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How Physical Mapping helps Speed Breeding? – A Review

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A B S T R A C T

Physical Map generally provides the actual details of the distance present between the genetic markers and the nucleotides present in between them and also it acts as the representation of the entire genome as the set of overlapping fragments of cloned DNA which makeup the genome. In this, the genes or the molecular markers are depicted within the equal order as they arise with inside the chromosomes, however the distances among adjoining genes/markers are depicted in the terms of base pairs. Speed Breeding is a new and interesting technique to breeding at the beginning stimulated by using the United States national Aeronautics and space administration (NASA) that promises to expand new crop varieties quicker, imparting wish for meals security in the continent. It is a device or approach for rapid technology advance that notably reduces the harvest time of plants so one can accelerate agricultural research and increase the production of meals to meet the call for of the growing population. Physical mapping helps in the identification of a particular gene or the marker or the primer in a particular gene sequence or in the chromosome whereas speed breeding helps in the acceleration of the breeding cycles of the crop.

Introduction

Physical Map generally provides the actual details of the distance present between the genetic markers and the nucleotides present in between them and also it acts as the representation of the entire genome as the set of overlapping fragments of cloned DNA which makeup the genome.

In this, the genes or the molecular markers are depicted within the equal order as they arise with inside the chromosomes, however the distances among adjoining genes/markers are depicted in the terms of base pairs. The distance present in between the basepairs of the chromosome is called physical distance and can be determined by the hybridization of the probes. It generally involves cloning of many pieces of chromosomal DNA, characterization of the fragments to the size, determining their relative locations along the chromosomes by using the techniques suitable for it. High resolution pictures of the physical mapping reveal the co-linearity regions and have important implications for studies related phylogenetically.

Speed Breeding

Since the population of the world is growing day by day and is also projected to increase 25% in the future and also the major problem right now is the change in the climate that has direct impact on the food security due to the limited food resources present. Change in the climate rapidly and the emergence of recent pests and diseases threatens the agricultural manufacturing. As a consequence, producing a higher quantity of satisfactory food for the ever-increasing population is a prime problem these days. The traditional breeding or conventional breeding techniques would not be enough to meet the future demands of the next generations so that the plant breeders and the cultivators are in steady pressure to improve the crop manufacturing and increase new form of crop that is of better pleasant and gives better yield which ought to be of superior best in every respect i.e. in terms of dietary values, sickness resistance and climatic adjustments etc. Out of those modern ideas from the researchers, one of the maximum trending techniques of the breeding software to accelerate the yield, improve nice of the crop and expand weather resilience is "speed Breeding".

Pace Breeding is a new and interesting technique to breeding at the beginning stimulated by using the United States national Aeronautics and space administration (NASA) that promises to expand new crop varieties quicker, imparting wish for meals security in the continent. It is a device or approach for rapid technology advance that notably reduces the harvest time of plants so one can accelerate agricultural research and increase the production of meals to meet the call for of the growing population. It shortens era time and hurries up breeding and research programs. Usually, crossing of selected determine lines, four-6 generations of inbreeding are generally required to expand genetically stable traces for evaluation of agronomic traits and yield. This is specifically time eating for field-grown plants that are regularly constrained to handiest 1-2 generations in keeping with year. Speed breeding is followed in an enclosed controlled-environment boom chambers can accelerate plant development for studies purposes, which include phenotyping of person plant developments, mutant research, and transformation offers extra outcomes.

Physical Map of Chromosome

A map generated through genetic strategies is rarely sufficient for guiding the sequencing phase of a genome challenge. This is for two motives:

The decision of a genetic map relies upon on the wide variety of crossovers that have been scored: This isn't a main hassle for microorganisms due to the fact those may be acquired in huge numbers, allowing many crossovers to be studied, resulting in an exceedingly precise genetic map wherein the markers are just a few kb apart. As an instance, while the Escherichia coli genome sequencing mission commenced in 1990, the cutting-edge genetic map for this organism comprised over 1400 markers, a median of one consistent with three.3 kb. This turned into sufficiently detailed to direct the sequencing application without the need for massive physical mapping. Further, the *Saccharomyces cerevisiae* project changed into supported by a nice-scale genetic map (about 1150 genetic markers, on average one in step with 10 kb). The hassle with humans and most other eukaryotes is that it's far genuinely now not viable to gain massive numbers of progeny, so notably few meiosis can be studied and the resolving strength of linkage analysis is restricted. Because of these genes which are several tens of kb apart may also seem at the equal position on the genetic map.

Genetic maps have restricted accuracy: while the assessment of Sturtevant's assumption that crossovers arise at random alongside chromosomes. This assumption is best partly correct because the presence of recombination hotspots manner that crossovers are more likely to arise at a few factors in place of at others. The effect that this may have on the accuracy of a genetic map was illustrated in 1992 whilst the complete series for *S. Cerevisiae* chromosome III turned into posted (Oliver *et al.*,

1992), allowing the first direct evaluation to be made among a genetic map and the real positions of markers as proven by means of DNA sequencing.

