Extrachromosomal circular DNA in cancer
history, current knowledge, and methods
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Extrachromosomal circular DNA (eccDNA) is a closed-circle, nuclear, nonplasmid DNA molecule found in all tested eukaryotes. eccDNA plays important roles in cancer pathogenesis, evolution of tumor heterogeneity, and therapeutic resistance. It is known under many names, including very large cancer-specific circular extrachromosomal DNA (ecDNA), which carries oncogenes and is often amplified in cancer cells. Our understanding of eccDNA has historically been limited and fragmented. To provide better a context of new and previous research on eccDNA, in this review we give an overview of the various names given to eccDNA at different times. We describe the different mechanisms for formation of eccDNA and the methods used to study eccDNA thus far. Finally, we explore the potential clinical value of eccDNA.

Healthy human somatic cells contain 23 pairs of chromosomes in the form of long, linear, condensable chromatin fibers. Besides the mitochondrial genes, our chromosomes contain all the genetic information needed for a cell to carry out all functions. During mitosis, all chromosomes are replicated once and the resulting sister chromatids are equally segregated, ensuring the formation of two genetically identical daughter cells.

This normally tightly regulated mechanism is often disrupted in the genomes of cancer cells. Cancers progress by a sequence of mutational events including nucleotide substitutions, translocations, and gene copy number gains or losses that result from an environment of genomic instability [1]. One of the most common genetic changes in tumorigenesis is oncogene copy number gains [2], leading to overexpression of oncogenic gene products, which provides the cancer cells with growth advantages. The mechanisms leading to oncogene amplification are not thoroughly understood, although it is widely acknowledged as an underlying cause of cancer development. A major challenge for current cancer therapies such as chemotherapy is the development of resistance to therapeutic drugs, ultimately leading to therapy failure. Therapeutic resistance depends on biological properties such as tumor heterogeneity, cell populations with stem-cell-like properties, regulation of the therapeutic target molecules’ expression, and activation of prosurvival pathways, which can all result from gene amplification [3].

Circularization of otherwise linear chromosomal DNA is one of the keys to understanding how gene amplifications arise. Circular DNA molecules, which are not plasmids, are found in the nuclei of all eukaryotic cells studied. This eccDNA has been described in the scientific literature under various names, which are covered below. eccDNA sequence content is homologous to the nuclear chromosomal DNA, which it derives from [4–9]. eccDNA can vary in size from less than 100 bp to several megabases, and can contain any element found in the human genome from small, noncoding regions to entire genes [7–9]. eccDNA was observed for the first time in boar sperm and wheat embryos in 1964 when Hotta and Bassel investigated using electron microscopy the extrachromosomal DNA in the nuclei of spermatids and embryos.
microscopy the theory that chromosomes of higher organisms are made of DNA circles [10].
Later in the 1960s and 1970s, eccDNA was observed in filamentous fungi and yeast as well as
birds and a variety of mammalian tissues, suggesting that eccDNA is a common phenomenon in eu-
karyotic cells [5]. The majority of eccDNA identified in these studies was too small (<500 bp) to contain
whole protein-coding regions [11]. In cancer cells, much larger extrachromosomal DNA structures
were discovered at approximately the same time through staining and light microscopic examination
of metaphase chromosomes [12]. These structures were initially denoted double minutes (DMs) due
to their small size (in relation to chromosomes) and distinct pairing in metaphase. DMs were large
enough that their circular structures were observed by light microscopy [13]. Later, sequencing of
the junction points supported the circularization relative to the linear chromosomal sequence [6].

Pioneering work from Wahl and others revealed how oncogenes are amplified on DMs in tumors [4].
The close link between eccDNA and most cancers has recently become even more clear. In an
influential paper from 2017, it was revealed how a large proportion of tumors from different cancer
types carry megabase-size eccDNA, specifically called ecDNA [8]. This was complemented by
reports showing how ecDNA evolves in different cancers of neurological origin [14,15] and how
tumors with ecDNA amplifications of some oncogenes are associated with higher mortality [16,17].

