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EVALUATION OF A GENOMIC MODEL FOR PLANT GENOME STUDIES

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ABSTRACT

Numerous plants have been the subject of recent research in the pharmacological, cosmetic, and agro-alimentary domains due to their chemical composition and multiple therapeutic capabilities. *Populus trichocarpa* is one of the most common trees found in deciduous forests (*Salicaceae* family). The current study examines *Populus trichocarpa* as a model plant for plant genomics research, as well as the most recent findings on phytochemical composition and medicinal potential. More than 45,000 potential protein-coding genes were discovered. In the *Populus* genome, a whole-genome duplication event was discovered, with approximately 8,000 pairs of duplicated genes surviving. Furthermore, the reproductive biology of *Populus* provides new opportunities and challenges in the study and analysis of natural genetic and phenotypic variation. In the present review, we endeavour to describe and compile the available knowledge on *Populus trichocarpa* as a model plant for genomic investigations and to bring that material up to date of *Populus trichocarpa's* phytochemical and medicinal properties.

Keywords: Genomic, Populus, *Populus trichocarpa*, Medicinal properties, Genomic sequence

INTRODUCTION

Over the beyond decades, the cultivation of medicinal flora has started attaining momentum. However still, a significant part of our requirements continues to be met from wild sources. Although there has been a significant increase in the use of herbal medicine in recent years, there is still a significant demand for research data in this field. Medicinal plants are rich sources of components that can be employed in the manufacture of pharmacopoeial, non-pharmacopoeial, and synthetic medications. We can't get away from nature since we are part of it. They must be promoted to preserve human lives **[1]**. *Populus trichocarpa* considered as the first tree whose entire DNA code is decoded. The genome sequence of *P. trichocarpa* is a significant tool for employing comparative mapping to investigate the structure and function of genomes in the poplar and related species **[2, 5]**. Genomics is the study of whole genomes of organisms, and incorporates elements from genetics. The objectives of the genomic research are to determine the function of genes and the factors that regulate genes throughout the genome. Based on available DNA sequences, it is propounded that trees have higher rates of genome-wide recombination (correlated with higher levels of genetic diversity) than short-lived herbs and shrubs, except conifers which exhibit lower recombination rates as compared to angiosperms **[1]**.

Table 1: Year Wise Utilization of Genomic Sequence of *Populus Trichocarpa*

Year	Highlights	Remarks
2006	**Discovery of Genomic Sequence of Populus**	• **Chromosome scale genome reconstruction from a combination of shotgun sequence assembly and genetic mapping.** • **Discovery of 45,000 recognized protein coding genes.** • **Assembled genome revealed genome duplication event (8000 duplicated gene pairs surviving in Populus genome)** • **One more duplication event coincides with Populus and Arabidopsis lineages but tandem gene duplication, nucleotide substitution and gross chromosomal rearrangement is slow in Populus as compared to Arabidopsis [2].**
2007	**Populus as a Plant Biology Model System**	• **Based on the complete *Populus trichocarpa* genome sequence and the development of various genetic, genomic, and biochemical tools, Populus now provides a wealth of opportunities to investigate questions that are difficult to answer in Arabidopsis and rice, the two most widely used model systems in plant biology and genomics** • **Although research into tree-specific qualities such as wood creation, long-term perennial growth, and seasonality is clear, including a tree in the model system improves research into other areas such as blooming control, biotic interactions, and adaptive trait evolution [3].**
2008	**Cytokinin Signaling Regulates Cambial Development in Poplar**	• **Despite the fact that vascular cambium activity accounts for a significant portion of plant biomass, there is largely unknown molecular basis of plant growth.** • **Cytokinin signaling for cambial activity was studied in the cambial zones of two tree species, poplar (*Populus trichocarpa*) and birch (*Betula pendula*) [4].**
2009	***Populus trichocarpa* 'Nisqually-1' Micropropagation- the Genotype from which the Populus Reference Genome was Derived**	• **The reference genome sequence of *Populus trichocarpa* (Torr. & Gray) genotype 'Nisqually-1' is available, and it is used as a reference for biotechnology and molecular biology research** • **However, 'Nisqually-1' has been shown to be resistant to micropropagation, regeneration, and transformation.** • **This study developed a highly efficient micropropagation strategy for 'Nisqually-1' shoot tips from greenhouse-grown shoot tips [5].**
2010	**Temporal dynamics of co-occurring changes in aquaporin expression levels, embolism and refilling in *Populus trichocarpa***	**The patterns of pip gene expression in *Populus trichocarpa* during xylem embolism recovery suggest that the pip1 aquaporin subfamily plays an important role as refilling process moderators [6].**

