Genome-wide repression of extrachromosomal circular DNA in Plants A-Review

Abstract:

Many years ago, scientist's keenly absorbed and pay attention to the Cytoplasmic genes and nucleus Chromosomes. In this era, Scientists also focused on the nucleus chromosomes since 1965. There are a lot of things that are fortunately or unfortunately neglected by the scientific community one is eccDNA. Mostly in the eukaryotic cell exons and eccDNA is a not-rare process. When the sequencing techniques have come into view this is highly appreciated that this eccDNA is due to the repeats again and again in genomic sequence, new and fresh studies and scientists admit that this eccDNA is due to the different regions of the genome taking part to the eccDNA pool. This eccDNA may be extra but plays a role as a DNA in the cell. Sometimes this is very dangerous for the wheat and in some conditions, it is very may be helpful and show their gene expression in the different plants to control their mechanisms such as stress and adaptation, this may also show the phenotypic effect as well as genotypic effect. In this review, we discuss different approaches and technologies that facilitate eccDNA identification and early discoveries in the eccDNA in wheat.

Key Words: DNA, EccDNA, Genome, Centromere, Plants Genomics.

Introduction:

Ecc DNA a well-defined type of circulating DNA that commonly exist in nature and is chromosome -independent. Extrachromosomal circular DNA was firstly discovered by BASSEL AND HOTTA in 1964 and researcher called it double minutes (DMs). EccDNA was firstly identified in wheat embryos and boar sperm(Li et al., 2022a).That is found in nucleus of cell plants and animals in

UNDER PEER REVIEW

eukaryotes. Ecc DNA is originate from chromosomal DNA. The size range of ecc DNA is, in length, 50 base pair to several mega –base pair , and this can encode full length genes and regulatory elements(“Extra chromosomal Circular DNA,” 2023).EccDNA mostly found in repetitive sequence, genic fragment, and intergenic regions in plants. Initially in weed crop Amaranthus palmeri 400-kb eccDNA founded (*Kiad380.Pdf*, n.d.). Ecc DNA is a type of gene amplification that carry complete information of genes including promoters and enhancer elements specifically oncogenic driver genes that are often contribute in tumor growth. In mouse cells, ecc DNA is discovered in 1978 that led to gene amplification of dihydrofolate reductase (DHFR) and arbitrate the methotrexate resistance in mouse cell. Researcher found that, DMs contribute 30% in etc. DNA. Their abundance is related to number of copies of genome(Li et al., 2022a).

In eukaryotic cells, the mostly circular DNA present in the chromosome, which is not part of the chromosome, but this is the eccDNA that have also attached with the histone which is inside the nucleus. Histone is vast important for the gene expression in the eukaryotic cells. Lysine methylation (histone) is used for the controlled the gene expression in plants. The eccDNA has been find in 1965 in wheat and some other crops, eccDNA is not too easy see with simple and compound microscopy so to see eccDNA by the electron microscopy. They displayed a heterogeneous size distribution, with a mean contour length ranging from 0.1 m to more than 5 m for T. aestivum. Compared to the distribution of short circular DNA in mitochondria, this distribution is very different. Additionally, using a quick microscale technique called mica-press adsorption for electron microscopy, small polydisperse circular (SPC) DNA/protein complexes were discovered. The size distribution of spcDNA/protein complexes was comparable to that of cccDNA. Over a hundred spcDNA/protein complexes were thought to be present on average in each nucleus. Discussion is had over the biological purposes and origin of nuclear circular DNAs(Kinoshita

UNDER PEER REVIEW

et al., 1985). Large quantities of cccDNA molecules were created using the traditional CsCl/ethidium bromide density gradient centrifugation technique, while tiny quantities of spcDNA/protein complexes were created using the quick microscale mica-press adsorption for electrons. Here, we refer to the recent broad classification to describe eccDNA as all the circular DNA in a plant cell, including, but not restricted to, small polydisperse circular DNA (spcDNA), extrachromosomal telomeric circles (t-circles), microDNA, double minutes, and extrachromosomal DNA (ecDNA). This avoids ambiguity and inconsistency between the numerous terms used to describe eccDNA(Liao et al., 2020). EccDNA is a common component of organism genomes that results from the combining of genomic fragments from many chromosomes. Their quantity and genomic copy number are correlated.