Although cancers can carry many eccDNAs in different sizes and with different genetic elements,
according to some reports [7,16,18], most research has focused on the large ecDNAs that
amplify genes, including oncogenes [4,8,14,19]. We still have little understanding of how mixtures
of thousands of different eccDNAs arise in tumors and affect cancer progression, and whether
eccDNA can be used as a cancer biomarker. In this review, we first give an overview of how
eccDNA was discovered and named several times in different scientific contexts. We then
describe the current knowledge of how eccDNA is generated and maintained in cells. We
describe the methods used in the field and finally discuss the potential use of eccDNA as a marker
for diagnosis, prognosis, and treatment of cancer.

Nomenclature and definitions

ecDNA

Historically, eccDNA has been isolated by a number of methods and in many different organisms
and cell types, which has led to a number of different names. eccDNA was suggested as a term to
cover all nuclear, extrachromosomal circular DNA of endogenous chromosomal origin in 1990 [5].

Covarley closed circular DNA

In the earliest literature describing eccDNA, the term covalently closed circular DNA was some-
times used. This was used to describe all known double-stranded circular DNA including viral
genomes, bacterial plasmids, mitochondrial DNA, and eccDNA [5,20], but the term is now mostly
used in the field of virology.

Small polydisperse circular DNA

The name small polydisperse circular DNA (spcDNA) was first used to describe eccDNA isolated
from HeLa cells by density separation from the chromosomal DNA and visualized by electron
microscopy in 1972 [11]. spcDNA was used to describe eccDNA at the smaller end of the size
spectrum (<100–10 000 bp) until the 2000s. The name comes from their heterogeneous size
distribution and sequence content [5,11]. spcDNA was described as mainly containing repetitive
genome sequences [5], although this could reflect the limited DNA sequence analysis methods
available at the time rather than the true frequency of repeat sequences on spcDNA. It was
found to be common in normal eukaryotic cells, but much more abundant in genetically unstable
cells such as cancer cells and cells from patients with Fanconi’s anemia [21,22].
microDNA
The term microDNA arose in 2012 when small, circularized DNA were isolated from mouse and human cell lines by density purification [7]. The vast majority of these were determined to be between 200 and 3000 bp [23]. Thus, the terms microDNA and spcDNA cover circular DNA molecules with similar sizes and physical properties. Sequencing of microDNA revealed that they arise from all parts of the genome, though microDNA from the 5’ and 3’ termini of genes and regions with a higher GC content appears to be overrepresented when compared to the whole genome [7].

The functions of microDNA and spcDNA in eukaryotic cells are not well-elucidated. The small size of these DNA molecules makes them unable to carry full protein-coding gene sequences and promoter regions. A 2019 study found that microDNA can express functional small regulatory RNA, including microRNA (miRNA) and small interfering RNA [24]. The authors also found that microDNA molecules could be transcribed without a canonical promoter. These results suggest that microDNA can regulate gene expression through transcription of regulatory RNA. Although the formation of microDNA is common in healthy individuals, the length distribution of microDNAs varies in different sample types such as tissue, plasma, or cancer cell lines [9,25,26].

Telomeric circles
Telomeric circles are a specialized group of eccDNA that have been found to be important in immortalization of telomerase-negative cancers though the alternative lengthening of telomeres (ALT) mechanism [27]. Telomeric circles serve as templates for telomere elongation and the ALT mechanism is reported to be responsible for telomere maintenance in 10–15% of all cancers [28]. Telomeric circles are found in the form of t circles, which are fully double-stranded and contain telomeric repeats, or c circles, which have a partially single-stranded C-rich region. Electron microscopy has shown that the telomeric circles vary in size from 100 to 30 000 bp [29]. ALT has been observed in a variety of tumors including osteosarcoma, soft tissue sarcoma, glioblastoma multiforme (GBM), renal cell carcinoma, adrenocortical carcinoma, breast carcinoma, non-small cell lung carcinoma, and ovarian carcinoma [27].

DMs
Large eccDNA in the megabase range was first described by Cox et al. in 1965, when they examined metaphase spreads of chromosomes from childhood cancer cells by light microscopy and discovered small, paired chromatin bodies, which they named DMs [12]. DMs are a DNA species without recognizable telomeres and centromeres [4,30] and serve an important role in oncogene amplification and overexpression. They tend to accumulate in malignant tumor cells when they amplify genes that provide a growth advantage [4].

