

Arabidopsis Thaliana: As a Model Organism

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Abstract - Due to its genetical nature and desirable traits for cultivation, *Arabidopsis thaliana* is considered as a model organism by researchers to several plants in the plant kingdom. The sequencing of entire plant genome enhances its value to consider for genomic analysis. This feature enables the plant to study various features in genetics and molecular biology like signal transduction pathways, phytochrome activity, circadian rhythms and several more. Also, *Arabidopsis* in the field of proteome research has proven to be an excellent model organism due to its outstanding results. Apart from these, it also withstands to conserve the genetic nature of eukaryotes by adopting few mechanisms. Considering all these characteristics *Arabidopsis* holds handful of advantages over other organisms in selecting as a model organism.

Index Terms - *Arabidopsis*, genomic, molecular, proteomic, model organism.

INTRODUCTION

Arabidopsis thaliana a well-known plant in Brassicaceae is now being widely used as a model organism of choice by the researchers (David W. Meinke, 1998). *Arabidopsis thaliana* was first picked as a model plant by Laibach in Europe and later concentrated in detail by Re'dei in the United States (Laibach, 1970). *Arabidopsis thaliana*, also known as the cress, mouse ear cress which is a short life cycle rabi weed is a little blooming plant of Africa (MH, 2002). *A. thaliana* has a short genome size of 135 Mega base pairs (Mbp). Having its genome sequenced entirely, this plant is used in molecular biology for studying plant characteristics like flowering habits and detecting lights. *A. thaliana* is presently generally utilized for examining plant sciences, including hereditary qualities, advancement, populace hereditary qualities, and plant development. (Rensink WA, 2004) (Coelho SM, 2007), (A.Platt., 2010). However, *Arabidopsis thaliana* has minimal direct impact on farming, it has a few attributes that make it a helpful model for studying the hereditary, cell, and

science of flowering plants. (Platt A, "The scale of population structure in *Arabidopsis thaliana*", 2010) The extensive assets which are accessible for *Arabidopsis*, for example, the whole genome grouping, a huge collection of characteristic variations and an increasing number of molecular devices, made it the positive model for post-genomic research. Due to diploid, and the low size of its genome made *Arabidopsis thaliana* useful for hereditary planning and gene sequencing with about 157 super base pairs and 5 chromosomes. (Bennett MD, 2003), by using *Agrobacterium tumefaciens* we can make a standard level of genetic changes in *Arabidopsis thaliana* to move the genetic material into plant genome. In current scenario Process like floral dip which means dipping of flowers in *Agrobacterium* solution with preferred plasmid and a detergent became popular. (Clough SJ, 1998) (Zhang X, 2006).

ARABIDOPSIS THALIANA AS A MODEL PLANT FOR GENOME ANALYSIS

A large portion of the strategies and asset materials required from a genetic model plant have been produced by the *Arabidopsis* research network. These involve clear chemical and insertional mutagenesis methodology, efficient cross-performing and DNA presentation strategies by plant transition, large mutant assortments of different phenotypes, and a range of mutant gene chromosome maps and molecular markers. Developed seeds are the favoured targets for chemical mutagenesis since a huge number of offspring seeds homozygous for recessive mutations can be created by selfing M1 plants got from a solitary trial. Insertional mutagenesis with transferred DNA (T-DNA) from *Agrobacterium tumefaciens* has gotten normal through advancement of entire plant transformation methods. The genome of *Arabidopsis thaliana* has five chromosomes with 20,000 estimated genomes, absence of polytene chromosomes and

because of little meiotic chromosome restricted cytogenic investigations of chromosome structure in spite of the fact that representation has improved lately with in situ hybridization techniques. (Fransz, 2002)

Exploration with Arabidopsis has given important bits of knowledge into all parts of current science. Now and again, long-standing inquiries in plant physiology and biochemistry were first settled through hereditary and molecular investigation of Arabidopsis mutants, explanation of ethylene signal transduction pathways in Arabidopsis gave the primary identification of a hormone receptor in plants (C. Chang, 1993), In the zone of light perception, mutant investigation with Arabidopsis has prompted the identification of plant receptors and signal transduction segments for phototropism (Huala, 1997) (M. Ahmad, 1998) and circadian rhythms (David W. Meinke, 1998) (M. Tobin, 1998) notwithstanding propelling our comprehension of phytochrome activity (David W. Meinke, 1998)