Repression:

The detection of eccDNA is firstly done by method of electron microscopy and inverse PCR amplification of LTR-LTR junction. By advance sequencing technologies, eccDNA detection method is useful with the tools of bioinformatics .circular sequencing for eccDNA is a first method of high – throughput that was developed for yeast that lead to illumine sequencing. The drawback of these tools were that they required a reference genome as an input file form and not applicable on plant data. For identification of origin of genome on basis of distribution of reads split reads coverage and discordant mapping by method of ECC splorer basis on short read. By using long reads, analysis of eccDNA is possible by CIDER-seq2. For plant tissue data, ecc-finder is another method. This can be used for both long and short read data and run in form of both reference genome and reference free method. For mobilization of monitoring past active well known transposing TEs in rice, tomato and Arabidopsis, eccDNA identification was very useful(*Fpls-13-1080993.Pdf*, n.d.). By tandem repeats, eccDNA is formed in plants. The assembly of

UNDER PEER REVIEW

genome depend upon the callus subline. By using REPEATE XPLORER analysis are performed for identification of eccDNA enriched in sample in ecDNA LIBRARIES. Like active elements, eccDNA reads Have LTR-RT. Recently many analysis shows that, eccDNAs fractions that derived from repeats is proportional to the repeats present in genome, as from random Damage of DNA eccDNA formed. The good indicator of the mobilization is an over-presence of reads that derived from LTR-RTs group in library of eccDNA(*The Plant Journal - 2022 - Kwolek.Pdf,*.).

Formation of the eccDNA in wheat:

EccDNAs seem to originate from random locations in the genome of cells that are mitotically dividing. Since hypoxia and chromosomal splitting (chromothripsis) can increase the amount of eccDNA in eukaryotic cells, DNA damage followed by DNA repair appears to be a significant source of circularization(Shoshani et al., 2021). Additionally, it has been proposed that mistakes in DNA replication might result in DNA circularization. Thus, it is believed that other processes exist in addition to DNA repair. The proportional contributions of different routes to this mechanism during DNA repair are less clear. Knowing the sequence of DNA surrounding the junction point of a circle, from which a specific DNA repair mechanism may be deduced, helps to partially overcome this. A high degree of homology between the recombined ends suggests the use of a homology-based repair process, such as mismatch repair, homologous recombination, or micro homology-mediated end joining (MMEJ) (MMR) (Dillon et al., 2015).On the other side, little to no homology suggests that circularization was aided by non-homologous end joining (NHEJ). While mechanistic studies have linked each of these pathways to the formation of eccDNA, the proportions of eccDNA formed by the various pathways likely depend on the type of cell, the organism, and the stage of the cell cycle that the damage occurs in the cell cycle damage take place.

UNDER PEER REVIEW

Circular extrachromosomal DNA: a multifaceted history:

Circular DNA has been given several various titles because it was independently extracted from a wide range of species and cell types. Following James Gaubatz's guidelines, we shall refer to extrachromosomal circular DNA (eccDNA) to ensure uniformity in terminology. Regardless of size, complexity, or content, this word refers to any chromosome-derived circular DNAs found inside eukaryotic cells, including ecDNA (extrachromosomal DNA), which is the name for mega-base sized eccDNA in to- mours with one or more genes and visible under a light microscope (Verhaak et al., 2019). Nomenclature: In addition to names for individual eccDNAs, names are occasionally required to designate discrete eccDNA. According to their locus of origin, we have thus far documented the genotypes of circularized genes, including [CUP1circle] and [HXT6-7circle] for circular DNA in yeast and [TTNcircle] for circular DNA in humans. Like how prions are denoted, non-chromosomal inherited material is denoted by square brackets (Ter-Avanesyan et al., 2005). Alternately, circles may be denoted using chromosomic coordinates like if nucleotide resolution is required. Professor Yves Barral also suggested using the letter "" to denote circular DNAs, for example, during the symposium "Circular DNA in development and illness" held in Berlin in January 2020, when this nomenclature was also presented. The symbol for diameter, a key element of every circle, is Ø.

What role do eccDNAs play in rapid adaptation as tools for gene amplification?

