Original Article

Received: 2021-09-15
Accepted: 2021-11-02

BCCR
2021, No 2, Vol 13 :92-104
www.bccrjournal.com

Application of Novel Molecular Biology in Cancer Therapy

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Running head: Molecular biology and cancer therapy

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ABSTRACT

Cancer is a genetic illness that develops for various reasons, including the activation of oncogenes, the failure of tumor suppressor genes, or mutagenesis induced by environmental stimuli. This article was produced using PubMed, Nature, Science Direct, Springer, and Elsevier data. Oncogenes are altered forms of normal proto-oncogenic genes that are important for cell proliferation, development, and regulation. The transformation of a gene to an oncogene is caused by chromosomal translocation or gene mutation due to addition, deletion, duplication, or viral infection. These oncogenes are targeted by medications or the RNAi system to limit malignant cell development. Various molecular biology methods for cancer detection and treatment have been developed, including targeting cancer stem cell pathways for cancer therapy, retroviral therapy, oncogene silencing, and alterations in tumor suppressor genes. Among all the techniques used, RNAi, zinc finger nucleases, and CRISPR have a greater chance of reaching a cancer-free planet.

Keywords: Brain Tumor, Cancer, Molecular Biology, Oncogenes

INTRODUCTION:

Cancer is the leading cause of death worldwide. In many malignancies, essential proteins have been discovered to impact signaling pathways controlling cell cycle progression, apoptosis, and gene transcription [1]. Identifying and developing effective pharmacological treatments for cancer remains a public health problem. Tumors are formed when a single cell undergoes an oncogenic transformation. Some cancers develop the potential to spread beyond their original location. The Rous sarcoma virus might be used to spread solid tumors, such as sarcomas, from one animal to another [2]. This research was created using PubMed, Science Direct, Springer, and Elsevier publications. The databases were searched using the following keywords: Tumor, Cancer, Oncogenes, Proto-oncogenes, Mutagenesis, and Viral Infections.

Oncogenes and cancer development

Oncogenes are genes that promote cancer development, while tumor suppressors prevent cancer formation. IntOGen collects data from large-scale sequencing initiatives to evaluate the importance of cancer genes. Infection with a virus is an uncommon source of oncogene activation in animals. As a consequence of mutations, some proto-oncogenes lose their function and become oncogenes [3, 4].

Viral infection

Researchers generate viral infections by introducing oncogenes into the host chromosomes. It is more likely to cause cancer when it infects a progenitor stem-like cell than a progeny differentiated cell. They believe the virus will prove a helpful tool and a viable method for identifying cancer genesis. Oncology recapitulates ontology for viral content. Viral material may be emperor, but cellular context is essential (Fig. 1) [5, 6].

Cancer and oncogenes

Proto-oncogenes, essential regulators of biological processes, exist in normal cells. These genes might behave as growth factors, cellular signal transducers, or nuclear transcription factors. When these oncogenes are produced, they stimulate cell proliferation and play a critical role in cancer etiology [7]. Next-generation TKis

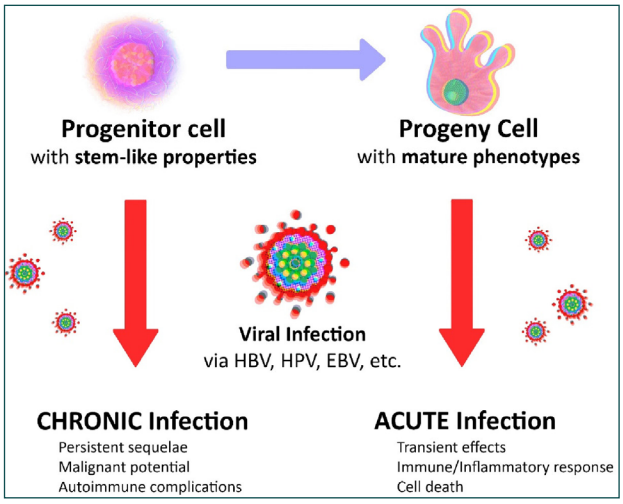

Figure.1. Viruses and cancer. When a virus infects a progenitor cell with stem-like characteristics rather than a progeny cell with mature phenotypes, it is more likely to cause malignant tumors, chronic infections, and autoimmune disorders [5, 6].

