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Cytogenetics, Types and its Application in Crop Improvement

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ABSTRACT

Cytogenetic analysis plays a vital role in the crop improvement. From last few years, cytogenetic analysis has extended in the laboratories for the routine testing and provides significant prognostic and diagnostic results for the human diseases and crop improvements. There are different approaches in the cytogenetic for the identification of the genetic imbalance like conventional cytogenetics, and molecular cytogenetics (fluorescence in situ hybridization, spectral karyotyping, comparative genomic hybridization). From the overall performance, resolution for the detection of alternation is slightly higher in the molecular cytogenetic techniques as compared to the conventional karyotyping. Conventional cytogenetics is more labor intensive, time consuming and many clinically relevant chromosomal abnormalities are undetected by this technique. But the molecular cytogenesis stunned the limitation of the traditional banding analysis. molecular cytogenetic techniques are the valuable additions to chromosomal banding, increases thorough complex chromosome aberrations and interpretation of numerical by linking the gap between molecular genetic studies and conventional banding analysis. Molecular cytogenetics improved the breeding and genetic studies of many horticultural and agronomic crop. Many chromosomal translocations, cytogenetic probes and molecular markers have been identified through cytogenetic applications.

Keywords: *Molecular cytogenetics, Agronomic crop, Cytogenetic probes, Fluorescence*

INTRODUCTION

In the limited exchange of humidity, gases, temperature, light and nutrients with abiotic stress including radiations, gravity, aboard air composition and vibration, plant reproduce and undergoes ontogenesis inside the ecological system. Plant development, growth and yield is linked with the gene expression which also influences their characteristics (De Micco et al., 2014; & Zheng et al., 2015).

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These genes expression reduced the seed size specially in the *Triticum aestivum* L., *Brassica rapa* L. and *Arabidopsis thaliana* (L.) Heynh when they grow under microgravity climate for complete life cycle in the International Space Station (Levinskikh et al., 2002, & Link et al., 2014). While some gene expressions are linked with the production of stress response protein (pathogenesis-related proteins, antioxidant proteins and heat shock proteins) which were detected in space environment in the *Hordeum vulgare* L., *B. rapa*, and *A. thaliana* plants (Shagimardanova et al., 2010; Paul et al., 2012; Zupanska et al., 2013; & Sugimoto et al., 2014). Other than this, *A. thaliana* plant leaves and roots showed responses of organ-specific proteome to the spaceflight environment (Ferl et al., 2015). Besides, some chemical contamination also influenced the plant growth and development which were cultivated in the artificial atmosphere of the spacecraft (Carman et al., 2015).

Pisum sativum was cultivated in the green house under controlled conditions (space) by maintaining their reproductive purposes and seed viability for the four life cycles through four successive expeditions (Sychev et al., 2007). Genetic polymorphism was checked by RAPD (random amplified polymorphic DNA) which showed not any changing in treated plants than ground plants (Gostimsky et al., 2007; & Sychev et al., 2007). Chromosomal rearrangement was also not observed in the plants through Polymorphic organization of constitutive heterochromatin. Ontogenesis process also influenced in the plants which cultivated in space in their genomes (Musgrave & Kuang 2003; & Carman et al., 2015).

Heterochromatin plays a vital role in the gene expression of epigenetic regulation in the eukaryotes. Heterochromatin increased the small interfering RNA which resulted from DNA repeats or transposable elements (Wang et al., 2016; & Zhang et al., 2016;). But in plants, gene regulation is controlled by a class of RNAs which is known as heterochromatic siRNAs (Djupedal & Ekwall, 2009; & Wang et al., 2016). But different environmental stress components can encourage the structural changes in the heterochromatin (Wang et al., 2016, & Probst & Scheid, 2015). DNA repeated sequences (simple sequence, satellite, microsatellites and transposable elements) are comprised by the C-heterochromatin (Heslop-Harrison & Schwarzacher, 2011; & Merritt et al., 2015). Microsatellites play several functions in the genome of eukaryotes like RNA structure, DNA metabolic process, modulation of the expression of the genes and chromatin regulation (Bagshaw, 2017). For the genetic study of the genome, polymorphic length of SSRs is used as genetic markers (Hodel et al., 2016). Plants quickly adopt the environmental changes by mutation in the microsatellites which are responsible for the gene functions (Richard et al., 2008; & Shi et al., 2013).

Ribosomal RNA gene are used as marker for the study of the cytogenetics and polygenetic of the plants. These rRNA genes are divided into two families i.e., 5S rDNA and 45S, which present at the specific regions of the chromosome. Detection of the rDNAs due to higher number of copies is provide the important information related to the evolution of the chromosome (Siljak-Yakovlev et al., 2017). Chromosomal distribution and number of copies of rDNAs vary in the plant genomes and within the intraspecific taxa which provide the landmarks of chromosome for the genome plasticity (Amosova et al., 2014; & Siljak-Yakovlev et al., 2017).

