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Genome-wide Repression of Extrachromosomal Circular DNA in Plants: A Review

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Authors' contributions

This work was carried out in collaboration among all authors. Author UA created and wrote the protocol. Authors AH and BF collected the data and prepared the materials. Authors AH and BF wrote and prepared the original draft. Authors SB, AA and MA literature researched and contributed a lot to the replication portion of the ECC DNA. Authors KS, AZ and IE wrote the final part of the manuscript which is about exonucleases and endonucleases in ECC DNA degradation in plants. Author AH managed references and citations. All authors read and approved the final manuscript.

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Review Article

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ABSTRACT

Many years ago, scientists keenly absorbed and paid 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.

Keywords: DNA; EccDNA; genome; centromere; plants genomics.

1. INTRODUCTION

Ecc DNA is a well-defined type of circulating DNA that commonly exists in nature and is chromosome-independent. Extrachromosomal circular DNA was first discovered by BASSEL AND HOTTA in 1964 and researchers called it double minutes (DMs). EccDNA was first identified in wheat embryos and boar sperm [1]. That is found in the nucleus of cells plants and animals in eukaryotes. Ecc DNA originates from chromosomal DNA. The size range of ecc DNA is, in length, 50 base pairs to several megabase pairs, and this can encode full-length genes and regulatory elements [2]. EccDNA is mostly found in repetitive sequences, genic fragments, 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 carries complete information of genes including promoters and enhancer elements specifically oncogenic driver genes that often contribute to tumor growth. In mouse cells, ecc DNA was discovered in 1978 that led to gene amplification of dihydrofolate reductase (DHFR) and arbitrate the methotrexate resistance in mouse cells. Researchers found that DMs contribute 30% of etc. DNA. Their abundance is related to the number of copies of the genome [1].

In eukaryotic cells, the mostly circular DNA is present in the chromosome, which is not part of the chromosome, but this is the eccDNA that is also attached to the histone which is inside the nucleus. Histone is vast important for gene expression in the eukaryotic cells. Lysine methylation (histone) is used the control the gene expression in plants. The eccDNA was found in 1965 in wheat and some other crops, eccDNA is not too easy to see with simple and compound microscopy so see eccDNA 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 cDNA. 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 [3]. Large quantities of EccDNA 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 (EccDNA). This avoids ambiguity and inconsistency between the numerous terms used to describe eccDNA [4]. 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. With advanced sequencing technologies, the eccDNA detection method is useful with the tools of bioinformatics Circular sequencing for eccDNA is the first method of high–throughput that was developed for yeast that led to illumine sequencing. The drawback of these tools was that they required a reference genome as an input file form and did not apply to plant data. For identification of the origin of the genome on the basis of the distribution of reads split reads coverage and discordant mapping by the method of ECC explorer 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 the 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 the genome depends upon the callus subline. By using REPEATE XPLORER analyses are performed for the identification of eccDNA enriched in samples in ecDNA LIBRARIES. Like active elements, eccDNA reads Have LTR-RT. Recently many analyses have shown that eccDNA fractions that are derived from repeats are proportional to the repeats present in the genome, as from random Damage of DNA eccDNA formed. A good indicator of the mobilization is an over-presence of reads derived from the LTR-RTs group in the 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 [5]. 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 microhomology-mediated end joining (MMEJ) (MMR) [6]. 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.

Circular extrachromosomal DNA: a multifaceted history: Circular DNA has been given 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- hours with one or more genes and visible under a light microscope [7]. 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 [8]. Alternately, circles may be denoted using chromosomic coordinates 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.

2. WHAT ROLE DO ECCDNAS PLAY IN RAPID ADAPTATION AS TOOLS FOR GENE AMPLIFICATION?

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.

However, 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 [9]. It is noteworthy that the genomic rDNA copy number for yeast revealed a substantial negative link to the amount of rDNA-derived eccDNA [10]. 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. [11] It has been demonstrated that cells with fewer rDNA copies produce more eccDNA in a replication-dependent manner, providing evidence that eccDNA may be integrated to increase the number of rDNA copies [12] 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 for chromosomes, leading to inherited glyphosate resistance [13].