2011	**Heat shock response Physiology and Transcriptional Networks in *Populus trichocarpa, Arabidopsis thaliana,* and *Glycine max***	• **The reactive oxygen network, and hormonal signaling are discovered, the heat shock response becomes more complex with new interactions and crosstalk between heat shock proteins (HSPs)** • **Comparative analyses of variation in each of these processes across species, on the other hand, are largely unknown** **in controlled environment experiments, photosynthetic response curves from 22-42 °C were measured and revealed that the temperature optimum of light-saturated photosynthesis was higher for *Glycine max* than for *Arabidopsis thaliana or Populus trichocarpa* [7].**
2012	***Populus trichocarpa* Sequencing Revisited**	• **The availability of genetic and genomic data, as well as the sequencing of the Populus genome, aided in the identification of candidate genes underlying physiological and morphological features of interest.** • **Genome-enabled research has helped us understand the relationship between phenotype and genotype, as well as the genetic mechanisms by which woody perennials adapt to environmental stress [8].**
2012	**Chemical Transformations of *Populus trichocarpa* during Dilute acid Pretreatment**	• ***Populus trichocarpa* was subjected to dilute acid pretreatment at various intervals. The three primary components of lingo-cellulosic biomass, cellulose, hemi-cellulose, and lignin, were separated from the beginning and dilute acid pretreated poplar** • **The structural changes in poplar during dilute acid pretreatment were studied using nuclear magnetic resonance (NMR) and gel permeation chromatography (GPC).** • **According to the findings, the pretreatment dissolved hemicelluloses and changed the structural properties of lignin and polysaccharides [9].**
2013	**Ptr-Mir397a is a Negative Regulator of Laccase Genes Affecting Lignin Content in *Populus trichocarpa.***	• **Laccases have been thought to catalyse the oxidative polymerization of monolignols. Genetic evidence in support of this theory has been difficult to come by due to the functional redundancy of laccase genes** • **A subset of laccase genes in *Populus trichocarpa* has been identified as targets of the microRNA (miRNA) ptr-miR397a.** • **To better understand the activities of ptr-miR397a and its targets, the laccase gene family was studied and 49 laccase gene models were identified, of which 29 were predicted to be ptr-miR397a targets. Ptr-MIR397a was found to be over-expressed in transgenic *P. trichocarpa* [10].**
2014	**Novel and Drought-Responsive LincRNAs in *Populus trichocarpa* Identified Genome-Wide and Functionally Predicted LincRNAs**	• **Although protein-coding genes are thought to be the most important component of the eukaryotic transcriptome, numerous studies have revealed that intergenic, non-coding transcripts also play an important role.** • **LincRNAs (long intergenic non-coding RNAs) have been found to be essential in both humans and Arabidopsis.** • **However, lincRNAs and their regulatory roles in woody plants, particularly *Populus trichocarpa*, remain unknown (*P. trichocarpa*).** • **A large set of Populus RNA-Sequence data were examined with high sequencing depth under control and drought conditions, yielding a total of 2542 lincRNAcandidates. 51 and 20 lincRNAs were identified as putative targets and target Mimi, respectively [11].**
2015	**Evolutionary Quantitative Genomics of *Populus trichocarpa***	• ***P. trichocarpa* evolutionary quantitative genomics provides a better understanding of the molecular basis of climate-driven selection in forest trees, and we show that important loci underlying adaptive trait variation are also related to the climate of origin.** • **The authors believe their approach is the most thorough because it investigates the molecular mechanisms of adaptation using a variety of methods and tests.** • **They also provide a detailed outline of the analyses needed to study environmental adaptation in a population genomics context in order to better understand the species' potential adaptive capacity to future climatic scenarios [12].**
2016	**During root development in *Populus trichocarpa*, genes regulated by histone acetylation were identified.**	• **Histone deacetylases (HDACs) are enzymes that remove acetyl groups from histones.** • **HDACs work with histone acetyltransferases (HATs) to regulate histone acetylation status, which influences gene expression.** • **The role of histone deacetylase (HDAC) in root organogenesis**