Episomes
In the 1980s, it was observed that tumor cells also contain autonomously replicating circular DNA in the submicroscopic size range. These could still be large enough to carry whole genes, and they were named episomes [31]. Episomes were isolated by denaturation and renaturation of DNA and visualized by gel electrophoresis. This work led to the development of an episome model in cancer genetics that states that episomes are formed by excision of linear DNA from chromosomes followed by circularization and amplification [4,32–34].

ecDNA
Next-generation sequencing (NGS)-based studies have in recent years allowed scientists to study the sequences of circular DNA from tumors in-depth. This also led to a new definition of mega-base-pair amplified circular DNA in cancer, namely ecDNA [8]. ecDNA with oncogenes is reported in a broad variety of tumors and in 46% of cell lines from 17 different cancer types.
ecDNA appears to be especially common in GBM and prostate, breast, lung, and renal carcinoma, as well as melanoma [8].

In the following text, we use eccDNA as the common term for all previously defined classes of eukaryotic, nonmitochondrial, and nonplasmid extrachromosomal circular DNA. ecDNA will be used as the term for the cancer-specific subset of large eccDNA with oncogenes, rather than DMs. Since small eccDNA and ecDNA are generally studied separately, many findings from the literature can only be considered valid for one of these subsets. In the following text, we have therefore chosen to differentiate between what is known about formation, functions and clinical relevance for small eccDNA and ecDNA, respectively.

**Formation and maintenance**

**Formation**

A number of models exist for how eccDNA is formed in human cells. They often involve damage to the chromosomal DNA and erroneous actions by different DNA repair pathways. For example, two double-strand breaks (DSBs) in the same chromosome can result in a stretch of DNA deleted, which could become circularized (Figure 1A), or secondary DNA loop structures formed in several processes, for example, mismatch repair (MMR) (see Glossary), could be excised and circularized [35–37]. Therefore, the mechanisms for eccDNA formation can be different depending on how and where chromatin is subjected to damage and which DNA repair mechanisms are active in a given cell.

In several studies, eccDNA were sequenced and their junctions were examined for evidence of which DNA repair mechanisms were likely to have generated them. Junctions that indicate where an eccDNA has formed can indicate whether they were formed by DNA repair mechanisms dependent on homology or not. eccDNA formed between regions with no homology is likely to have formed through nonhomologous end joining (NHEJ) (Figure 1A) [38], which has been observed in several studies of eccDNA and ecDNA in the eukaryotic model organism Saccharomyces cerevisiae (baker’s yeast) and human cancer cells [6,35,36,39,40]. To directly validate that eccDNA can be generated by DSBs, the clustered regularly interspaced short palindromic repeats (CRISPR)/Cas9 method was used to create two DSBs in the same chromosome. Subsequently, endogenous eccDNAs of various sizes were formed and the formation happened in regions without homology [41]. There are also reports of eccDNA forming between regions with high homology, potentially through homologous recombination (HR) [36,42–45]. The newer reports of this were all studies in S. cerevisiae, but this was also observed in early human cell studies as reviewed by Gaubatz in 1990 [5]. eccDNA formed by HR is expected to be rare, since HR is primarily active in mitosis and most healthy mammalian cells are postmitotic, where NHEJ is the primary repair mechanism for DSBs. The studies in S. cerevisiae indeed suggest that HR contributes only a minority of eccDNA, but that eccDNAs formed by HR form repeatedly from the same loci [36,42–45].

NGS-based studies of eccDNA may underestimate HR effects. This is because sequence reads from repetitive DNA are often filtered out in bioinformatics analysis because they are difficult to accurately map to the human genome. Human eccDNA from repetitive regions has been estimated in a few studies, after removal of all linear DNA. One study indicated that DNA repeat sequences are slightly more common in eccDNA compared with the whole human genome (72% of eccDNA to 52% of the genome) [46], while another indicated that they had occurrences of repeat elements at the same level as the whole genome [35].

