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### Arabidopsis Thaliana: Its Emergence as a Model Organism

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**ABSTRACT**: Various studies have been made since then to study about Arabidopsis thaliana plant which is native to Eurasia and Africa. It is a eudicotyledonous angiosperm belonging to family Brassicaceae. Because of rapid life cycle and high production of seed it has been chosen as a model for scientific research. Friedrich Laibach is the founder of experimental Arabidopsis research. In 1907 Laibach described the correct chromosome number during his PhD research. The Arabidopsis Information Resource (TAIR) provides central access for Arabidopsis data, annotates gene function and expression patterns. Recently, A. thaliana has even become a model organism for the study of the biochemical and molecular processes involved in human diseases and flowering plants. Genetic transformation using agrobacterium tumefaciens was done in Arabidopsis species by floral dip and vacuum infiltration method. Various transgenic lines were produced. Agar plate culture system was used to study root growth responses in plant species. The Arabidopsis Genome Initiative (AGI) was established in 1996 to coordinated sequencing of the Arabidopsis genome. Because of small and tractable genome it can be easily and rapidly manipulated through genetic engineering than any other plant genome. All these studies helped us to consider its emergence as a model organism.

KEYWORDS: Eudicotyledonous, transgenic, genome, miRNA, flowering

#### I. INTRODUCTION

is native Arabidopsis thaliana is also called thal It as mouse ear or cress. to Eurasia and Africa. It is a small, annual and rosette plant belonging to family Brassicaceae. It is a vascular plant eudicotyledonous angiosperm. The plant is closely related to oilseed crops, vegetables and spice plant like cabbage, cauliflower, garden radish, mustard and brussel sprouts. The name thaliana is given after Johannes Thal who first discovered the plant in Harz Mountain of Northern Germany in 1577. First study on Arabidopsis was started by Laibach in 1907. Arabidopsis thaliana emerged as a model organism from 1980's when researchers started combining genetics with powerful molecular biological tools. The first genome sequence was published in 2000 as first nuclear genome of flowering plant<sup>[1]</sup>

Some favorable feature of plant which makes it model organisms is:

- 1. High seed yield
- 2. Easy cultivation in small spaces
- 3. Fast development
- 4. Variability in photoperiodic response
- 5. Easy crossing with full fertility of the hybrids
- 6. Not too high chromosome number
- 7. Hundreds of plants can be raised to flowering when soaked on filter paper with tap water in a petri plate.
- 8. They can be grown from seed to maturity on agar media in a test tube
- 9. Both induced and spontaneous mutation can be isolated <sup>[2]</sup>.

Various studies made in research; genome analysis made it an important plant for studying flowering plants. All these traits make Arabidopsisan ideal model organism for biological research and help researchers to study complex multicellular eukaryotic organism.



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#### **II. HISTORY**

In 16th century, botanical information has been available on Arabidopsis thaliana. In 1577 a German physician Johannes Thal described the plant in his Harzflora<sup>[3]</sup>. Johannes Thal discovered Arabidopsis thaliana hence the name called thaliana. Several name changes have occurred but originally, he called it Pilosella Siliquosa. Due to its rapid life cycle and high production of seed, it has chosen as a model for scientific research. The plant is commonly known as Thal cress due to this cultivation. Small cress plant can be grown in a small area <sup>[4]</sup>. Some centuries later nearly three dozen botanical synonyms have been used and many common named are known including the "mouse ear-cress" or "wall cress"<sup>[5]</sup>. Arabidopsis thaliana is popular as a model organism that discovered in the 1980s, and thenrapidly gained momentum when researchers successfully began to combine genetics with powerful molecular biology methods <sup>[1]</sup>. Due to adoption as a model organism Arabidopsis is useful to genetic experiment. Arabidopsis thaliana stands alone as the most thoroughly studied plant<sup>[5]</sup>. In 2000, the Arabidopsis reference genome sequence was published as the first nuclear genome sequence of a flowering plant<sup>[1]</sup>. In 1935 Drosophila vegetative was translated from which R. Owhyte (1946) gave the nickname "Botanical Drosophila". Genetic investigation was begun in the 1940s by Friedrich Laibach. Fredrich Laibach was the professor of botany at the University of Frankfurt. Friedrich maintained a research laboratory with his personal funds in his hometown Limburg. The genetic carrier of Arabidopsis was started by the doctoral thesis of a student of Laibach, Erna Reinholz which was published in 1947<sup>[3]</sup>. In 2008 more than 3500 papers on Arabidopsis were added to the Pub Med database.

