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ROLE OF CYTOPLASMIC GENES IN CROP IMPROVEMENT

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Introduction:

Nucleus is the main organelle where genetic information is stored. DNA is also present in the cytoplasm called as Plasmon. Plasmon located as plastome in plastids (pt-DNA) and as chondriome in mitochondria (mt-DNA). The organelle genomes are circular DNA molecules, smaller than genomic DNA (about 200kb/plastid, up to 2500kb/mitochondrion), present in multiple copies and do not follow Mendelian inheritance. Most of the crop improvement researches focus on genetic information within genomic DNA. Despite smaller size of organelle DNA, it has role in inheritance of few specific traits. They interact with the nuclear genes and also with each other to carry out biological processes such as photosynthesis, ATP synthesis, and cytoplasmic male sterility (CMS), reactions to diseases, susceptibility to insecticides, drought resistance etc., hence cannot be undermined. Nevertheless, in plant breeding programs, the importance of genetic information about mitochondria and chloroplasts is often ignored or excluded in studies of DNA polymorphisms and their correlation to phenotypes.

Eukaryotic plant cells contain pt-DNA and mt-DNA that interact with the nuclear genetic information and interact with each other. They contribute in cell metabolism to photosynthesis and respiration. Furthermore, cytoplasmic genes contribute to the operation of the sexual reproductive systems and to the differentiation and evolution of plant species, including maize and teosinte potato, rubber tree, soybean and wheat. Thus, mitochondria and chloroplasts represent a source of genetic diversity, as they contain DNA and the machinery to express that information as RNA and, after RNA editing and tRNA import, by their own translation system, as proteins. The expression of plastid genes may be enhanced under light and may show tissue specificity that leads to increased protein production in chloroplasts of photo synthetically active tissues.

Role in Crop Improvement:

A first area in cytoplasm research was the production and use of alloplasmic lines by combination breeding, where by successive backcrossing of two parents the cytoplasm of one is changed. A second tool was provided by the field of somatic cell fusion, circumventing uniparental inheritance and permitting complete combination of cytoplasm's. The third application is opened up by direct transfer of genes into organelles, resulting in the case of plastids in transplastomic plants.

In order to further enhance the performance of cultivars, plant breeders can exploit minor effects of plasmone on quantitative traits by characterizing the cytoplasmic variability and assist it in breeding programmes to select favorable genotypes. New variability may be created either by undirected process-hybridization and meiotic recombination or by directed process i.e., chloroplast genetic engineering approach (Frei, U., 2003). Chloroplast transformation has become an attractive alternative to nuclear gene transformation due to its advantages: high expression, the feasibility of expressing multiple proteins from polycistronic mRNAs, and gene containment through the lack of pollen transmission (Wang, H. et al, 2009). Chloroplast transformation was generally achieved by the biolistic process or PEG-mediated gene transfer and follow integration by site-specific recombination. Chloroplast genome has been engineered for traits like herbicide resistance, insect & pest resistance, drought tolerance, tolerance to mercuric compound toxicity, etc. for example, Tobacco chloroplasts were shown to correctly process a bacterial operon and express the Cry2Aa2 proteins at levels up to 46% total soluble proteins (tsp.) (Grevich & Daniell, 2005).

In higher plants, CMS is a maternally inherited defect in pollen production that is thought to be associated with altered mt-genome organization or mt-gene expression at transcriptional or post-transcriptional level (Frei, U., 2003). Pollen sterility can be suppressed by nuclear restorer-of-fertility genes and allows the commercial exploitation of CMS systems in the production of hybrid seed (Chase, C.D., 2006). It eliminates the need for hand emasculation which incurs high cost for resource and time. Since cytoplasmic genes are maternally inherited their role on phenotype can be detected via reciprocal crosses or by the use of alloplasmic lines. Influences of cytoplasmic genes on several agronomic traits such as yield and yield contributing characters, resistance to diseases, combining ability, adaptability, etc. have been reported by several workers (Tao *et al*., 2011).

Agronomic Traits influenced by Cytoplasmic factors:-

Problem in applied reports of cytoplasmic effects on agronomic traits is that, many have been evaluated in populations carrying different sources of cytoplasm's, or do not differentiate plastome and chondriome. In addition there is the problem of accurately assessing cytoplasmic variation with respect to quantitative agronomic traits. Thus, a comparison of the phenotypes of alloplasmic isonuclear lines with different backgrounds in order to evaluate their use for hybrid breeding programs is difficult. Furthermore, a clear distinction of cytoplasmic effects and nuclear-cytoplasmic interactions is complicated, depending on the nuclear genome that is combined with the cytoplasm under evaluation. The differentiation between cytoplasmic types is primarily based on their sterile phenotype controlled by CMS of the mtDNA and the corresponding nuclear restorer system. Less important and obvious are variations of the ptDNA due to differences in chloroplasts or other plastid types. Agronomic traits influenced are; i. Cytoplasmic Male Sterility. Eg: Cotton, Maize etc. ii. Yield and quality parameters. iii. Disease resistance. Eg: Yellow berry in wheat. iv. Combining ability. Eg: Pearl millet v. Adaptability. vi. Fertility.

Conclusion:

Information on genetic variability and genetic distance is most useful for optimal selection of parents, especially for hybrid breeding. Thus, increasingly molecular markers based on genome polymorphisms are mapped on the chromosomes and used for marker aided selection (MAS). This nuclear genomic picture should be backed by an understanding of plasmone variability. Different reports on the influence of the plasmone emphasize the importance of the non-nuclear DNA for breeding processes, in particular for hybrid production using CMS. In contrast to the complex nuclear genome, mt- or pt-probes may allow a simpler but faster classification due to less complex polymorphisms. Cytoplasmic genes are known to have role in pollination control systems, differentiation and evolution of plant species, cell metabolism and in the field of somatic cell fusion. Deciphering the precise inheritance of traits under the influence of Plasmon is rather difficult. However, it could have enormous implications in genetic enhancement of feed, food, and non-food crops. The importance of the mtDNA for CMS in hybrid breeding highlights the potential of non-nuclear genes. Chloroplasts have, however, become an object for transformation since under the aspect of safeguarding transgenes, plants carrying the transformation in the pt-genome minimize the ecological risk of vertical and horizontal gene transfer. Chloroplast genetic engineering technology has opened the door to a new era in biotechnology. Chloroplast genetic engineering can be used for developing crop cultivars resistant to herbicides, insects, disease and drought, and for production of biopharmaceuticals. The expression of foreign genes in chloroplasts offers several advantages over their expression in the nucleus.

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