A complementary approach to determine how eccDNA forms is to measure it in cells deficient in different DNA repair proteins. In two studies, deficiency of genes involved in MMR has been
(A) DSBs

- Damage
- Deletion
- Repair
- Circularization
- Junction
- Fusion
- Chimeric eccDNA (and ecDNA)

(B) Chromothripsis

- Centromere
- Telomere
- Chromothripsis
- Reassembly and circularization
- ecDNA

(C) BFB cycle

- Centromere
- Telomere
- Telomere loss and replication
- Fusion
- Bridge
- Multiple BFB rounds
- HSR
- ecDNA

(See figure legend at the bottom of the next page.)
shown to result in a decreased amount of eccDNA in chicken lymphoma and human cancer cells [35,37]. In the most recent of these, deficiency of genes involved in damaged DNA resection and microhomology-mediated end joining (MMEJ) also resulted in decreased eccDNA amounts [37]. In cells lacking proteins essential for NHEJ, both decreased and increased amounts of eccDNA have been reported [22,37,47]. These results might be explained by the different methods used for quantification or a context- or cell-type-dependent role of NHEJ. Thus, proteins from the DNA damage repair pathways MMR, NHEJ, and MMEJ, and DNA resection prior to repair are indicated to be involved in eccDNA formation at least in some cell types. In these studies, cells with defective HR, single-strand annealing repair, base excision repair, and nucleotide excision repair were found to have unchanged amounts of eccDNA compared to wild-type cells [35,37].

When profiling eccDNA in cancer cells, it has been observed that sometimes their size distribution displays clear peaks in a periodicity of approximately 200 bp [18,25]. This is reminiscent of the ladder pattern observed in linear DNA from apoptotic cells, which reflects the breakdown of chromosomal DNA into fragments corresponding to one or more nucleosomes. Recently, it was demonstrated that inducing apoptosis in mouse embryonic stem cells indeed massively increased their amounts of eccDNA [48]. When sequenced, the apoptosis-induced eccDNA displays the characteristic size distribution peaks and originates from genetic loci found evenly across the whole genome. The increase is dependent on the apoptotic enzymes DNase 1 and DNA ligase 3, confirming that apoptotically fragmented DNA is indeed converted to eccDNA.

In a study of telomeric circles, collapse of replication forks in telomeric DNA with single-strand breaks was shown to induce the formation of c circles [49]. In S. cerevisiae, re-replication and oligonucleotide-stimulated DNA amplification have also been suggested as sources of eccDNA [50,51], although none of these mechanisms has been tested in mammalian cells.

DNA damage is also suggested to be an initial step in the formation of ecDNA, while less is known about the pathways that lead to their circularization. Circularization could be mediated by the DNA repair pathways also involved in forming small eccDNA, as described previously. In some cases, ecDNA is suggested to arise by multistep processes, potentially from smaller precursors [32,40]. In others, large-scale DNA damage events have been proposed as the sources of ecDNA in cancer. Chromothripsis is one such single-step catastrophic event involving multiple DSBs, which in essence shatters a whole chromosome into small pieces. Repair of the chromosome is then attempted by error-prone DNA repair mechanisms, leading to many different genetic errors [52,53]. In several studies, chromothripsis was shown, directly or indirectly, to lead to ecDNA formation (Figure 1B). When human chromosomes were pulverized in a process similar to chromothripsis in human–rodent hybrid cells, new stable ecDNAs were generated [54]. Furthermore, analysis of whole-genome sequencing (WGS) data from human cancers and chemotherapy-resistant clonal...
cell lines have suggested that chromothripsis is an important driver of cancer genome rearrangements including ecDNA formation [55,56].

A breakage–fusion–bridge (BFB) cycle is another type of event known to lead to severe genetic aberrations in cancer cells. The BFB cycle starts with a DSB in a chromosome such that it loses a telomere. The chromatid ends lacking telomeres can fuse to form a dicentric chromosome. At anaphase, the dicentric chromosome is pulled apart to form a chromatid bridge that breaks and generates a variety of chromosomal aberrations, including ecDNA (Figure 1C) [2,56]. Although BFB cycles and chromothripsis have historically been considered separate types of events, recent studies have suggested that they are mechanistically linked, in the sense that chromothripsis can be caused by consecutive rounds of BFB cycles [56,57] (Figure 1B,C).

Evolution
Several studies suggest that ecDNA can evolve over time. This was first proposed by Wahl and coauthors [4,31]. This was also observed in several later studies, generally showing that smaller ecDNA can gradually increase in size over time by fusing with, for example, other ecDNA (Figure 1A). In several recent studies chimeric ecDNA, consisting of several noncontiguous chromosomal DNA segments, has been detected, which also supports an evolutionary process after the initial formation event [14–17,48,58].