#### The early years (before 1975)

Friedrich Laibach is the founder of experimental Arabidopsis research. In 1907, Laibach described the correct chromosome number during his PhD research and returned to this species in the 1930s when he was established botanist. In 1943 Laibach made a seminar paper for the suitability of Arabidopsis for genetic studies. Laibach and his students emphasized the use of natural variation for the analysis of physiological traits such as flowering time (Laibach 1951) and seed dormancy (Kugler 1951). Interest in Arabidopsis research increased throughout the 1950s.one landmark event was the emigration in 1956 of George Re`dei from Hungary to the United States (Koncz 2006). Laibach joined researchers in Germany (Nappzinn, Robbelon, Muller) the Czech Republic (Veleminsky, Gichner, Cetl) the Netherland (Feenstra, Vanderveen) and Belgium (Jacobs, Bouharmont) to form an active research community in the 1960s (Somerville and Koornnef, 2002). Gerhard Ro¨bbelen organized the first international Arabidopsis conference in 1965 in Gottingen, Germany<sup>[5]</sup>.

#### The Renaissance Period (1976-89)

Renewed interest in Arabidopsis began in the late 1970s with the search for a suitable plant model for research in molecular genetics. In 1975 the excellent review article published by Arabidopsis by Re`dei. David Meinke began to work on embryo-lethal mutants in the area of plant development as a graduate student with Lan Sussex at Yale in 1976. The work of Andreas Muller was expanding 15 years before in Gatersleben, Germany. Ultimately, this led to publications is developmental biology on the use of Arabidopsis and the study of plant embryo development. Muller's work was first introduced by Meinke, when he convinced the landlady of his apartment in new haven to translate the original paper from German in return for cleaning out her basement. Language problem encountered by some when attempting to access the early literature and this illustrates a barrier to advances in Arabidopsis research. In 1980s Somerville and colleagues were instrumental in promoting Arabidopsis. Marten Koornneef and Jaap Van Der Veen were performed informative mutant screens at the same time in Wageningen. Several events in the growth of Arabidopsis research community took place in the mid-1980s<sup>[5]</sup>.

#### **III. TIMELINE**

**2005**: TAIR took over responsibility from TIGR to improvise the annotation <sup>[6]</sup>. TAIR's first Genome version 6.0 was released; it contains 26,751 protein coding gene, 31,407 genes (838 non-coding RNA genes and 3818 pseudogenes). 437 new genes were added and 9 genes were declared as obsolete. Many more updates were made to the genes, coding sequences (version TAIR 6.0, Nov 2005) <sup>[7]</sup>.

**2004**: Final TIGR Genome release (version TIGR 5.0, March 2004) - The final genome reannotation released contained annotation for 26,207 protein-coding genes, 2rDNA cassettes, 631 tRNAs, 57 snoRNAs and 15 snRNAs. There was overall improvement of annotation and gene structure <sup>[7, 8]</sup>.

**2003**: TIGR 4.0 Genome release (June 2003) – In this release the output of the gene prediction algorithms and homology-based computes were compared with the pre existing gene models. New gene models were generated and the



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already existing gene models were updated based on different classes of evidence. There is continuous improvement in the process of automating gene structure as new data is available and pipeline components become sturdier<sup>[9]</sup>.

2001: Increased emphasis on functional and comparative genomics which was supported by NSF 2010 Program<sup>[7]</sup>.

**2000**: The sequence of first ever plant genome was completed <sup>[10]</sup>.

1999: Microarrays and DNA chips was made available<sup>[7]</sup>.

**1999**: Chromosomes II and IV of Arabidopsis was sequenced. Analysis of 17.38 megabases of unique sequence and other revelations with sequencing of chromosome IV was carried out by Mayer, et al. <sup>[11]</sup> and the sequencing of chromosome II from the Columbia ecotype was completed by Lin, et al. <sup>[12]</sup>.