are designed to enhance intracranial activity and reduce ROS1-inherent resistance mechanisms. ROS1 is a proto-oncogene that codes for a receptor tyrosine kinase with no known physiological function in humans. Patients may develop intrinsic or extrinsic mechanisms of resistance to ROS1 TKIs. Physical alterations that cause proto-oncogenes to activate can be divided into two categories. Point mutations and chromosomal translocations that create hybrid genes, such as the Philadelphia translocation, are examples of mutations that influence structure (BRC-ABL). Amplification of genes or chromosomal translocation cause increased expression in human malignancies [8, 9]. Inactivated forms of 50 to 60 carcinogenic genes have been discovered in human tumor genomes thus far. Oncogenes are activated by transcription. Gene amplification is the process of integrating numerous copies of an oncogene into a cell (e.g., c-MYC in neuroblastoma) [10].

Oncogene types and classification

Mutations in growth factors cause cancers such as fibrosarcoma, glioma (brain cancer) [11], and osteosarcomas (bone cancer) [12]. These growth factors are thought to be the root cause of many cancers. Five mutations produce oncogenes or dysregulation of these chemicals [13]. The Epidermal Growth Factor Receptor (EGFR) is

a protein found on the skin surface. EGFR mutations are most prevalent in the gastrointestinal tract, breast, and lung malignancies. Mutations can affect many signaling pathways by interacting with other cytoplasmic proteins [14]. Ras and other deregulated GTPases stimulate the MAPK pathway, causing unregulated signaling and cell proliferation, leading to myeloid leukemia. Overexposure to Raf-1 kinase and cyclin-dependent kinases can result in thyroid and ovarian cancer [15, 16].

The role of oncogenes in cancer therapy

Oncogenic malignancies are treated with drugs that inhibit oncogene formation or downregulate signaling oncoproteins [17, 18]. Multiple oncogenic driver changes have been identified in the recent decade, each of which might be a potential therapeutic target [19]. Investigation of KRAS's underlying biology in patients with non-small cell lung cancer (NSCLC) might aid in identifying prospective candidates for evaluating novel targeted drugs and combinations [20]. The overexpression and activation of ABL1 in hepatocellular carcinoma (HCC) lead to poor patient survival [21, 22].

Cancer tumor suppressor genes

In most cancers, tumor suppressor genes (TSGs) are inactivated, resulting in abnormal cell proliferation and malignancy [10, 23]. TSGs that have lost function have been linked to resistance to cancer treatments [24]. Thus, drug resistance substantially impacts the efficacy of anticancer drugs [25].

The function of TSGs

- Tumor suppressor genes have been shown to play essential roles in the following areas:
- Hormone receptors that limit cell growth and proliferation
- Enzymes that play a role in DNA repair
- Checkpoint proteins that stop the cell cycle if DNA or chromosomes are damaged
- Proteins that promote programmed cell death proteins (apoptosis)
- Proteins that control or stop cells from progressing through a certain cell cycle stage [26, 27]

Double agents: tumor suppressors with oncogenic functions

Traditional TSGs are anti-proliferative, recessive, and commonly inactivated or mutated in malignancies [23, 28]. Tumor suppressor genes have various cell functions in vivo and play different roles in cancer etiology [29]. Due to haploinsufficiency, epigenetic hypermethylation, or interaction with numerous genetic and neoplastic processes, specific tumor suppressors may operate as "double agents," performing opposing roles [30]. This indicates a higher proliferative capacity and contributes to cancer etiology (Table 1) [31]. Several instances of a TSG that does not fit the conventional classical behavior and has oncogenic potential have been discovered via research throughout the years (Fig. 2) [31]. Most contemporary molecular treatments attempt to create inhibitors