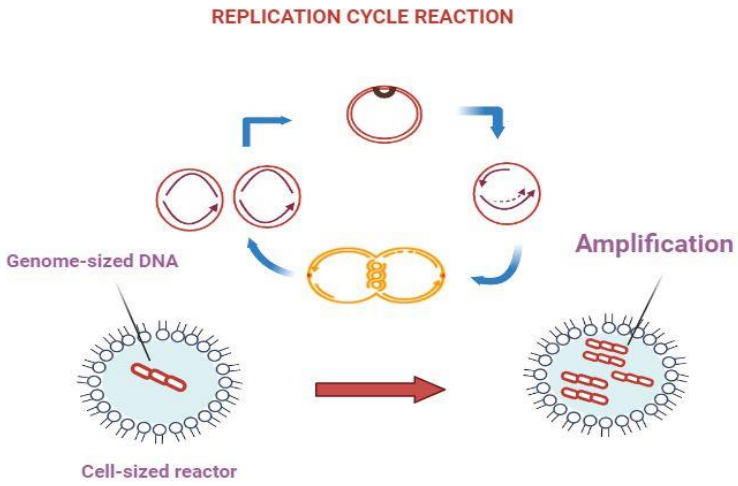

Fig. 1. Replication cycle of EccDNA

Formation; Acquisition of ecc DNA:

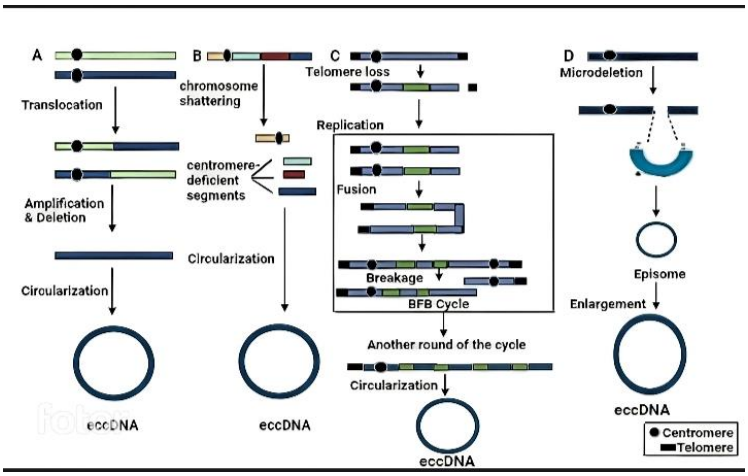

Fig. 2. Formation of Ecc DNA

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: The first one is Homologous Recombination, the second one is Non-Homologous end-joining, replication of DNA, and R-loops formation [14].

We can produce eccDNA from the mediated chromosomes through recombination-independent and dependent mechanisms. 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, the chromothripsis model, and the translocation Deletion Amplification model. We will study these all in detail [15].

Episome model: It is one of the oldest and most widely used models of eccDNA biogenesis. In this eccDNAs can be produced through the R-loops formation and DNA slippage during the process of DNA synthesis. These newly formed eccDNA are also called episodes. Episomes can replicate themselves and can also be expanded by inserting other components of DNA, like enhancers or promoters and transposable elements [14]. According to this model, the fusion or enlargement of chromosome-derived, smaller episomes and other episomes results in the formation of large complex eccDNA [16].

The Breakage- fusion- Bridge model: In the 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 and make a dicentric anaphase bridge. This whole process repeats again and again to enlarge the telomere-free bridges, this will result in the instability of the genome which will ultimately release the eccDNAs [17].

Chromothripsis model: In the 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 homolog recombination. During the mechanism of repairing, the 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 part of eccDNA biogenesis [14].

Translocation–excision–deletion–amplification: During the process of gene translocation, the amplification or deletion of fragments occurs 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 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 [18].

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 a 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 was organized in a large form of tandem repeats. In wheat, 40kb long 18S Rdna have formed large circles [19].

Implication of ECC DNA Repression: In TE mobilization eccDNA acts as a 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 in 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 [20].