**1997**: Physical maps of all chromosomes were completed <sup>[13]</sup>.

**1996**: Arabidopsis Genome Initiative (AGI) was organized by bringing together the efforts of international teams who had been decoding the genome sequence since the early 1990s<sup>[10]</sup>.

1995: Standard BAC and P1 libraries of an Arabidopsis were constructed <sup>[7]</sup>.

**1993**: A successful High-efficiency transformation of Arabidopsis was developed which is widely used in laboratories <sup>[14]</sup>.

**1992**: The chromosome walking experiment was initiated and published <sup>[10]</sup>.

**1991**: Stock centers in US, the Arabidopsis Biological Resource Centre (ABRC) and database was organized which also serves in Asia and Australia in addition to the America. The first stock center Nottingham Arabidopsis Stock Centre (NASC) was launched by Dr Bernard Mulligan in 1990<sup>[5]</sup>.

**1990**: The Multinational Coordinated Arabidopsis thaliana Genome Research Project was initiated as a cooperative international effort <sup>[15]</sup>.

**1989**: First T-DNA tagged mutant gene was cloned. It has become a valuable resource for the studies of gene function in Arabidopsis. Zambryski and colleagues have reviewed its identities and functions<sup>[16]</sup>.

**1988**: First Restriction Fragment Length Polymorphism (RFLP) linkage map for the nuclear genome of Arabidopsis thaliana was constructed by C Chang and colleagues<sup>[17]</sup>.

**1988**: Chris Somerville and collegues organized a conference in United States and established electronic Arabidopsisnewsgroup to help researchers to keep in touch<sup>[18]</sup>.

1986: The First genetic sequence of Arabidopsis was published and co-authored by C Chang and E M Meyerowitz<sup>[19]</sup>.

**1986**: Arabidopsisthaliana was transformed by the leaf disk transformation-regeneration method which was modified by inoculating it with Agrobacterium tumefaciens strain<sup>[20]</sup>.

1985: Arabidopsis was promoted as model for molecular genetics for the first time <sup>[5]</sup>.

**1984**: With the help of many methods complexity of Arabidopsis was characterized and genome size was estimated and the first technique to determine genome size of Arabidopsiswas proposed by Leutwiler et al; in 1984<sup>[21]</sup>.

**1983**: The first complete map of Arabidopsis genes with mutant phenotypes was published. 76 genes were included in the map with phenotypes covering seed coat pigmentation, altered trichome morphology to increased hypocotyls length and reduced surface waxes<sup>[13]</sup>.

**1980**: The awareness of Arabidopsis uses for the study of plant biochemistry, physiology, and development was expanded <sup>[5, 22]</sup>.

**1976**: Second International Arabidopsis Conference was held <sup>[5, 18, 23]</sup>.

**1970**: First major review article published which was written by George Redei. He gave a bibliographic review <sup>[24]</sup>.

**1965**: The First International Arabidopsis Conference was held in Göttingen, Germany and organized by Gerhard Röbbelen<sup>[5, 18, 22]</sup>.

**1964**: The First Arabidopsis newsletter was published <sup>[5, 18, 23]</sup>.

#### IV. TAXONOMICAL CLASSIFICATION

Arabidopsis is a vascular plant which is the main character of phylum Tracheophyta. Being a eudicot plant resemble it in class Magnoliopsida. It is a rosette plant. Fruits pedicels are ascending, divaricate or slightly reflexed or slender. In flowers sepals are erect or ascending, usually oblong or ovate. Petals are white, lavender or purpulish. Stamens are slightly tetramendous, filaments are not dilated basally, and anthers are oblong or ovate. Fruits are subsessile. They have 15-80 ovules per ovary. Seeds are usually uniseriate, plump or flattened, not winged or margined, oblong, ovoid or ellipsoid. It has mucilaginous seed coat. All these characters of Arabidopsis evolved it multiple times in family Brassicaceae<sup>[25]</sup>.