UNDER PEER REVIEW

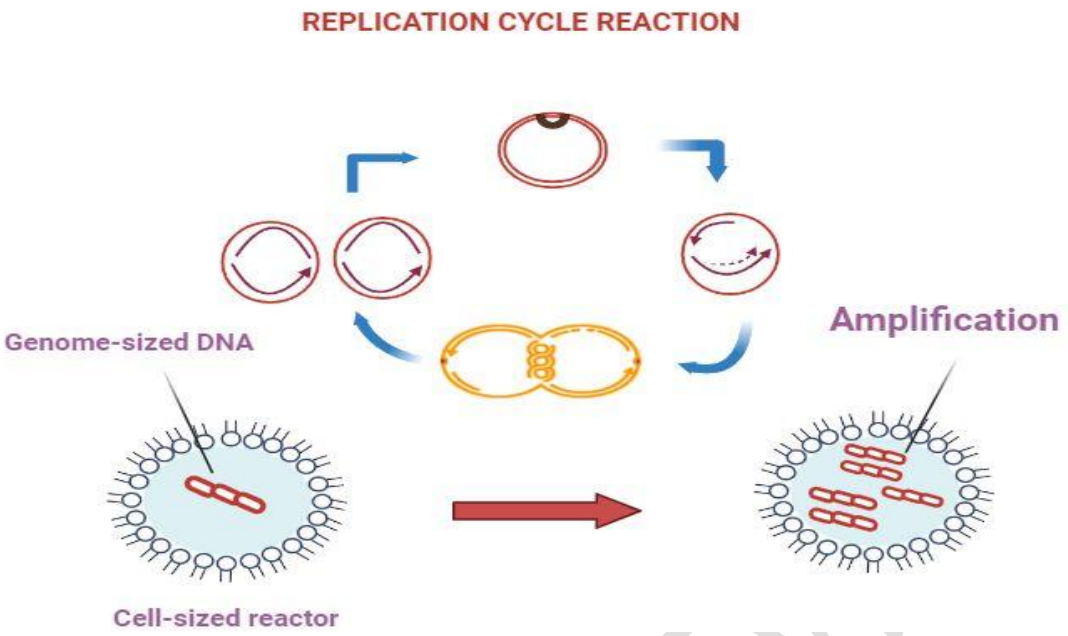

Fig 1; Replication cycle of EccDNA

Even while eccDNAs in plant genomes have been known to exist for a while, we have just recently begun to have a more comprehensive repertory of genomic sites that create eccDNA. But there are still a lot of unanswered concerns concerning the biogenesis and use of eccDNA. What are the eccDNA biogenesis's favorable and unfavorable regulators? Do feedback loops exist that prevent excessive accumulation? If so, how can a plant know how much eccDNA there is? Forward genetic mutant screening for eccDNA accumulation in Arabidopsis may yield useful information to help with these inquiries. Additionally, candidate gene techniques that concentrate on DNA repair may be useful, even if they have had mixed results in the past. (Møller et al., 2015).It is noteworthy that the genomic rDNA copy number for yeast revealed a substantial negative link to the amount of rDNA-derived eccDNA. (Sinclair & Guarente, 1997). Double strand breaks and DNA circulation in yeast are brought on by the replication fork barrier protein Fob1 binding to the intergenic spacer region of the rDNA. [13] It has been demonstrated that cells with fewer rDNA copies produce more eccDNA in a replication-dependent manner,

UNDER PEER REV

providing evidence that eccDNA may be integrated to increase the amount of rDNA copies(Mansisidor et al., 2018)Notably, a rise in eccDNA coexists with genomic rDNA copy reduction. The existence of comparable systems in plants must be investigated. It appears that telomere rings and loops are frequently involved in telomere maintenance. For instance, research in human cells revealed a significant association between the creation of telomere eccDNA and telomere shortening. EccDNA controls copy number variations. Indeed, the EPSPS-containing eccDNA may also be transmitted to germ cells without the need of chromosomes, leading to inherited glyphosate resistance(Koo et al., 2018).