Classification		Genes
Protein-Coding	Transcription factor	FOXL2[49], RUNX1[50], DNMT1[51], DNMT3A[52], ETS2[53], ETV6[54], EZH2[55], FOXO1[51], FOXO3[10], GLI1[56], HDAC1[57], FOXO4[10], MXI1[58], NOTCH1[59], NOTCH2[50], NOTCH3[60], PAX5[37], RARB[61], SKIL[62], TCF3[63], WT1[43], ZBTB16[64], NR4A3[65], NCOA4[66], KLF4[67], LITAF[68], YAP1[51], SALL4[69], HOPX[70], LHX4[71], FUS[72]
	Kinases	BCR[51], CDKN1B[31], MAP3K8[73], FLT3[74]
	Protein binding	RHOA[75], ECT2[76], IDH1[77], NPM1[63], PHB[78], PML[47], PTPN11[79], SPOP[80], RASSF1[81], ARHGEF12[82], SIRT1[83], SUZ12[84], WHSC1L1[85], WDR11[86], RB1[10], CBL[87],DMBT1[88]
Noncoding RNA (ncRNA)		MIR106A[33], MIR107[34], MIR125B1[35], MIR146A[36], MIR150[37], MIR155[38], MIR17[33], MIR18A[39], MIR194-1[40], MIR194-2[41], MIR196A2[42], MIR20A[43], MIR203A[33], MIR210[44], MIR214[45], MIR222[43], MIR223[46], MIR24-1[47], MIR27A[48], MIR18B[39]

Table 1. List of TSGs with a potential oncogenic role (adapted from TSG2.0)

against oncogenes to target them. Using TSGs to share the therapeutic load with other compounds might be beneficial. TSGs, on the other hand, are reported to be changed more frequently than oncogenes in human malignancies. The presence of two roles offers up additional possibilities while also complicating the approach [32].

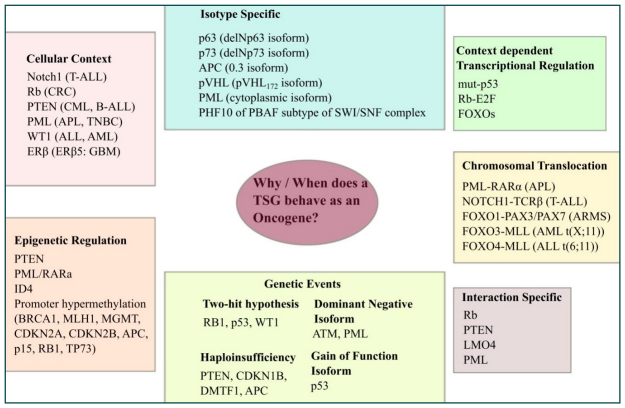

Figure.2. Identification of probable circumstances with examples of candidate TSGs where TSGs do not exhibit conventional tumor-suppressive activity [31]

RUNX family dual role in cancer

Runt-related transcription factor (RUNX) proteins are members of a family of embryonic development master regulators that play a role in proliferation, differentiation, cell lineage specification, and even apoptosis [89]. RUNX proteins may be valuable biomarkers exploited to create cancer early detection methods. The protein RUNX has been found to transform TSGs into oncogenes, causing them to negatively regulate oncogenic processes in patients [90]. This implies that they can activate tumor suppressors while suppressing oncogenes, resulting in a positive tumorigenic activity. Researchers discovered decreased function in two patients with breast cancer in two of the three RUNX genes [91].

Tumor suppressor gene TP53

P53 plays a role in cell cycle regulation and programmed cell death [92]. P53 mutations cause uncontrolled cell growth and poor DNA repair. When p53 detects a break in the DNA, it can either stop the cell cycle or enable the DNA to self-repair [93]. This is accomplished by activating genes involved in cell cycle control and regulation. It is mutated in almost half of all human malignancies, including pancreatic ductal adenocarcinoma (PDAC) (58.7% mutation frequency), esophageal squamous cell carcinoma (93.7%), invasive breast cancer (32.7%), and non-small-cell lung cancer (58.7% mutation frequency) (66.5%). However, point or missense mutations induced by UV radiation, aflatoxins, smoking, or other environmental factors cause the bulk of TP53 gene dysfunctions in sporadic malignancies. Therapeutic methods targeting mutant TP53 have piqued attention due to the high incidence of TP53 mutation in various malignancies [94-96].

BRCA1/2 tumor suppressor gene

Breast cancer-1 (BRCA1) and breast cancer-2 (BRCA2) genes have been linked to familial breast cancer. BRCA1, a tumor suppressor gene, contains 100 kilobits of DNA and 21 exons. It contains a zinc-finger domain comparable to those found in DNA binding proteins. BRCA2 is a tumor suppressor gene as well [97, 98].