**Kingdom:** Plantae **Phylum :** Tracheophyta



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Class: MagnoliopsidaOrder: BrassicalesFamily: BrassicaceaeGenus: ArabidopsisSpecies: Arabidopsis thaliana

#### V. CHARACTERIZATION

Arabidopsis thaliana having a relatively small genome size no genes of double number, most of the plant genome contain the double number of genes. A. thaliana genome size is approximately 19 times smaller than the Maize genome it is about 2400 Megabase pairs (Mbp), wheat genome is also 128 times larger than A. thaliana and 5 times larger than Homo sapiens<sup>[26]</sup>. It is difficult to isolate, sequence and clone of larger genome in mutant loci. Small genome of A. thaliana simply analyze genetically, it grows faster and its response to disease and stress.

1. Expression, organization and DNA-binding characteristics of GATA factors in A. thaliana :

In animal and fungi, there are some proteins identified as GATA factors i.e. Type-IV zing-finger proteins are GATA-1, GATA-2, GATA-3 and GATA-4 as well as DNA-binding characteristics of their identified proteins. At the transcription level the genes are not regulating developmentally and cannot be detected. GATA-1 is different from the other three proteins by their DNA binding specificity<sup>[27]</sup>.

#### 2. Characteristics of RbcX proteins :

RbcX is one of the factors of Rubisco (Ribulose-1, 5-bisphosphate carboxylase/oxygenase). Rubisco is composed of eight larger (Rbc1) and eight small (Rbcs) subunits and the RbcX is the subunit that converts the enzyme into functional holoenzyme. In CynobacterialRubisco complex RbcX is considered to act as the chaperon in that assembly <sup>[26]</sup>. Two homologous genes of RbcX of cyanobacteria are: AtRbcX1 (At4G04330) and AtRbcX2 (At5G19855). These proteins contain the same function acting as a chaperon during Rubisco synthesis.

#### 3. Characterization of root hair-line under physiological stresses of A. thaliana:

Calcium binding protein associated with the plasma membrane of A. thaliana involved in growth of root hair tips. N-terminal domain contain 23 residues of some transgenic lines over express it and EXPANSIN A7 is a root hair-specific promoter completely lack the root hairs<sup>[28]</sup>.

#### 4. A robust circadian rhythm of metabolites :

VP16-02-003 and VP16-05-014 are enhanced growth phenotypes obtained by the genome-wide reprogramming of A. thaliana mutants. These studies showing that eighteen observed biomarkers of circadian rhythm for increased characteristics growth phenotypes mutants of VP19-02-003 and VP16-05-014<sup>[29]</sup>.

#### 5. Identification and prediction of microRNAs and their target mRNA :

The method uses characteristics of known plant miRNAs having conserved sequences between A. thaliana and Oryza sativa related species having conserved miRNA. Interaction of miRNAs (miRNA) and target messenger RNA expression can be regulated by sequence complementarity<sup>[29]</sup>.

6. Structural and functional characteristics of cGMP-dependent methionine oxidation in A. thaliana proteins :

Some observable evidences of enhanced structural and biochemical properties shows post-translation methionine oxidation of proteins is not result of cellular damage but can provide the cell with information on cellular oxidation status the cell with information on cellular oxidation status <sup>[30]</sup>.

#### VI. GEOGRAPHICAL DISTRIBUTION

A. thaliana is native to Europe and central Asia and now it is acclimated at many places in the world. Hoffmann illustrated the biogeographic of the species in detail and stated that the too - low spring and autumn temperature, high temperature and low precipitation in summer limits. A. thaliana distribution range Hoffmann also concluded that if conditions with sufficient water and high mean temperature in laboratory are artificial for more raise except in the south



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eastern north American range. Arabidopsis has wider climatic amplitude than other species of the Brassicaceae. Arabidopsis occupies habitats often on sandy or loamy soil such as riverbanks, rocky slopes, waste places, roadside and cultivated grounds. It has also been found from the sea level which is up to 4250m<sup>[31]</sup>. Pigliucci was reviewed the ecology of Arabidopsis<sup>[32]</sup>.