Formation; Acquisition of ecc DNA:

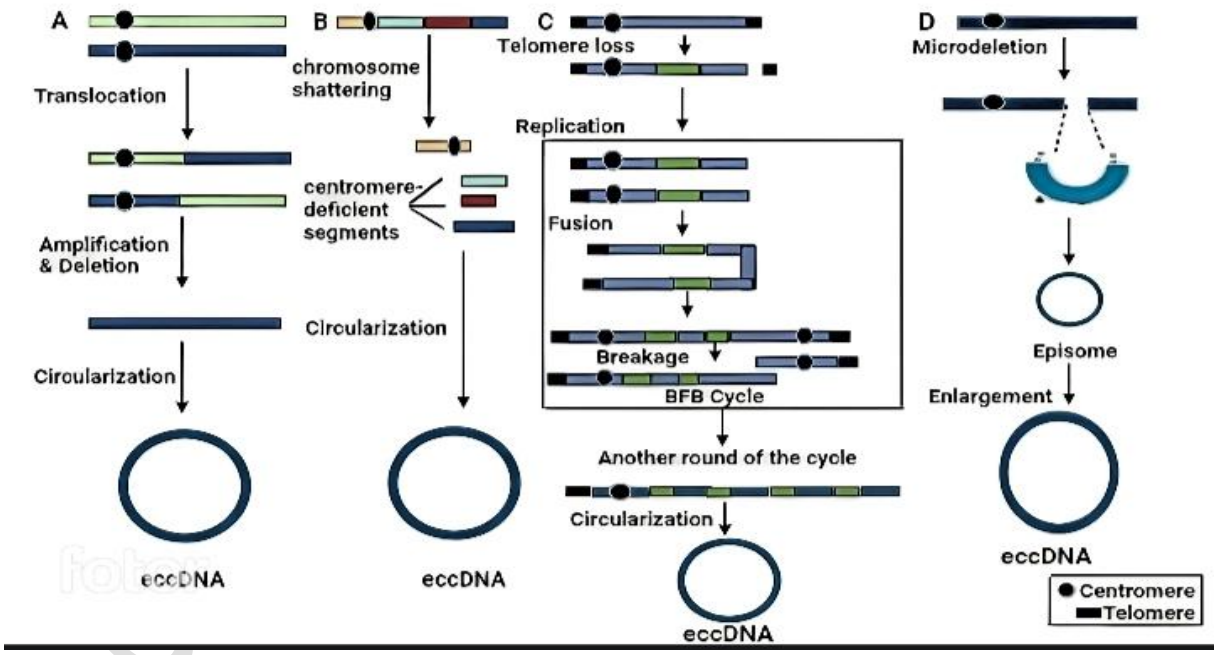

Fig 2; Formation of Ecc DNA

The mechanism underlying the generation of ecc DNA:

There are many ways to generate EccDNA depending upon the context manner. There are 4 different categories of the formation procedure of eccDNA: First one is Homologous Recombination, second one is Non-Homologous end-joining, replication of DNA and R-loops formation (Yang et al., 2022).

We can produce eccDNA from the mediated chromosomes through recombination independent and dependent mechanism. DNA replication is a very important phase in the formation process. Different models of eccDNA acquisition and formation have been proposed including: the Episome model, the Breakage Bridge Fusion model, chromothripsis model and the translocation Deletion Amplification model. We will study these all in detail(Wang et al., 2021a).

Episome Model:

It is one of the old and most widely used model of eccDNA biogenesis. In this eccDNAs can be produced the through the R-loops formation and DNA slippage during the process of DNA synthesis. These newly formed eccDNA are also called episodes. Episome have the ability to replicated themselves and can also be expanded through inserting other components of DNA, like enhancers or promoters and transposable elements(Yang et al., 2022). According to this model the fusion or enlargement of chromosome derived, smaller episomes and other episomes results in the formation of large complex eccDNA(Arrey et al., 2022).

The Breakage- fusion- Bridge Model:

In BFB cycle first of all there will be the telomeres loss in chromosomes. After the process of replication, the chromosomes that are free form telomeres fuse together and make a anaphase bridge that is dicentric. This whole process repeats again and again to enlarge the telomere-free bridges, this will result in the instability of genome which will ultimately release the eccDNAs(Zhao et al., 2022a).

Chromothripsis Model:

In chromothripsis model of eccDNA formation, a catastrophic event occurs which results in the breakage of chromosomes into pieces. Some pieces of DNA are ligated randomly, and most of the fragments are removed through different systems like DNA repair which includes Non-homologous end joining and homologue recombination. During the mechanism of repairing, generation of eccDNA takes place and the loss of their chromosomal segments. From studies it is also revealed that the damage to DNA which is related to this model is also the part of eccDNA biogenesis(Yang et al., 2022).