Wilms' Tumor 1 (WT1) gene

The Wilms' Tumor 1 (WT1) gene encodes a repressor protein that inhibits the transcription of many growth factor-inducible genes [99]. WT1 is inactive in Wilms' tumor, the juvenile kidney tumors [100]. Inactivation causes a tumor in the immune system [101]. The WT1 gene, overexpressed in Wilms' tumors and contributes to aberrant cell proliferation, targets insulin-like growth factor II (IGF2) [102]. Several investigations in recent years have shown WT1 protein in the cytoplasm of several benign and malignant cancers, indicating its complex regulator activity in transcriptional and translational processes. Although WT1 cytoplasmic staining has been seen in various benign and malignant cancers, it is rare [103].

Tumor suppressor genes and their application

Various techniques may be used to investigate tumor suppressor genes at the DNA, mRNA, and protein levels in normal and malignant cells. Individuals susceptible to retinoblastoma and other cancers might benefit from tests that detect heterozygosity. The growing prevalence of p53 mutations expands diagnostic and analytical possibilities. RNase preservation tests, single-strand structural variation, and denaturing gel electrophoresis can be used to study the alterations. In tumor cell line lysates and tissue homogenates, immunometric methods successfully detect p53 mutations [27, 104].

Cancer diagnosis using molecular pathology

Next-generation sequencing (NGS) helps uncover cancer's actual variety and identify recurrent mutations that may be targeted with novel treatments. Things are not just categorized by morphological and descriptive methods, but by a mix of histopathological and genetic taxonomy [105, 106].

Treatment for cancer back then and today

Different therapeutic techniques and treatments have been utilized to treat cancer. The most commonly used methods are surgery, radiation treatment, chemotherapy, hormone therapy, immunotherapy, adjuvant therapy, targeted-growth signal inhibition, apoptosis-inducing drugs, nanotechnology, RNA expression and profiling, and the most recent, CRISPR. Cancer cells may be destroyed by altering genes or turning off oncogenes. Oncolytic viruses may be used in combination with chemotherapy medicines to destroy cancer cells [95, 107, 108]. This review will go through a few more prevalent approaches later on.

Cancer treatment by targeting cancer stem cell pathways

Cancer stem cells (CSCs) have been regarded as prospective therapeutic targets for cancer treatment since they were initially discovered in leukemia in 1994. These cells can self-renew, differentiate, and play various cancers, including recurrence, metastasis, heterogeneity, multidrug resistance, and radiation resistance [109]. Several pluripotent transcription factors, including OCT4 [110], Sox2 [111], Nanog [112], KLF4 [113], and MYC [114], govern the biological activity of CSCs. Wnt [115], NF-κB (nuclear factor- κB) [116], Notch [115], Hedgehog [117], JAK-STAT (Janus kinase/signal transducers and activators of transcription) [118], PI3K/AKT/mTOR (phosphoinositide 3-kinase/AKT/mammalian target of rapamycin) [119], TGF/SMAD [120], and PPAR (peroxisome proliferator-activated receptor) [121], TGF/ To selectively target CSCs, molecules, vaccines, antibodies, and CAR-T (chimeric antigen receptor T cell) cells have been produced. Some of these components are now being studied in clinical trials. This study outlines CSC classification and identification, displays main determinants and processes that govern CSC growth, and considers possible CSC targeted treatment [109, 112].

CAR treatment is a type of gene therapy

The FDA has authorized Kymriah™, a ground-breaking cancer therapy that inserts the CD19 gene ex vivo into the patient's white blood cells or T cells. Chimeric antigen receptors (CARs) are synthetically designed antigen receptors that reprogram the specificity, activity, and metabolism of T cells in a single molecule. Car-T cell treatment has been related to serious systemic adverse effects that need immediate medical attention and, in rare circumstances, results in patient death. Third-party CAR-T cells that can be used "off the shelf" would allow more rapid and less expensive treatment. [122, 123].