These repeated DNA sequences play an important role in the genome of plants for the adaptation under the stress. That's why it is important to study the polymorphism in karyotypes and distribution of chromosome in these DNA fractions in the plants. The study of the relationship between genetic adaptation and chromosomal aberrations in the plants is known as cytogenetics (Li & Pinkel, 2006).

There are different approaches in the cytogenetic for the identification of genetic imbalance. Which are described below.

Conventional cytogenetics:

Conventional cytogenetics is well known as the best standard for the identification and scenario of genetic diagnosis. Traditionally, it is used for the scanning of alteration in the genome (both losses and gains of genome portions) and changes among and within the chromosome (Kang & Koo, 2012). It also used to investigate the relationship between clinical syndromes and specific chromosomal abnormalities (Nowakowska & Bocian, 2004). As it is the banding analysis, it required more labour and time. Usually, two weeks are minimal time period to get the results. But many chromosomal abnormalities belong to clinical studies are invisible by this conventional technique (Simons et al., 2012).

Molecular cytogenetics:

Molecular cytogenetics is the modern technique for the chromosomal studies. It's stunned the limitation of the traditional banding analysis. Molecular cytogenetic has some techniques, used as effective diagnostic tool.

1. Fluorescence in situ hybridization (FISH)
2. Spectral karyotyping (SKY)
3. Comparative genomic hybridization (CGH)

These techniques are widely used and employed in the conventional cytogenetics for the identification of chromosomal aberration and alteration (Dave & Sanger, 2007; Kang & Koo, 2012; & Chandran et al., 2019). But molecular cytogenetic techniques are the valuable additions to chromosomal banding because it increases thorough complex chromosome aberrations and interpretation of numerical by linking the gap between molecular genetic studies and conventional banding analysis (Bejjani & Shaffer, 2008; & Russo & Degrassi, 2018).

Fluorescence in situ hybridization (FISH):

Fluorescent labeled DNA probes and specific chromosomal region are used in the FISH method. These DNA probes are the clone pieces of genome of DNA that distinguish their harmonizing DNA sequences and make FISH technique ideal by producing the fluorescent signal for the detection of background strained chromosomes (Qiu et al., 2009). FISH detect the small genomic alteration (from 50 Kb to 100 Kb) and also visualized these alternations in the uncultured cells (Li and Andersson, 2009). From last few years, FISH technique has made quick growth in the field of genomic alterations detection irrespective to the complexity by reducing the gap between molecular cytogenetics and conventional chromosome karyotyping (Kang et al., 2007; & Mohamed et al., 2018). The use of multicolor and divers Fluorescence in situ hybridization assays increased thorough description of arithmetical and multifaceted chromosome aberrations irrespective to their complexity (Chandran et al., 2019). But, the complication of the staining pattern produced by the Fluorescence in situ hybridization is limited on the basis of numbers of FISH probes that can be illustrious. Furthermore, the same chromosome structure and optical reflections can disturb the chromosome banding (Krause et al., 2006; & Li & Pinkel, 2006).

Comparative genomic hybridization (CGH):

CGH is used to screen the whole genome for the identifying the aberrations and showed the variation of Fluorescence in situ hybridization technique by revealing the imbalances in the entire genome (George et al., 2016). While, aberration i.e., balanced mosaicism, chromosomal translocations, changes and inversions in whole genome ploidy cannot be perceived by using this method due to limited resolution of metaphase chromosomes from 5 to 10 Mb (Gullotta et al., 2007). Form the overall performance, resolution for the detection of alternation is slightly higher in the molecular cytogenetic techniques as compared to the conventional karyotyping (Melissa et al., 2011).

Molecular cytogenetic has been used to identify the wheat derived lines by developing the addition lines, translocation line, substation lines and intergeneric amphiploids (Li et al., 2020; & Bai et al., 2020). Chen et al. (2021) used cytogenetics and found that natural hybrid plant of family

triticeae is the natural cross of *Roegneria stricta* and *Roegneria turczaninovii* because Phylogenetic showed that the single copy chloroplast gene rps16 and nuclear gene DMC1 was closely related to the *Roegneria turczaninovii* and *Roegneria stricta*. Cytogenetic analysis indicated the ploidy variation (2*x*, 4*x*, 6*x* and 8*x*) among the intra and interspecies of Asparagus (Viruel et al., 2021). However, Norup et al. (2015) reported the hermaphroditism by gynodioecy produced the dioecy in Asparagus.

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