Arabidopsis most abundantly flowers in spring and early summer and mature seeds are available from May to July<sup>[33]</sup>. Natural environmental conditions differ throughout the year, and therefore, the timing of the transition from the vegetative to reproductive phase of a plant is a major determinant of its reproductive success. Currently, flowering variation is especially studied among sorts of cultivated species. This variation present in cultivated species probably had a natural origin<sup>[34]</sup>. Although Arabidopsis has been used mainly for studies related to development and general biology, it will also be useful for dissecting traits that are required for plant breeding and ecology, of which growth and reproductive success are probably the most important traits. Absolute growth and RGR are the integrative results of a complex set of parameters, including directly related components such as carbon fixation, water and mineral uptake, partitioning of reserves and respiration<sup>[34]</sup>.

#### VII. METHODS OF RESEARCH

Arabidopsis is first established model organism. The first paper on experimental research on **individuality and continuity of chromosomes** in Arabidopsis was published in 1907 by Friedrich Laibach. **10 somatic and 5 meiotic chromosomes** were accurately counted by him in the Arabidopsis species. He noted that though much lower amount of chromatin in Arabidopsis but they are at most 1/3 rd of Brassica concluding thatnot all the chromatin are essential for maintaining individuality of chromosomes. Arabidopsis was published by Robellen (1962a). Also great efficiency of **ethylmethane** sulfonate in Arabidopsis was demonstrated by Robellen (1962b) and McKelvie (1963) <sup>[2]</sup>. Arabidopsis is widely used in genomic research. It has served to develop and improve proteomic and metabolomic analysis technique. Hence, all the initial integrative omics studies on plant level are based on Arabidopsis genome annotation. The Arabidopsis Information Resource (TAIR) provides central access for Arabidopsis data, annotates gene function and expression patterns<sup>[36]</sup>.

Feldmann and Marks (1987) described the method for genetic transformation using Agrobacterium in Arabidopsis thaliana species. The method used was **floral dip method** which includes seed imbibitions in suspension of Agrobacterium and plant was grown in a natural condition until next generation and then it was screened on medium supplemented with Silwet L-77 agent More than 100 transgenic lines were obtained on a single selection plate in this experiment using primary transformant of kanamycin + carbenicillin<sup>[37]</sup>.

New method of transformation was described by Bechetold (1993). In this method vacuum is applied to the early uprooted plant which is placed in a bell jar in a solution of Agrobacterium. Then these plants are planted in soil and next generation is selected using antibiotic selection system. Then finally flower buds were inoculated with agrobacterium suspension which contains surfactant Silwet L-77, which facilitates bacteria to explore intercellular spaces. The method is known as **vacuum infiltration method** <sup>[37, 38, 39]</sup>.

Study was carried out to compare the efficiency of these two methods wherein floral dip method of transformation proved to be best. Also transgenes were detected by PCR for the presence of reporter gene sequence (gusA or GUS Plus) which were used in the procedure of transformation. Single DNA band at 488-bp was the positive control for GUS Plus and those at 604-bp represented amplified fragments of gusA which are most stable transgenic plants. With the help of GUS assay in the tissues of inflorescences, leaves, stems and roots of putative transformants the gene expression for gusA and GUS Plus were visualized. No GUS activity was observed in wild type whereas with localization and intensity GUS Plus expression varied in seedlings and mature plants<sup>[38]</sup>.

Agar plate culture system was used for improved plant growing method to study root growth and natural responses of Arabidopsis thaliana.

**i]** Traditional agar-plate culture system (TPG, traditional plant growing): In this system, both the roots and shoots are exposed to illumination. Into the agar medium in which about 1%-3% sucrose is added roots are grown. Because of root lighting or sucrose addition artifact root response can be caused as it is not the natural environment.



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**ii] Improved agar-plate culture system (IPG, improved pant growing):** A new system IPG was developed to study root growth and response of Arabidopsis thaliana. In which shoots are illuminated and roots are grown in darkness without sucrose addition. While investigating the root growth responses, some Arabidopsis natural accessions, relevant Arabidopsis mutants and transgenic lines were used. The total root length, lateral root length, primary root length, root hair density, PIN2 abundance (an auxin efflux carrier), gravitropic response,  $H^+$  or  $Ca^{2+}$  flux in the root tip were investigated in IPG or TPG. It was concluded that though the root growth and responses are directly regulated by lighting and sucrose the most approximate natural growth environment such as IPG should be adopted for studying in vitro cultured Arabidopsis plant species<sup>[40]</sup>.