Translocation–excision–deletion–amplification:

UNDER PEER REVIEW

During the process of gene translocation, the amplification or deletion of fragments occur which are close to translocation positions. The circularization of the fragments of DNA results in the formation of eccDNA(*81412.Pdf*, n.d.). Plants may amp up their genes through a process called translocation-excision-deletion-amplification (TEDA)(*Extrachromosomal Circular DNA: Biogenesis, Structure, Functions and Diseases | Signal Transduction and Targeted Therapy*, n.d.). Once the translocation event arises close to a gene, this process takes place, and the segment next to the crossing site may get amplified, deleted, or circularized. Extrachromosomal circle DNA, or eccDNAs, are generated from fragmented or maintained DNA fragments that are created following DNA damage repair. The amplification of MYC and ATBF1 in SJNB-12 the cells, where a reciprocal relocation between chromosomes 8 and 16 occurs followed by deletion and deletion close to the translation breakpoint, supports the TEDA explanation (Cao et al., 2021a).

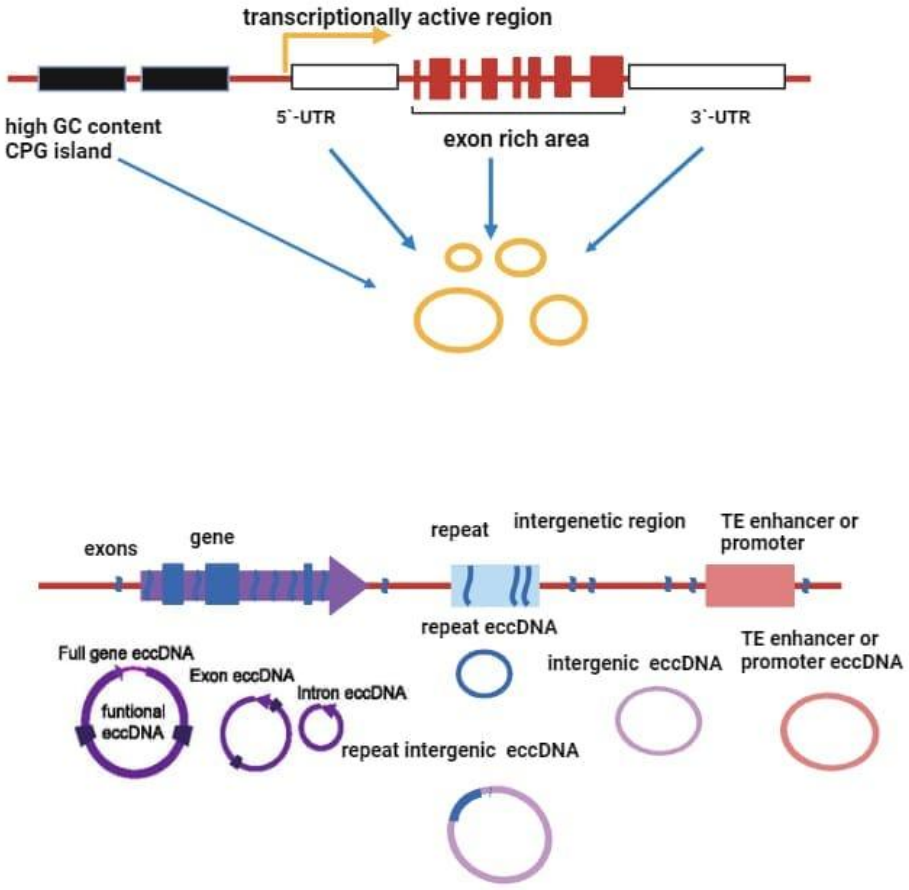

Fig 3; Translocation–excision–deletion–amplification

Sources of eccDNA in plants:

In eukaryotic plants ecDNA is present in prokaryotic region organelles like chloroplast and mitochondria that are evolved through endosymbiosis. Some of the viruses also need extra-34 behavior to maintain themselves. While in prokaryotes eccDNA is maintained in the form of Plasmids. These plasmids encode some non-essential genes and in few conditions such genes can be helpful. To spread these plasmids bacterial colonies will be used through the process of horizontal transfer of genes(*10.4*, 2016).

Repetitive Genome Sequences are the point of origination of all founded eccDNAs, most importantly taken from ribosomal DNA, which were being organized in a large form of tandem repeats. In wheat, 40kb long 18S Rdna have formed large circles(Peng et al., 2022a).

