using a pair of long primers complementary to a specific sequence [5, 6].

CAPS. The CAPS (Cleaved Amplified Polymorphic Sequences) methodology, as well as SCAR, belongs to the STS (Sequence Tagged Site) group, since it is based on the amplification of strictly defined fragments of the genome with a known sequence. The principle of the method is as follows: genomic DNA is amplified using a pair of highly specific primers, then the resulting fragment is processed with a restriction endonuclease; differences between genomes manifest themselves in the form of different numbers and lengths of restriction fragments during agarose gel electrophoresis.

SSR-markers. Microsatellites, also called Simple Sequence Repeats (SSRs), are short tandem repeats of simple nucleotide motifs that contain from one to ten nucleotides in a repeating unit. They are found in all eukaryotic genomes, and in plants the most common repeats are (A) n, (AT) n and (GA) n motifs, where n varies between 10 and 80. Microsatellites, first obtained using PCR, are highly polymorphic markers for individual loci which are classified as dispersed tandem repeating sequences [6, 7].

Conclusion

The future is impossible without conducting biotechnological and molecular researches. One of the priority areas of research In Sumy National Agrarian University – Polymerase Chain Reaction (Pcr): An Alternative of Immunological Studies with the Determination of Disease Resistance Gene in Winter Bread Wheat Genotypes. The Purpose of the Research – breeding lines differentiation of bread winter wheat with resistance against diseases with Lr, Sr, Pm, Ug, Sr1AR genes for new varieties origination using molecular diagnostic methods. Materials of this Research – seeds of Triticum aestivum (cultivars-carriers of wheat-rye translocations) and hybrid material newly created of bread winter wheat. The Tasks of the Work: to identify by means of the polymerase chain reaction of 1BL/1RS and 1AL/1RS wheat-rye translocations in bread winter wheat genotypes; to investigate the genetic effects of 1BL/1RS combinations and 1AL/1RS translocations in bread winter wheat genotypes; to carry out the genotype selection of bread winter wheat with a mix of signs from carriers of various wheat-rye translocations.

The perspectives for molecular research of bread wheat

- The identification of bread winter wheat lines with resistance to fungal diseases (Erysiphe graminis, Tilletia caries, Ustilago tritici, Puccinia recondita, Puccinia graminis in particular the TTKSK strain Ug99 strain, etc.) with an introgressive rye component (1RS);
- Combination in one genotype of the 1RS chromosome shoulder on genomes of different orders to get new-generation wheat lines that will provide the index increasing of the genetic potential realization of the grain crop productivity;
- Establishing the reasons for the significant presence of the pathogens on winter wheat;
- Recommendations for breeding for resistance and production of resistant varieties;
- Comparison of classical methods with molecular diagnostics.

Acknowledgement

None.

Conflicts of Interest

No conflicts of interest.

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