The effects of exposure to vernalization (winter-like temperature) is mediated by **FRI** (**FRIGIDA**) and **FLC** (**FLOWERING LOCUS C**) traits of Arabidopsisthaliana. In short days, they account for about 23% of the phenotypic variations in flowering time of Arabidopsisthaliana. Both the traits are light dependent but most of the characterized natural allele affects either seedling growth or flowering time. A cross of Fr-2 to Col-0 shows simple segregation in phenotype of  $F_2$  population that they flower early. The PHY-C the red light receptor gene was responsible for this flowering behavior. The frequency of PHY-C receptor varies with latitude. The *p*-values for the association of PHY-C ranked first for latitude and for the FRI-dependent interaction with latitude it was fourth. Through this work it was concluded that, major agents of natural variation in flowering and growth responses are photoreceptor genes<sup>[41]</sup>.

#### VIII. LAB STRAINS

There are over 750 natural accessions all over the world that are collected and are available from two major seed stock centers, ABRC and NASC. Every accession is quite different from each other in terms of form, development, and physiology <sup>[7]</sup>. The frequently used ecotypes are Landsberg erecta (Ler), Columbia and Wassilewskija <sup>[42]</sup>.

The **Landsberg erecta** (**Ler**) line was selected from the population of Landsberg seed that had been irradiated. It was called Landsberg erecta (Ler) by Will Feenstra and was the background line for all the mutants that have successively been produced by Feenstra, Van der Veen and Koornneef at Wageningen University <sup>[43]</sup>.

Monogenic mutations of the first accession Landsberg erecta were selected on the basis of late flowering under long-term conditions (LD) after treatment with ethyl methanesulphonate or radiation<sup>[44]</sup>.

The lab strain Landsberg erecta (Ler) yielded 66.6% more seeds than the accession **Cape Verde Islands(Cvi)**, but the Cvi seeds were twice heavier than Ler seeds <sup>[45]</sup>. Arabidopsis accession also differs greatly in their seed dormancy behavior. The behavior of lab strain Ler and Col is almost nondormant when in water germination is measured under white light whereas other accession such as **Enkheim-2(En-2)** or Cvi from Cape Verde Islands appears to have much stronger seed dormancy under the same condition. Ler seed took 12-17 days for 50% germination, depending on the maternal environment, while Cvi seeds took between 74 and 185 days <sup>[46]</sup>.

**Columbia** (**Col**) is the ecotype that is being sequenced in the Arabidopsis Genome Initiative. The Columbia accession is mostly used for the investigation of genome size among the A. thaliana accessions. It is believed that there are intraspecific variations between the accessions for e.g. between Cape Verde Islands ecotype "Cvi-0" and "Columbia".

It's said to be that the nuclear genome of accessions (natural strains) of Arabidopsis can differ by few percent of their sequence which was suggested by Whole-genome hybridization studies; the reference accessions was Col-0, and two divergent strains "**Burren**(**Bur-0**) and **Tsu**(**Tsu-1**)"<sup>[47]</sup>.

"C24" is usually mistaken as Columbia, however it's an independent ecotype based on several data <sup>[48]</sup>.

FISH experiments were used to check whether the use of 5s rDNA to identify chromosomes can be generalized to other ecotypes using six different strains: **Wassilewskija** (**WS**), Ler, Col, (**Kashmir**) **Kas**, and C24, Cvi. Three different hybridization patterns of 5SrDNA were observed in the six ecotypes tested, showing polymorphism between the ecotypes with reference to 5S rDNA loci <sup>[49]</sup>. The crosses between the most widely used laboratory strains Col and Ler and Cvi showed natural variations which helped in attaining changes in the circadian period of leaf movement. An



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examination in Recombinant Inbred Lines (RILs) between Ler\*Cvi and Ler\*Col identified four presumptive Quantitative Trait Loci (QTL) that regulate the period of the circadian clock <sup>[50]</sup>.