Interference with RNA

RNA interference (RNAi) uses small noncoding RNA that may bind to other mRNAs and inhibit their processing of proteins. RNAi may be employed in cancer therapy to inhibit the activity of cancer genes. In mammals, including humans, endogenous siRNAs have not been discovered. There are no universal pathways for delivering exogenously synthesized RNA to cells in a targeted manner (Fig. 3) [124]. RNAi can knock down numerous target genes, and there are several methods for delivering these genes to the body.

Cancer gene therapy using viral vector systems

Gene therapy is a possible therapeutic method for various illnesses (including hereditary abnormalities, certain forms of cancer, and some viral infections). The method remains hazardous and is being researched to ensure effectiveness and safety. No one delivery technique can treat all cell types [125].

Retrovirus vectors

Retroviruses (RV) are limited RNA viruses with a diploid single-stranded RNA (ssRNA) genome and at least four genes: gag, pro, pol, and env. Replication-competent retroviruses cause malignant illness and some other pathogenic states in various animals. A novel type of retroviral-vector-mediated gene transfer has been revived. The capacity of RV to integrate into the host cell genome increases the risk of insertional mutagenesis and oncogene activation [126, 127].

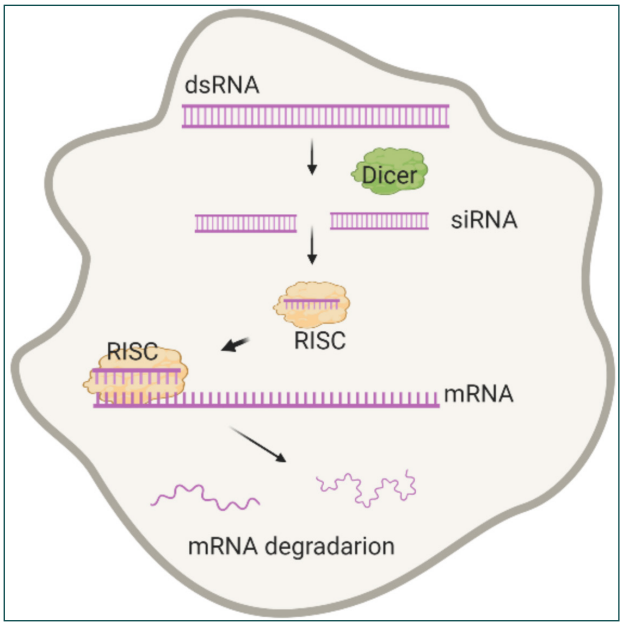

Figure.3. A diagram of RNAi in cells [124]

Lentivirus vectors

Lentiviruses, a kind of RV, have a single-stranded positive-sense RNA sequence translated into DNA and integrated into the host genome, resulting in long-term infection. The overwhelming majority of lentiviral vectors (LVVs) are produced from HIV-1 and can integrate into the genomes of infected cells. LVVs have been used to alter T cells by adding genes to generate immunity to combat cancer by injecting chimeric antigen receptors (CARs) or cloned T-cell receptors [128]. CAR T-cell therapies generated using lentiviral (LVV) stem cells are successful in individuals with B-cell neoplasia. The long-term safety of these treatments is even being researched. While LVV systems are derived from HIV, their dispersion over multiple plasmids and the deletion of many HIV proteins decrease the likelihood of generating HIV-capable virus. Developing LVVs incapable of reproduction in human cells is one way to solve safety concerns [129, 130].

Adenovirus vectors

Adenoviruses (AV) (Fig. 4) are another method for delivering target pieces for dsRNA synthesis. They offer many benefits over lentiviruses [124]. Adenoviruses (AV) are DNA viruses with a double-stranded genome of 34- to 43kb and utilize alternative splicing to encode genes in sense and antisense orientations. Some genetic anomalies associated with AV, such as induced immunity to the AV capsid and low-level AV gene expression, may now help develop anticancer immunotherapies. Because of the combination of AV immunity and the short-expression time, AV may be a feasible vaccine development option [131].