The gradual fusing of smaller ecDNA has been suggested as a formation mechanism for ecDNA. Later in its evolution, ecDNA has been demonstrated to integrate into chromosomes to create regions of gene amplifications known as homogeneously staining regions (HSRs) [32,59,60].

Maintenance
Maintenance in cells has mainly been described for ecDNA. During mitosis, chromosomes are replicated once and then pulled apart at the centromeres by the mitotic spindle. This process ensures an equal distribution of chromosomes in the two daughter cells. ecDNA molecules have also been shown to replicate once per cell cycle [61], but unlike normal chromosomes and ring chromosomes, these elements lack recognizable centromeres [62], and they are thus not segregated evenly by the mitotic spindle. Their dynamic behavior during the segregation process has been studied in cell models, where it has been shown that they ‘hitch-hike’ during segregation by tethering to the ends of chromosomes furthest away from the mitotic spindle poles [63–65]. Their distribution in daughter cells after cell division is highly variable from cell to cell and has been suggested in separate studies to follow either a binomial random distribution or a Gaussian distribution [65,66].

This uneven segregation can lead to accumulation of ecDNA molecules with oncogenes in subpopulations of cells, accelerating cancer progression, and increasing tumor heterogeneity with daughter cells that contain increasingly amplified copy numbers of the oncogene [64,66] (Figure 2). Thus, some daughter cells can achieve survival and proliferation advantages as discussed further in Box 1. ecDNA amplification elevates oncogene copy number faster than chromosomal amplification [8], which can promote the further propagation of ecDNA. Similar observations have been made for S. cerevisiae, where maintenance of, for example, nutrient transporter genes on ecDNA provides selective advantages in nutrient limiting conditions [45]. Loss of ecDNA has been observed as a result of DNA damage, induced by, for example, hydroxyurea. They have been observed to aggregate in micronuclei and eventually be extruded from cells [67,68].

The mechanisms of replication, segregation, and loss of small ecDNA from cells are not well described. In one recent study, it was observed that cells had reduced ecDNA levels immediately
after mitosis, indicating that at least a proportion of the eccDNA did not replicate [37], and would therefore have been lost from cells over time.

**Methods for descriptive and functional studies on eccDNA**

**Methods from the pre-NGS era**

In the first report describing eccDNA from 1965, eccDNA was isolated as a fraction of DNA using sedimentation in a sucrose gradient and the circular structure was visualized by electron microscopy [10]. This launched a new field and led to investigation in other mammals, including humans. Larger DMs were discovered using light microscopy by Cox et al. using human tumor biopsies [12]. Southern blotting showed that eccDNA was homologous to genomic DNA [5,69,70]. In situ hybridization and later **fluorescence in situ hybridization (FISH)** enabled scientists to distinguish extrachromosomally amplified oncogenes from those on chromosomal DNA in preparations of metaphase chromosomes from cancer cells [71,72]. This use of FISH is exemplified by a study of cells from a transplanted tumor, showing how the oncogenes MYC and EGFR were amplified on circular elements early in tumor development and later integrated into chromosomes to form HSRs [3]. In the 1990s, 2D gel electrophoresis was used to separate eccDNA from chromosomal DNA based on their different physical properties, such as supercoiled and relaxed states [73].
NGS methods

NGS-based methods have undergone technological advances in the recent years and have been the primary drivers of the recent research into eccDNA. These methods allow for the analysis of the sequence content of these DNA elements in-depth and to map their structure relative to the reference genome (Figure 3).

When a certain eccDNA is highly amplified in a cell population, it will be apparent as a copy number amplification in WGS data. The presence of soft-clipped reads spanning the circle junctions as well as discordant read pairs are features that can be analyzed by bioinformatics algorithms to determine whether amplifications are circular (Figure 3A) [74,75]. In a series of papers, WGS data has been analyzed for these features to identify amplified ecDNA and...
Chimeric eccDNA detection with paired-end short reads

Chimeric eccDNA detection with long reads

See figure legend at the bottom of the next page.
techniques such as FISH and electron microscopy used to confirm their extrachromosomal status and circular structure [8,19,76]. Further features of ecDNA have been studied by overlapping the genomic coordinates of circular amplicons with whole-genome assays of chromatin accessibility, methylation and 3D contacts and comparing to the features of linear amplicons [14,15,76,77].