Implication of ECC DNA Repression:

In TEs mobilization eccDNA act as marker but its role is still undisclosed in TE mobilization. Plants are sensitive to alterations in gene copy number that sometimes results in gene silencing. Interaction is found between eccDNA and DNA methylation by some studies. Like DNA methylation inhibits methyl transferase that results in reducing DNA methylation and it enhance rDNA eccDNA formation by recombinations. Equivalently reduction in DNA methylation by inhibitors results in LTR-RTs bursts(Peng et al., 2022b).

Influence On gene Expression and Transcription regulation:

Many kinds of eccDNA may alter to each other to execute distinct regulatory functions to look towards environmental stress. They found that micro DNA plays part in gene silencing. It may hinder gene expression (Khan & Khan, 2022a).DNA recombination was monitored by introducing DNA by in vivo alteration(Fromm & Walbot, 1987).

Impact on genome Stability and mutation rates:

UNDER PEER REVIEW

Herbicide resistance in plants is improved by existence of eccDNA. Genomic changes are caused by eccDNA by guiding gene amplification as well as by activation of cis regulatory elements on same chromosome. It also contribute in oncogene expression by adjusting transcription. For gene expression eccDNA perform well as transcriptional element like promotor/enhancer. Expression of RNA regulated by transcription is also a key function of eccDNA. Fluorescence in situ hybridization is utilized to view eccDNA placement and highly aggregated eccDNA is observed known as eccDNA hubs. These hubs are major sites of oncogene transcription. Alteration of gene copy number for somatic cell genotypes are affected by eccDNA from gene rich regions of chromosome(Li et al., 2022b).

Role In plant development evolution and stress response:

In plants for stress resistance and evolution eccDNA plays an important role to transfer resistance genes for herbicides in crop weed that results in quick glyphosate additionally eccDNA was observed in C.elegans germ line and a t as genetic material by offspring(Zuo et al., 2022a).Herbicide resistance to glyphosate by gene amplification as eccDNA is developed in plants by Amaranths palmeri.In germ cells circular molecules are introduced to develop resistance by adaptive evolution and genome plasticity. Bt promoting DNA, retrotransposons that produce eccDNA are introduced to genome for improvement against environmental stress(Cao et al., 2021b).

Future prospective and challenges:

Regulatory mechanism of eccDNA in disease development need to investigate. Due to limited tools for eccDNA analysis, advanced methods are essential to develop. For diagnostic and prognostic biomarkers are used. EccDNA also play an important role in therapeutics for disease treatment(Zhao et al., 2022b). Prospects for fundamental and applied studies on eccDNA in plants are

UNDER PEER REVIEW

presented in the future. Further investigation is necessary in fundamental research to fully understand the development of eccDNA, its biological activities, and its participation in many pharmacological and pathologic procedures. In conclusion, eccDNA is a characteristic shared by all plants. It also plays a part in transmissible herbicide resistance and supports several processes related to DNA transcription, DNA replication, and other activities. Prospects for fundamental and clinical research on eccDNA in plants are presented in the future.

Emerging teachings for studding eccDNA:

Research on eccDNA is still at the stage of identification and discovery. In order to identify and discover eccDNA, it is often necessary to evaluate the type and content of eccDNA. Yet nearly all techniques for purification and enrichment of eccDNA depends on its circular structure. Cells and tissues from DNA are identified and isolated, linearized DNA is deleted by nuclease without damaging its circular DNA and it is expanded by rolling loop amplification. After that eccDNA is assessed by examining copy number variation and circular DNA sites with double terminal sequencing. In plants eccDNA identification by automation processes includes DNA extraction, mapping assembly and mapping, clustering and assemble(Khan & Khan, 2022b).

Examination of technological procedure for eccDNA in plants by HTS includes DNA extraction, continues DNA molecules are elaborated by rolling circular amplification. After debranching DNA segments are offered short read sequencing and long read sequencing. Assembly and algorithms of cluster and mapping sequencing are utilized for short read sequencing by analyzing eccDNA loci(Peng et al., 2022c).