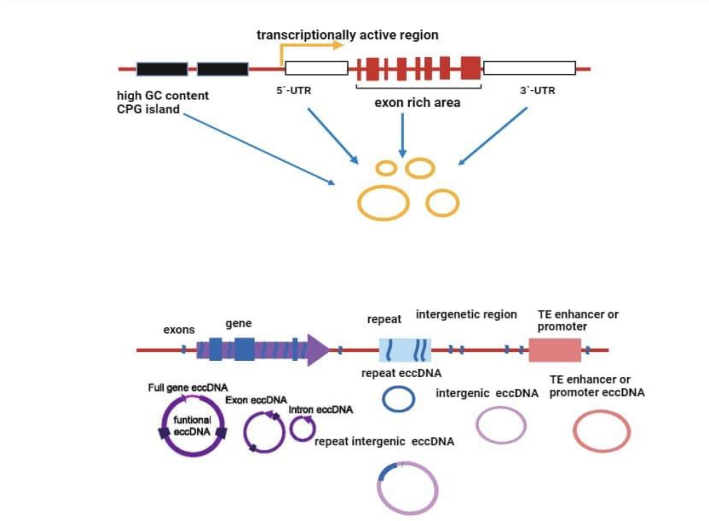

Fig. 3. Translocation–excision–deletion–amplification

Influence on Gene Expression and Transcription Regulation: Many kinds of eccDNA may alter each other to execute distinct regulatory functions to look towards environmental stress. They found that microRNA plays a part in gene silencing. It may hinder gene expression [21]. DNA recombination was monitored by introducing DNA by in vivo alteration [22].

Impact on genome Stability and mutation rates: Herbicide resistance in plants is improved by the existence of eccDNA. Genomic changes are caused by eccDNA by guiding gene amplification as well as by activation of cis-regulatory elements on the same chromosome. It also contributes to oncogene expression by adjusting transcription. For gene expression, eccDNA performs well as a transcriptional element like a 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 numbers for somatic cell genotypes is affected by eccDNA from gene-rich regions of chromosomes [23].

Role In plant development evolution and stress response: In plants for stress resistance and evolution eccDNA plays an important role in transferring resistance genes for herbicides in crop weed that results in quick glyphosate additionally eccDNA was observed in the C.elegans germ line and a t as genetic material by offspring [24]. 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. By promoting DNA, retrotransposons that produce eccDNA are introduced to the genome for improvement against environmental stress [25].

Future prospective and challenges: The regulatory mechanism of eccDNA in disease development needs to be investigated. Due to limited tools for eccDNA analysis, advanced methods are essential to develop. Diagnostic and prognostic biomarkers are used. EccDNA also plays an important role in therapeutics for disease treatment [26]. Prospects for fundamental and applied studies on eccDNA in plants are presented in the future. Further investigation is necessary for 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 studying eccDNA: Research on eccDNA is still at the stage of

identification and discovery. 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 depend 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 assembly [27].

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 [28].

Unanswered questions and research gaps: Despite repeated regions eccDNA begins from additional loci also it is effective for TE assembly. Yet the role of eccDNA In TE assembly is undisclosed so it appears that they may act as a side product of eccDNA and are brought together by plant defense mechanism. Now no sign found that any circle that appears in a plant can also fuse to the genome. Besides, we were not sure that molecular structures are involved in plant cell duration. In conclusion, we became aware of TE repression. Many stresses exhibit well secure link between mammalian cells and yeast eccDNA [20].

Potential application and implication of eccDNA manipulation: In the last few years, the main focus of scientific research has been eccDNA and its contribution to extensive biological actions. It appears that contrasting types of eccDNA own well-defined tasks. Beyond gene regulation, if the biological purpose is known for eccDNA it was guided to explain epigenetic mechanisms under common and pathological conditions. Another application of eccDNA involves results in replication, deletion, translocation of genes, and mutation, dominating genetic heterogeneity and evolution. They also act as useful characters in cell physiology when transferred under cells [29].

Significance: In mammal cells and tissues, eccDNA is very small to carry coding genes of protein. For different biological groups, eccDNA are potential marker for difference. EccDNA are mutation elements commonly in NSCLC. In NSCLC tissue, eccDNA is commonly found. EccDNA originated mainly from the region of intergenic, 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 phenotype of the plant [30]. The majority of ecDNA in plants is made up of repeated sequences, which may also be found 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 [31]. 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 the detection of eccDNA including 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 [32]. To study the aging yeast as a model organism, the eccDNAs cause aging in the yeast cells by accumulating in old cells [33].

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. Except those that may self-amplify, the majority of eccDNA quickly degrades. It's unclear exactly how eccDNA amplification works [34]. In various circumstances, it has been proposed that

enzymes such as TREX1, three prime, and Plasmid-safe ATP-dependent DNAse are involved in the breakdown of eccDNA [35]. 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 [36]. 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. [37] 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 [38]. On the other side, misfolded and short-lived proteins are broken down by the ubiquitin-proteasome system (UPS) [37]. 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. Protease substrate delivery is delayed as a result, although the catalytic activity is unaffected. Some people think that the proteasome can be activated by genetically or pharmacologically inhibiting autophagy. In eukaryotic cells, two main processes 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-dependent interaction, autophagy and the UPS are crucial for preserving the quality of proteins [38-42].

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 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 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 [43-47].

3. 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 the 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 about 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.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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