WGS data will generally only reveal eccDNA and ecDNA that are highly amplified (Figure 3A). As a different approach, a method called Circle-Seq enables genome-scale screening for eccDNA of all sizes and is not dependent on their copy numbers [36,78] (Figure 3B). In this method, circular DNA is first separated from linear DNA by denaturation under alkaline conditions and renaturation. Next, any remaining linear DNA is removed using an exonuclease to degrade DNA from free ends. Finally, the remaining circular DNA undergoes rolling-circle DNA amplification to increase the signal before NGS. The method is highly sensitive and has uncovered thousands of eccDNAs in S. cerevisiae, pigeon, healthy human tissue, and neuroblastoma [9,16,36,46]. Although it can reveal more individual eccDNAs in tumors than WGS can, the Circle-Seq method is less accurate at determining copy numbers of unique eccDNAs, since the rolling-circle amplification method has a bias towards amplification of smaller eccDNA molecules [9,79]. In some studies, better quantification has been achieved by foregoing rolling-circle amplification for transposase-based tagmentation during NGS library preparation, which achieves more linear amplification [26,48].

The aforementioned strategies for eccDNA detection have mainly been applied to short-read, paired-end sequencing datasets. However, short reads have limitations in accurately identifying complete eccDNA and ecDNA structures. In several studies, long read sequencing methods have been applied to perform de novo assembly of eccDNA structures. This allows for more confident identification of repeat-containing and chimeric eccDNA; that is, those consisting of several noncontiguous genomic sequences [15,16,19,48,58] (Figure 3C).

Sequencing of DNA from cells and tissues in bulk provide an average of eccDNA content across a population of cells and does not reflect cell-to-cell heterogeneity, even though this is expected to be high (Figure 2). Single-cell sequencing has the potential to address questions on this in great detail, although the likely low amount of eccDNA in single cells could be technically challenging, as it has been for other variations such as copy number variations and single-nucleotide variations [80].

**Imaging**

In addition to FISH, which is based on sequence-specific probes and can only be applied to dead cells, other microscopy techniques were developed for imaging ecDNA. Epstein–Barr virus vectors and plasmids have been used to specifically recombine with ecDNA to introduce lac operator repeats that are specifically bound by a lac repressor–green fluorescent protein (GFP) fusion protein...
This method enables visualizing ecDNA independently of sequence content and imaging ecDNA in live cells.

Recently, a technique using catalytically dead Cas9 and guide RNAs with binding sites for fluorescent reporter molecules was used to image specific ecDNA in live cells based on guide RNAs targeted towards their breakpoint sequences [66]. This technique thus enables sequence-specific imaging of ecDNA in live cells and contributed to the discovery of transcriptionally active hubs of ecDNA in cancer cells [66].

Imaging of ecDNA independently of sequence has historically been done by electron microscopy [10,11,82]. However, the recent advances in microscopic methods allows for high resolution microscopy of fluorescently labeled ecDNA with structured illumination microscopy [58] and ecDNA in its native form with atomic force microscopy [83].

**Cell model systems**

Many cancer cell lines with defined oncogenes amplified on ecDNA exist [8,17]. The isogenic colorectal cancer cell lines COLO320-DM and COLO320-HSR each carry an MYC amplification in ecDNA and HSR-form, respectively. These cell lines are frequently used for comparative studies of ecDNA behavior in cancer, as they allow for comparison between chromosomally and ecDNA amplified oncogenes [77,84]. However, to further understand and investigate the functional impact of small ecDNA in cells and tissues, it is also important to develop cell and animal models that mimic these.

A major challenge in the development of models for ecDNA research beyond ecDNA in cancer cells is producing specific ecDNA in vivo and in vitro. EcDNA cannot be produced massively in vitro via typical *Escherichia coli*-dependent DNA cloning workflows, because ecDNAs do not possess prokaryotic replication origins or selection markers. Instead, ecDNA can be directly synthesized. For this, the ligase-assisted minicircle accumulation (LAMA) approach, invented in 2007, can be used to produce covalently closed DNA minicircles [85]. The LAMA method relies on cycles of denaturation, annealing, and ligation, and has been used to synthesize microDNAs that encode small regulatory RNAs with gene-suppression effects [24].