The coming of Arabidopsis functional genomics and the accessibility of enormous quantities of Arabidopsis mutants inadequate in known gene become progressively significant for those examining different groups of organisms to stay informed concerning proceeding with propels in plant sciences gives a novel occasion to plant scholars to add to explore endeavours in a variety of related controls. Thus, it will turn out to be progressively significant for those examining different groups of organisms to stay up to date with proceeding with propels in plant science. The momentary objectives were to finish the genomic succession and screens for mutations, get insertional knockouts of each significant class of gene, proceed with point by point portrayal of cell, physiological, and formative pathways, proceed with the boundless utilization of Arabidopsis as a model to consider fundamental standards of genetics, build up improved registering frameworks to coordinate data on cell measures associated with plant development and advancement, and make progresses obtained through the Arabidopsis genome project accessible to those taking working at different activities. Technological developments, for example, the utilization of DNA chips and microarrays to consider global patterns of gene expression (M. Schena et al.) (J. Hodgson, 1998) plays a vital role in Arabidopsis research during this era.

ARABIDOPSIS: MAINTAINANCE OF GENETICAL CONSERVATION AND ITS FUNCTIONS

Arabidopsis encodes orthologous genes of most proteins utilized by eukaryotes to keep up genomic integrity, with some significant special cases (initiative, 2000). These orthologous genes incorporate proteins that straightforwardly converse DNA injuries, without separating base-sugar or phosphodiester bonds and glycosylases that start alleged base excision repair (BER) by perceiving altered DNA bases and isolating them from sugars, some of the time likewise cutting the sugar-phosphate backbone. AP endonucleases that perceive the apurinic/aprimidinic sites created by glycosylases, or basic sites emerging from spontaneous depurination/depyrimidination, and advance BER by cutting the DNA backbone, also the parts of multi-protein framework that collaborate to perceive bulky helix-distorting base adducts and cuts the damaged strand on both sides of the lesion, so called nucleotide excision repair (NER). Segments of mismatch repair (MMR) pathways, which perceive base mismatches and certain DNA lesions, and forestall replication errors by explicitly eliminating and supplanting broadened plots of nascent DNA that include base mismatches, proteins that utilize homologous recombination to fix broken chromosomes without loss or increase of nucleotide pairs, by utilizing data in sister chromatids or homologs. End-joining proteins that legitimately interface DNA ends (with some risk of DNA arrangement alteration). DNA replication/repair polymerases that perform semi-conservative chromosome duplication or potentially DNA synthesis related with excision repair (BER, NER, MMR) or break repair, with high or high fidelity and DNA ligases that seal strand discontinuities, and also specialized DNA polymerases—some able to synthesize DNA past inadequately replicated lesions, as a result of permissive nucleotide-selection and primer extension properties, some assuming ineffectively characterized functions in different cycles (R.M.A. Costa, 2001), (A.B. Britt, 2002) (E.J. Vonarx, 1998).

ARABIDOPSIS THALIANA FOR PLANT PROTEOME RESEARCH AS A MODEL ORGANISM

The accessibility of an entire genome arrangement in Arabidopsis gives novel opportunity to genome-based systems biology approaches. It empowers the utilization of post-genomic tools, for example, proteomics in its full limit. The presentation of shotgun proteomics empowered the high-throughput investigation of huge arrangements of tests alongside the identification of a several proteins inside each example. (Weckwerth W, 2008)

Proteomics, the complete and quantitative examination of proteins that are exhibited in a given organ, tissue, or cell line, gives novel experiences into natural systems that cannot be given by genomic or transcriptomic approaches (Wolters DA, 2001) (Gerster S, 2010)

Plastids are key plant cell organelles that perform numerous basic strides in plant cell digestion. One of the attributes is their capacity to form and separate into various plastid types, contingent upon their cell and tissue environment (Neuhaus HE, 2000) Arabidopsis does not create complex storage organs, flowers or fruits meristem is confined to a couple of cells in the shoot apex, most plastid types are essentially rejected from Arabidopsis proteomics research. Conversely, Arabidopsis has been the life forms of decision for the examination of chloroplasts and is right now the main plant for which a genuinely far-reaching set of chloroplast proteins are accessible. (Jung HS, 2010)

Review of a proteomic-tool kit for systems biology provides a focal proteome/peptide spectral information serves in as a base for the determination of proteotype peptides, appropriate for the focused-on Mass Western analysis of complex proteome tests. The MAPA-technique (MAPA = Mass Accuracy Precursor Alignment, (Hoehenwarter W v. D., 2008)) takes into account the recognition and measurement of new proteins.