A main factor that prevents A. thaliana from flowering quickly without vernalisation is FRI (FRIGIDA). The mainly used laboratory strains Landsberg erecta (Ler) and Columbia (Col-0) lacks FRI activity because of the deletion of FRI locus <sup>[51]</sup>. Ler, C24, **Shahdara** and **Da(1)-12** all have FLC alleles which is often described as "weak" due to their enervated reactions to active FRI alleles. **Drahonin (Dra-0), Estland (Est), Warschau(Wa-1)** and **Wilna(Wil-1)** which are early flowering accession appears to have intact FRI coding sequence and, except Wil-1, express the FRI transcript, which is the good reason for having effect in FLC.

In **Vancouver** (**Van-0**), defects in the FLC may be the source of its rapid flowering phenotype, and the effect of the inactive FLC allele lying in Bur-0 is obscured by the presence of other late flowering loci <sup>[52]</sup>.

#### IX. ROLE AND IMPORTANCE AS A MODEL ORGANISM

The usefulness for genetic experiments that involves important features like short generation time, small size that limited the requirement for growth facilities, and prolific seed production through self-pollination, Arabidopsis was adopted as a model organism<sup>[5]</sup>.

It's not an economically important plant but it is being closely related to economically important crop plants as turnip, cabbage, broccoli, and canola, Arabidopsis thaliana belongs to Brassicaceaeor mustard family, a small dicotyledonous species. For several years it is desirable for laboratory studies because it is in focus for over 40 yearsbecause of several traitsintense genetic, biochemical and physiological study. To complete its life cycle it requires only light, air, water and a few minerals. It produces numerous self-progeny showing fast life cycle with very limited space requirements. It has relatively small, genetically tractable genome that can be manipulated through genetic engineering more easily and rapidly than any other plant genome. It can be is easily grown in a greenhouse or indoor growth chamber. It produces very small seeds & has a small genome ~114.5 mb. It is genetically well characterized due to the volume of work being focused on this plant. A. thaliana is a versatile model organism for use in the biology laboratory. Exposing A.thalianatoagrobacterium tumifaciens provides a means of efficient transformation vector making. It helps to understand plant science, genetics and evolution and germination and aspects of plant growth. Recently A.thaliana has even become a model organism for the study of the biochemical and molecular processes involved in human diseases & flowering plants<sup>[53]</sup>.

The first plant genome sequenced is Arabidopsis in 2000. The Arabidopsis information resource (TAIR), functions have been credited to 27,000 genes encoding 35,000 proteins they encode. Because of its diploid and small size genome (135mbps) and five chromosomes makes Arabidopsis useful for genetic mapping and sequencing. Arabidopsis as a valued genetic model plant<sup>[54]</sup>.

Lipid breakdown, photorespiration and  $H_2O_2$ -detoxificaton are three metabolic pathways that play a pivotal role in higher plants peroxisomes. Arabidopsis thaliana is the first higher plant to have its entire genome sequenced and the study was begin by forward-/reverse genetics and post-genomic. These studies explain that plant peroxisomes have more different functions than we previously thought. Arabidopsis thaliana is helping us to understand the function of plant peroxisomes using research<sup>[55]</sup>.

#### X. GENOME

**GENOME SEQUENCE:** The genomic sequence of the flowering plant Arabidopsis thaliana is that the sequenced regions covers about 115.4Mb from 125Mb genome and extend into centromere regions. The estimation of Arabidopsis thaliana involved whole-genome duplication, followed by subsequent gene loss and substantial local gene duplications, giving rise to an active genome enhance by lateral gene transfer from a cyanobacteria like ancestor of the plastid. Arabidopsis thaliana has many families of new proteins but also they have lacks of several common proteins families, indicating that the sets of common proteins have undergoes differential expansion and contraction in the three multicellular eukaryotes. This is the first complete genome sequence of a plant which supplies the foundations for more comprehensive contract of conserved processes in all eukaryotes, identifying a wide range of plant specific gene functions and accepted rapid systematic ways to identify genes for crop improvement <sup>[56, 57]</sup>.