A recent advance has been the application of CRISPR-Cas9 genome editing to generate ecDNA [41]. As described, evidence suggests that endogenous ecDNAs can be produced after DSBs occur in chromosomes [36,37,43]. This event can be modeled by CRISPR/Cas9-mediated introduction of DSBs. Targeting the Cas9 endonuclease to specific genetic sites with guide RNAs is widely used for gene deletions by simultaneous cleavage at two sites in the same chromosome [86]. This gives rise to an extrachromosomal fragment of deleted DNA, which has the potential to be circularized [36]. Based on this principle, the CRISPR-C strategy was successfully implemented in cell culture to produce endogenous ecDNAs ranging in size from a few hundred to millions of base pairs and even ring chromosomes in human cells [9,87] (Figure 4). CRISPR-C is adaptable and efficient, but the long-term stability of CRISPR-C-induced ecDNA in cells is not well characterized [9]. Nonetheless, CRISPR-C is a promising tool for functional investigations of endogenous ecDNA in a broad range of sizes.

**Perspectives for ecDNA in clinical applications for cancer**

Small ecDNA elements have been identified in human plasma in several studies [25,26,88]. Cell-free ecDNA has been detected in plasma and serum from both humans and mice and human lung tumors have been shown to release ecDNA to the circulation [25]. Plasma samples collected prior to tumor resection contained more ecDNA compared with samples from the same patient weeks...
after surgery, suggesting that the eccDNA load in plasma can serve as a marker for cancer. Although the idea is attractive, designing a test for eccDNA in plasma samples to identify tumors and follow their progression is still challenging [89]. This is mainly due to the low quantity of eccDNA in plasma and that methods for their quantification in patients have yet to be developed.

ecDNA has a more significant and functional role in cancer compared with small eccDNA. Since the presence of certain ecDNA in tumors is correlated with an aggressive phenotype and poor prognosis [15–17], it is reasonable to propose that targeting these DNA elements would be a good therapeutic strategy. Several studies have shown that the amount of oncogene-bearing ecDNA molecules can be reduced by drug treatment in cells [90–93]. This was also demonstrated in a study of 16 patients with advanced ovarian cancer, who were prescribed a noncytotoxic oral dose of hydroxyurea, suggesting that this might be a way to target ecDNA and slow cancer progression in patients [94].

In addition to drug treatment, radiotherapy is commonly used to treat certain cancers. The number of ecDNA molecules carrying MYC and MDR1 genes has been shown to be significantly reduced by ionizing radiation in human epidermoid and colon carcinoma cell lines [95,96].

**Concluding remarks**

eccDNA can be formed in human cancer cells by several different mechanisms and can result in amplification of cancer-associated genes. In particular, the uneven segregation of large ecDNA
that happens at mitosis, can lead to a rapid increase in the DNA copy number and protein products of oncogenes. ecDNA promotes greater tumor heterogeneity, malignant phenotype, and development of drug resistance; all of which contribute to poor patient prognosis.

Research in eccDNA has advanced in recent years, relying greatly on different NGS-based technologies. However, model systems to study different kinds of eccDNA functionally in vitro and in vivo still need to be developed to a more mature stage. For this purpose, CRISPR/Cas9-based methods show great promise (see Outstanding questions).

Due to their apparent role in cancer progression, targeting of ecDNA in tumors is a promising therapeutic strategy, but methods to target them specifically need to be developed. eccDNA of all sizes may prove to be an important biomarker for cancer, both for diagnostics and for targeted treatment. Cell-free eccDNA is found in the blood, and although eccDNA can also originate from healthy cells, preliminary evidence indicates that eccDNA in plasma can serve as a cancer-specific biomarker. The research results so far create an opportunity to develop technologies for sensitive, specific detection of eccDNA in both tumor biopsies and plasma samples for directing diagnosis, treatment, and surveillance of cancer.

There has been great progress in our understanding of eccDNA in recent years, but many findings are still novel. Studies of eccDNA in cancer are often based on one or few specific cancer types or a small number of human samples. In the years to come, more extensive research on eccDNA could advance development of novel, eccDNA-based therapeutic strategies to target the most aggressive cancer cell populations, monitor cancer progression via blood tests, and overcome the issue of drug resistance.

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Declaration of interests
The authors declare no conflict of interest.

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