There had been full-size discrepancies, even to the quantity that one pair of genes had been ordered incorrectly with the aid of genetic evaluation. Undergo in mind that *S. Cerevisiae* is one of the two eukaryotes (fruit fly is the second one) whose genomes had been subjected to intensive genetic mapping.

Methods of Speed Breeding

Speed Breeding I

Speed Breeding II

Speed Breeding III

Techniques of Physical Mapping

Restriction Mapping

FISH mapping (Fluorescentinsitu hybridization)

STS mapping (Sequence Tagged Sites)

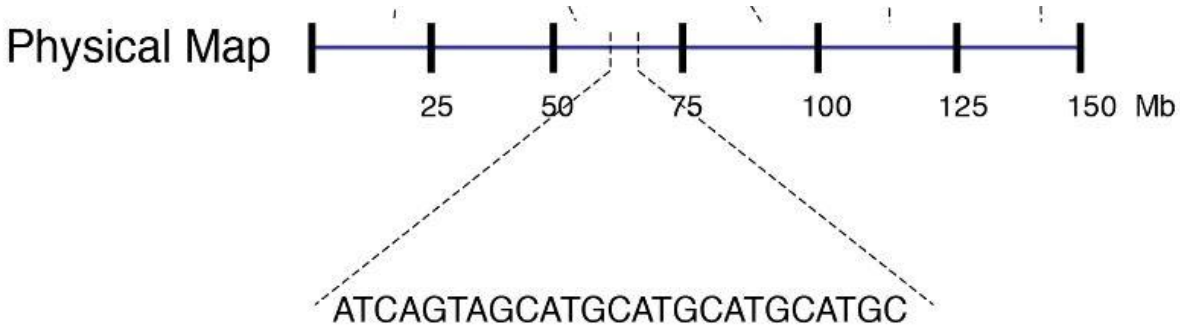
Generally, Physical mapping helps in the identification of a particular gene or the marker or the primer in a particular gene sequence or in the chromosome whereas speed breeding helps in the acceleration of the breeding cycles of the crop.

The physical map acts as an alternative tool for speed breeding by changing the gene or the primer and by inserting the primer that will be helpful for the particular crop either to develop the resistance or tolerance helps in increasing the breeding cycles within a short span of time. The breeding program must be adapted to climate change, and breeding climate-sensitive plants is an immediate challenge that can be achieved with new speed breeding ideas. Speed amplification can be considered as an effective tool for achieving the target of 2050 genetic gain in four Fs (Food, Feed, Fiber and Fuel). Faster breeding combined with new technologies such as marker help selection, genomic selection, CRISPR genetics editing etc., can be used to get the result very quickly. In a country like ours, where resources are severely limited, breeding can be one of the most effective options for reducing the breeding cycle and speeding up the research process. Excellent bioinformatics tools are currently available to compile genetic and physical mapping.

Table.1

Speed Breeding, I	Speed Breeding II	Speed Breeding III
• **Controlled environment chamber conditions (John Innes Centre, UK)** • **Photoperiod: 22Hrs (light)/ 2Hrs Dark Temperature: 22°C (photoperiod)/ 17°C (Dark)** • **Humidity: 70%** • **Light: white LED, far-red LED & Ceramic metal hydrargyrum quartz iodide lamp** • **Light Intensity: 360–380 µmol m−2 s −1 (highest value after ramping) at bench height and 490 – 500 µmol m−2 s −1.**	• Glasshouse conditions (Hickey Lab, Univ. of Queensland, Australia) • A temperature-controlled glasshouse fitted with high pressure sodium vapor lamp • Photoperiod: 22Hrs (light)/ 2Hrs Dark • Temperature: 22°C (photoperiod)/ 17°C (Dark) • Humidity: 70% • Light Intensity: 440-650(Adult Plant height) µ mol m−2 s −1	• low-cost homemade growth room design (Hickey Lab, of Queensland, Australia) • Photoperiod: 12Hrs-12Hrs (Light-Dark) for four weeks then increased to 18Hrs6Hrs • Temperature: 21°C (photoperiod)/ 18°C (Dark) • Light: 7 -8 LED light boxes (Grow Candy) • Intensity:210–260 (bench height) & 340–590 (Adult Plant height) µ mol m−2 s −1

Fig.1 Physical Map of Chromosome



Ref: NIH-National Human Genome Research Institute

These tools play a major role in the preservation and visualization of visual mapping sites. With the development of such tools, the entire visual genome map and visual genetic map have become a regular feature. The ever-changing computer tools and advanced genomic technology (molecular marker genotyping similar to the SNP detection and sequencing system) will surely usher in a new generation of genetic projects and visual mapping.

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