		and development in Populus trichocarpa51 was investigated using trichostatin A (TSA), a selective inhibitor of HDAC [13].
2017	*Populus trichocarpa* encodes small, effector-like secreted proteins that are highly induced during mutualistic symbiosis.	• Organisms communicate with one another through a variety of metabolic and protein-based signals during symbiosis. Small secreted proteins (SSPs) that cause phenotypic and physiological changes in another organism are one type of protein signal. • Protein-based effectors have been identified in aphids, nematodes, fungi, and bacteria • RNA sequencing was used to look for genes encoding effector-like proteins in *Populus trichocarpa* roots that were in mutualistic symbiosis with the ectomycorrhizal fungus Laccariabicolor [14].
2018	Annotation of *Populus trichocarpa*Micrornas from a Variety of Tissue Sets	• *Populus trichocarpa* is an important woody model organism whose entire genome has been sequenced • This resource has aided in the annotation of microRNAs (miRNAs), which are short non-coding RNAs with important regulatory functions. • To perform miRNA annotation, three separate next-generation sRNA sequencing runs from separate leaves, xylem, and mechanically treated xylem, as well as a fount, were used [15].
2018	Ptnf-Ya9, a Multifunctional Transcription Factor from *Populus trichocarpa,* regulates Arabidopsis seed germination, Abiotic Stress, Plant growth, and development	• NF-YAs have a critical role in abiotic stress. However, their characteristics and actions in abiotic stress have yet to be fully investigated in poplar, a model woody plant • For the first time, the biological functions of *Populus trichocarpa's* PtNF-YA9 (Potri.011G101000), an NF-YA gene, were investigated in depth. PtNF-YA9 exists in the nucleus. • PtNF-YA9-overexpressed Arabidopsis (OxPtNA9) lines displayed sensitivity to drought, ABA, and salinity stress, as well as growth regions, during the germination stage. • PtNF-YA9 not only inhibits plant development, but it also plays a critical role in the acclimation process in response to harsh climatic conditions [16].
2018	Through genome and population sequencing of American and European aspen, functional and evolutionary genomic conclusions on Populus have been made.	• To improve evolutionary and functional genomics investigations in Populus, two aspen species, *Populustremula* L. and *Populustremuloides*Michx, have genome assemblies and population genetics resources. • The two aspen species are widespread in the Northern Hemisphere, where they are important keystone species that support a diverse range of dependent ecosystems and produce a diverse range of secondary metabolites. • A variety of factors, including expression level, co-expression network connectivity, and regulatory variation, influence genetic diversity and molecular evolution patterns in aspen [17].
2019	*Populus trichocarpa* Anatomy and Chemistry with Genetically Modified Lignin Content	• Transgenic *Populus trichocarpa* (black cottonwood) trees were studied for vessel and fibre properties, diameter growth, and chemical compositions after six months of growth in a greenhouse. • When the genetic groups were compared to the wild-type control, trees with lower lignin concentrations were found to have distinct vessel and fiberqualities [18].
2019	Various lines of evidence were used to find new cell wall regulatory genes in *Populus trichocarpa*.	• Understanding the regulatory network controlling cell wall production in Populus trichocarpa is of great interest due to its reputation as a model woody perennial and its relevance for lingo-cellulosic products. • Researchers used an extended network-based Lines of Evidence (LOE) pipeline in *P. trichocarpa* to combine multiple genomics data sets, including gene co-expression, gene co-methylation, population-level pair-wise SNP correlations, and two distinct SNP-metabolite Genome-Wide Association Study (GWAS) layers, to find genes with putatively unknown roles in regulating cell wall biosynthesis [19].
2020	Genomic Diversity Evaluation of *Populus trichocarpa*Germplasm for Rare Variant Genetic Association Studies	• Genome-wide association studies are effective techniques for determining the genetic basis of phenotypes. A vast number of people and a wide range of genetic variations must be researched to explain the majority of the observed heritability of phenotypic traits. • Large-scale genome-wide genetic variation discovery is now possible thanks to advances in high-throughput technology and cost-effective genome-wide genetic variation discovery.

		• It was observed that there are unique and common small genetic differences across individual genomes using a pre-filtered data set of 1,014 pure *Populus trichocarpa* complete genomes [20].
2020	**Sequencing and Analysis of the Sex Determination Region of *Populus trichocarpa***	**• The ages and sizes determination of a sex-determination region is difficult in a non-model species. The quality of assembly with short sequencing reads is universally low because of the scarcity of recombination and the concentration of repetitive regions in SDRs.** **• Several Populus species have male heterogametic sex (XX/XY system) mapped on chromosome 19, although the specific placement of the SDR varies between species, and none of these SDRs have been properly assembled in a genomic context [21].**
2020	**A Genome-Wide Association Study of Populus trichocarpa Wood Anatomical and Morphological Traits**	**• This study published the first detailed GWAS (Genome-wide association studies) for wood anatomical features in Populus, revealing the genes that control functional and structural properties crucial for plant function, stress tolerance and development.** **• Construction of multi-trait sets based on functional interactions and genetic correlations of features in and between anatomical and morphological wood structures [22].**
2021	**Various species and hybrids of Populus (Populus Spp.) leaves were studied for their polyphenolic composition and antioxidant capabilities.**	**• TLC and HPLC-DAD/ESI-MS were used to determine the chemical composition of flavonoid and salicylic compounds in leaves from six species and three hybrids of poplars (Populus)** **• Salicylic compound content was determined using the HPLC-UV method and expressed as free and total fractions on salicin [23].**

CONCLUSION

Populus has been used as an anti-inflammatory, antiseptic, anti-scorbutic, balsamic, febrifuge, diuretic, expectorant, stimulant and tonic for centuries. The improvement of the Populus genome sequence has opened up new options for comparative plant genomics, as proven in this investigation. Further in-depth analysis is currently underway to characterize the active compounds that cause the observed effects and confirm the mechanism. The rising expense of energy and chemical raw materials, as well as major environmental concerns associated with synthetic pharmaceuticals, will undoubtedly make herbal therapies more suitable soon. Populus is getting used as a version for plant genetic studies in this work.

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