Unanswered questions and research gaps:

UNDER PEER REVIEW

Despite repeated regions eccDNA begins from additional loci also it is effective for TEs assembly. Yet role of eccDNA In TE assembly is undisclosed so it appears that they may act as side product of eccDNA and are bring together by plant defense mechanism. Now no sign found that either any circle that appears in plant can also fuse to genome. Besides we were not sure that molecular structures are involved in plant cell deration. In conclusion we became aware of TE repression. Many stresses exhibit well secure link was found between mammalian cells and yeast eccDNA(Peng et al., 2022b).

Potential application and implication of eccDNA manipulation:

In last few years, main focus of scientific research is eccDNA and its contribution in extensive biological actions. It appears that contrasting types of eccDNA owns well defined tasks. Beyond gene regulation if biological purpose is known for eccDNA it was guided to explain epigenetic mechanism under common and pathological condition. Other application of eccDNA involves results in replication, deletion, translocation of gene and mutation, dominating to genetic heterogeneity and evolution. They also act as useful character in cell physiology when transferred under cells(Wang et al., 2021b).

Significance:

In mammal's cells and tissues, eccDNA are very small to carry coding genes of protein. For different biological groups, eccDNA are potential markers for difference. EccDNA are mutation elements commonly in NSCLC. In NSCLC tissue, eccDNA are commonly found. EccDNA are originated mainly from region of itergenic,intron and exon(*S13059-017-1265-4.Pdf*, n.d.). EcDNA-mediated gene amplification is one type of genome plasticity that can propel the process. This may result in many gene copies, which may have different impacts on the phenotypic of the plant(Pereira & Dunning, 2023). The majority of ecDNA in plants is made up of repeated sequences, which may also be found

UNDER PEER REVIEW

in repeating satellite DNA and the centromere portions of chromosomes. The function and stability of ecDNA in plants may be affected by its repeating nature(“Extrachromosomal Circular DNA,” 2023b). Gaining more knowledge about the role ecDNA plays in plants might help us better understand plant variety, adaptability, and its uses in genetic engineering and agricultural enhancement. EccDNA plays a very crucial role in the heterogeneity and development of mutant uncontrolled cells. The evolution of different methods for detection of eccDNA include sequencing and microscopic approaches, has enhanced the knowledge the of role of eccDNA in evolution. It also promotes oncogene expression by the increase in the copy number and the interaction between chromosomes and act as a reservoir for the recombination of DNA by rebuilding into and being cut off from chromosomes. EccDNA promotes the expression of oncogene by hijacking enhancers. It forms the hubs of eccDNA and interact with the chromosomal DNA for the oncogene regulation. It is the storage place for the DNA recombination.(Dong et al., 2023) To study the aging yeast is a model organism, the eccDNAs cause aging in the yeast cells by accumulating in old cells(“Extrachromosomal Circular DNA,” 2023c).

Removal and degradation of ecc DNA:

Double-stranded circular DNA that originates from and is not associated with chromosomes is known as extrachromosomal circular DNA, or eccDNA. It is prevalent in all eukaryotes, including plants, and has been found in both normal and cancerous cells(*Extrachromosomal Circular DNA: A Neglected Nucleic Acid Molecule in Plants - ScienceDirect*, n.d.). Though research on other organisms has led to certain theories, the removal and destruction of eccDNA in plants is not fully understood. With the exception of those that may self-amplify, the majority of eccDNA quickly degrades. It's unclear exactly how eccDNA amplification works(Zuo et al., 2022b). In various circumstances, it has been proposed that enzymes such as TREX1, three prime, and Plasmid-safe