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**GENOME SEQUENCING INITIATIVE:** The Arabidopsis genome initiative (AGI) was established in 1996 to coordinated sequencing of the Arabidopsis genome. This initiative is followed by advances in EST sequencing project, construction of standardized YAC (Yeast Artificial Chromosomes) and BAC (Bacterial Artificial Chromosomes) libraries, establishment of physical maps for limited region of the genome, and the scanning of many isolated genes. AGI participants from Europe, Japan, and also in the United States (UK) agreed on a strategy that integrate bacterial artificial chromosome end sequencing, fingerprinting, hybridization tie up with Yeast Artificial Chromosomes (YACs) and molecular markers, and to take the first step in spread across the genome to begin sequencing adjacent of Bacterial Artificial Chromosome) clones because they had already invested in this approach. Each group was assigned a chromosomal region to begin sequencing with the understanding that assignment could be modified later to reflect progress and accessibility of funding <sup>[58]</sup>.

**GENOME ORGANIZATION AND DUPLICATION:** The Arabidopsis genome sequence provides anentire view of chromosomal organization and signals to its evolutionary history. Gene families organized in together arrays of two or more units have been described in C. elegans1 and Drosophila2. Huge segmental duplications were recognized either by directly aligning chromosomal sequences or by aligning proteins and searching for tracts of conserved gene order.

The only duplicated segment in the centromere regions was a 375 kb segment on chromosome 4. Much duplication appears to have sustained further shuffling, such as local inversions after the duplication incident. We used TBLASTX5 to findcollinear mass of genes occupy in huge duplicated chromosomal segments. The duplicated regions enclose 67.9Mb, 60% of the genome, moderately more than was found in the DNA-based order and these data extend earlier findings.

The diploid genetics of Arabidopsis and the substantial division of the duplicated segments have masked its evolutionary history. The determination of Arabidopsis gene functions therefore is pursued with the possible for functional repetition taken into account. The long period of time over which genome stabilization has take place has, however, bring sufficient opportunity for the divergence of the functions of genes that appear from duplications <sup>[57, 58]</sup>.

#### MicroRNAs and their mRNA targets

MicroRNAs (miRNAs) are non-coding RNA molecules with necessary regulatory functions in eukaryotic gene expression. The majority of studied mature miRNA are about 21-23 nucleotides long and have been found in a wide range of eukaryotes, from Arabidopsis thaliana and caenorhabditis elegans (c. elegans) to mouse and human. Over 300 miRNA have been recognize in different organisms to date, essentially through cloning and sequencing of short RNA molecules <sup>[59, 60, 61, 62, 63, 64, 65]</sup>.

#### Prediction of Arabidopsis miRNAs:

MicroRNAs (miRNAs) are used to predict new miRNAs by computational methods; it defines sequence and structural properties that differentiate known Arabidopsis miRNA sequences from random genomic sequence, and uses these properties as constraints to screen intragenic regions in the A. thaliana genome. Sequences for candidate miRNAs were evaluated for the following computable sequence properties: G+C content in mature miRNA sequences, hairpin-loop length in their precursor RNA structures. Sequence of all 19 known Arabidopsis miRNA had a G+C content ranging from 38% to 70%. The first step was to explore for potential hairpin structures in the Arabidopsis genome intragenic regions. The second step was to analyzed miRNA candidates according to their nucleotide composition and sequence conservation. If two or more overlapping 21-mer miRNA candidates from the same precursor were collected in the final miRNA claimant set, each miRNA candidate was scored using the following formula:

miRNA score = number of mismatches +  $(2 \times \text{number of nucleotides in terminal mismatches})$  + (number of nucleotide in internal bulges / number of internal bulges) + 1 if the miRNA sequence does not start with U<sup>[66, 67]</sup>.

#### **XI. CONCLUSION**

The main aim of our study was to collect information about emergence of Arabidopsis as a model organism. Its small genome, production of numerous progeny showing fast life cycle with limited space requirement makes it a very significant research tool. It is the first higher plant to have its entire genome sequenced. Various transgenic lines can be produced through genetic transformation. Various strains are available for studies, most widely used are Ler and Col. All these factors made it a significant model organism.



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