Coordination of proteomics and metabolomics is a promising and amazing methodology that offers another stage for investigations of complex organic functions including huge quantities of compounds and networks. (W., 2008) Arabidopsis thusly served to likewise create and improve proteomic and metabolomic investigation techniques. Hence, all underlying integrative – omics studies on a plant level depend on Arabidopsis genome explanations. (Malitsky S, 2008) (Lippold F, 2009) (Fukushima A, 2009)

Morgenthal, Wienkoop and others performed studies to exhibit improved example recognition complex quantitative MS examinations in Arabidopsis. Here firstly, detailed interpretation about the Arabidopsis has been done regarding the environmental change due to large scale samplings. Also, the coordination of various data collections acquired from one sample brought about a refinement of data interpretation and hence a more holistic approach. (Morgenthal K, 2007) (Wienkoop S, 2008) Considered that Arabidopsis has been the principal model plant is not unexpected, that these generally new integrative proteomic approaches have just arisen likewise for other model plant species. It is evident that the Arabidopsis genome is the most precisely useful explained to date because of integrative proteomics information. (Wienkoop, 2010) The occurrence of exclusively undifferentiated proplastids is confined to meristematic tissues and undifferentiated cells. Since Arabidopsis does not create complex organs, flowers or fruits and the meristem is limited to a couple of cells in the shoot apex, most plastid types are basically avoided from Arabidopsis proteomics research. (Jung HS, 2010)

It is consequently beneficial to gather data about the subcellular confinement of proteins in Arabidopsis that has been collected so far. The SUBA data set gives data about the sub-cell restriction of Arabidopsis proteins and is an excellent source of data about protein limitation. SUBA gathers all data that is accessible on the limitation of a specific protein, for example MS/MS information, GFP localization and prediction tools, and permits assembling list of organellar proteins with certain, self-characterized dependability criteria (Heazlewood JL, 2007). MAPA is an arising strategy free of genomic data, it has at first been created utilizing Solanum tuberosum, a solitary partial sequenced model yield (current sequence coverage ~70%). A powerful high throughput examination of about 1.5 million spectra from 107 investigations were adjusted for data mining and factually analyzed in around 1 day. Autonomous of the accessible EST-data bases a prevailing protein polymorphism was relegated solely to a particular potato cultivar. Normally, this methodology has likewise been applied to Arabidopsis. An ongoing global quantitative examination of the Arabidopsis hosphor proteome (Chen Y, 2010) was acted in response to a period course of treatments with different plant hormones utilizing phosphor peptide

enhancement and resulting MAPA (Mass Accuracy Precursor Alignment). This brought about 324 000 precursor ions from 54 LC-Orbitrap-MS examinations measured and adjusted in a data matrix with the dimension of 6000×54 utilizing the Prot Max calculation.

ADVANTAGES OF USING ARABIDOPSIS THALIANA AS A MODEL ORGANISM

Arabidopsis thaliana can be grown easily when compared with any other model organisms. This short duration crop produces tiny seeds, has a small genome size of ~114.5 Mb and its genetic nature makes suitable for research to work on this plant. As Arabidopsis belongs to the family of Cruciferae, it is more closely related to vegetables such as mustard, cabbage, and radish. The application of Arabidopsis thaliana to Agrobacterium tumefaciens makes it a versatile model organism that is helpful in the biology laboratory. A.thaliana is used extensively in the fields of evolution, genetics ,plant science which is helpful for the understanding the processes like Stages of germination and plant growth, which are important in the production of commercial crops. Just recently, A. Thaliana has been a model organism in the study of human disease-related molecular and biochemical processes. (homa Saeidfirozeh, 2018) (Matsunaga., 2016)

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