UNDER PEER REVIEW

ATP-dependent DNAse are involved in the breakdown of eccDNA(Paulsen et al., 2018). Potential processes for the destruction of eccDNA have been proposed, including DNA recombination and rearrangement. For instance, eccDNA synthesis may be inhibited by eliminating ADF (an enzyme generated by caspase-activated DNase, endonuclease G, or DNase γ), suggesting that ADF is a need for eccDNA synthesis(Li et al., 2022c).Ageing cells are known to collect eccDNA. With cellular senescence, the process that keeps eccDNA out of the nucleus eventually breaks down, causing a huge buildup of eccDNA in the nucleus. More research is needed to fully understand the mechanisms of eccDNA removal and degradation in plants. In eukaryotic cells, two main processes that break down the majority of cellular proteins are autophagy and proteolysis.(Raffeiner et al., 2023) In eukaryotes, autophagy is a highly evolutionarily conserved degradation system that targets and selectively breaks down intracellular bacteria and viruses (xenophagy), excess endoplasmic reticulum (reticulophagy), ribosomes (ribophagy), protein aggregates (aggrephagy), peroxisomes (pexophagy), damaged mitochondria (mitophagy), and mid-body ring structures.(Liu et al., 2016) On the other side, misfolded and short-lived proteins are broken down by the ubiquitin-proteasome system (UPS).(Raffeiner et al., 2023) The UPS and autophagy are two parts of the protein quality control system that depend on one another. Autophagy is enhanced by protease shortage, but autophagy inactivation affects the UPS because it produces too much p62. Proteasel substrate delivery is delayed as a result, although catalytic activity is unaffected. Some people think that the proteasome can be activated by genetically or pharmacologically inhibiting autophagy. In eukaryotic cells, there are two main processes that selectively break down various components such as protein aggregates, peroxisomes, damaged mitochondria, intracellular bacteria, viruses, excess endoplasmic reticulum, ribosomes, and mid-body ring structures. These mechanisms are called autophagy and proteolysis. Because of their intricate and context-

UNDER PEER REVIEW

dependent interaction, autophagy and the UPS are crucial for preserving the quality of proteins(Liu et al., 2016).

Exonucleases and Endonucleases In ecc DNA Degradation in Plants:

It is known that macromolecules including proteins, lipids, and nucleic acids are broken down during plant leaf senescence in order to be reabsorbed into the higher tissues(*Nucleases in Higher Plants and Their Possible Involvement in DNA Degradation during Leaf Senescence | Journal of Experimental Botany | Oxford Academic*, n.d.). It is believed that this process involves nucleases, which are enzymes that cleave phosphodiester links between nucleotides in nucleic acids(*Nucleases in Higher Plants and Their Possible Involvement in DNA Degradation during Leaf Senescence | Journal of Experimental Botany | Oxford Academic*, n.d.). Nonetheless, it is still unknown exactly what physiological function nucleic acid degradation—specifically, the breakdown of genomic DNA—serves. Several endonucleases (BFN1, CAN1, and CAN2) and an exonuclease (DPD1) in Arabidopsis have been demonstrated to be induced at the mRNA level and are believed to be implicated in the case of DNA degradation during leaf senescence(*Nucleases in Higher Plants and Their Possible Involvement in DNA Degradation during Leaf Senescence | Journal of Experimental Botany | Oxford Academic*, n.d.). This points to DPD1 as a possible target for understanding nucleotide salvage in plants and implies a major role for organelle DNA degradation during leaf senescence. Endonucleases break phosphodiester bonds inside a nucleic acid strand, whereas exonucleases are a kind of nuclease that cleaves phosphodiester bonds at the end of a nucleic acid strand(*Nucleases | Exonucleases and Endonucleases - YouTube*, n.d.). Nucleic acid strands from the 5' to 3' or the 3' to 5' end can be broken down by exonucleases. DPD1 is an example of a DnaQ-like exonuclease that mostly breaks down double-stranded DNA (dsDNA) and is dependent on magnesium ions to function. Overall, even though it is believed that nucleic acid

UNDER PEER REVIEW

degradation happens during plant leaf senescence, nucleases may play a function in this process that should be carefully examined, and further study is required to completely understand the physiological significance of DNA degradation in this process.

Conclusion:

Ecc DNA is a chromosome-independent type of circulating DNA found in nature, originating from chromosomal DNA. Initially discovered in wheat embryos and boar sperm, it is found in cell nuclei of plants and animals. Ecc DNA can encode full-length genes and regulatory elements, and is mostly found in repetitive sequences, genic fragments, and intergenic regions in plants. It is a type of gene amplification that carries complete information of genes, including promoters and enhancer elements, particularly oncogenic driver genes that contribute to tumor growth. In 1978, ecc DNA was discovered in mouse cells, leading to methotrexate resistance. EccDNA, a type of circular DNA found in eukaryotic cells, is attached to histones in the nucleus, which is crucial for gene expression. In plants, lysine methylation controls gene expression. EccDNA was discovered in 1965 in wheat and other crops, but its size distribution is difficult to see with simple and compound microscopy. Electron microscopy revealed small polydisperse circular DNA/protein complexes, which differ from short circular DNA in mitochondria.

ETHICS APPROVAL:

Not Applicable

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UNDER PEER REVIEW

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