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REVIEW PAPER

Quantitative scoring of mutations using plants

Sijila J. & Jasmine M. Shah*
Department of Plant Science, Central University of Kerala, Kasaragod – 671314, Kerala
*Corresponding author Email: jas109@gmail.com

Abstract

Genomic instability can be due to the changes in the chromosome number (eg. ploidy changes), structure (eg. translocations and breakage) and sequence information [eg. point mutation (PM), homologous recombination (SHR), frame-shift mutation (FSM) and transposition].Quantitative scoring of mutations caused due to the influence of mutagens and other factors is more often done using Ames test where, mutant *Salmonella* strains are used as a tool to detect mutations. In this review, we describe how mutant plants (*Arabidopsis* and tobacco detector lines) can also be used to quantitatively score mutations like PM, HR, FSM and transpositions.

Keywords: Mutations, *Arabidopsis*, GUS, homologous recombination, point mutations

Introduction

Mutations are the heritable changes in DNA happens either spontaneous or induced manner. These heritable changes are of two types based on where it happens. It can be either chromosomal level or molecular level. Mutations at the chromosomal level lead to ploidy changes and translocations. Mutation at the molecular level lead to single nucleotide changes (point mutation), homologous recombination (HR), frame-shift mutation (FSM) and, transpositions (leading to either HR or FSM). Ploidy changes and large translocations are detected by karyotyping. Other changes are detected using PCR, DNA page, genome sequencing, Ames test, etc. Of these methods, quantitative scoring of frequency is possible only through sequencing and Ames test (or similar strategy). This review is about scoring of mutations using a method similar to Ames test, where, the model plants *Arabidopsis* and tobacco is used as the detection tools.

Ames test

Detection of mutation rate can be done by 'Mutagen Test' (Ames test). In 1975, Bruce Ames developed a simple test for evaluating the potential of chemical to cause cancer. Mainly the test can be used for the detection of chemical mutagens and their carcinogenicity. This is very widely used assay for screening of various pollutants, drugs, cosmetics, food additives and metals. Ames test employs the use of a special mutant strain of bacterium namely *Salmonella typhimurium* (His^-). This organism cannot synthesis histidine; hence the same should be supplied in the medium for its growth. Addition of chemical carcinogens causes mutations (reverse mutation) restoring the ability of this bacterium to synthesis histidine (His^+). By detecting the strain of Salmonella (His^+) in the colony of agar plates, the chemical mutagens can be identified (Fig. 1). The Ames assay can detect about 90% of the chemical carcinogens (Pierce, 2008).

Starting from Bruce Ames's *Salmonella*, most quantitative mutagenesis research has largely been based on similar *in vitro* analysis using other bacteria, yeast, isolated animal cell lineages and model plants (*Arabidopsis* and tobacco). Although research using cell lineages has played a critical role in current understanding of the mechanisms of mutation, including the molecular pathways involved in DNA damage and repair, it is generally not likely to reflect the types of parameters