Adeno-Associated Virus (AAV)

Another viral vector utilized in gene therapy is the adeno-associated virus (AAV) [132]. AAV was discovered as a contaminant in a simian adenovirus preparation for

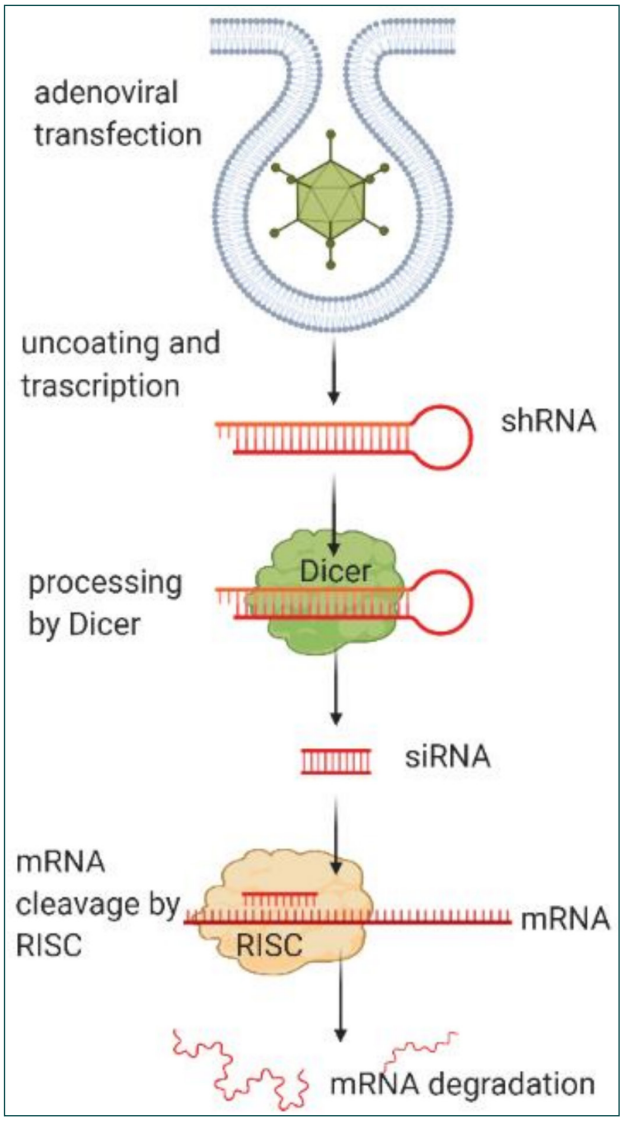

Figure.4. Mechanism of action of adenoviral particle transfection [124]

the first time. The 4.7kb ssDNA within a non-enveloped viral particle contains the p5, p19, and p40 promoters and the rep and cap genes flanked by two 145-nucleotide-long inverted terminal repeats (ITR) [133]. AVR has been discovered as a universal host cell receptor for AAV infections. As a result, AAV is a beneficial method for transducing a specific cell or tissue type. AAV1 has high transduction effectiveness in muscles, neurons, the heart, and the retinal pigment epithelium. Many kinds of cancer cells, neurons, kidneys, retinal pigment epithelium, and photoreceptor cells have been demonstrated to be infected by AAV2. The only serotype capable of infecting and delivering a therapeutic gene to the kidney is AAV2 [134].

Gammaretroviruses

Early gene therapy experiments utilizing gammaretroviral vectors detected the most severe cases of cell proliferation linked with vector integration. These vectors have potent enhancers in the long terminal repeats (LTRs), increasing gene transcription and cell proliferation when integrated near cancer-related genes. The challenge of forecasting pathogenic clonal growth is highlighted by the late cancer start and sudden lymphoproliferation. The pre-leukemic clone with the LMO2 proto-oncogene integration site was never found in more than 2% of the peripheral blood lymphocytes in this patient [135, 136].

Cancer gene therapy using nonviral delivery methods

Nonviral delivery approaches, like proteins, synthetic oligonucleotides, tiny chemicals, and genes have been used to improve tumor-selective delivery of therapeutic medicines [137]. Table 2 lists nonviral delivery methods such as liposomes and polymer-based delivery materials for systemic delivery, physical methods such as electroporation, sonoporation, and others for locally injecting therapeutic molecules, and virosomes for using infectious viral machinery for therapeutic molecule delivery [138].

Genome editing nucleases

Genome editing is a technique that allows humans to use designer endonucleases to edit the target genome and

DDS	Administration	Characteristic properties	Clinical use for cancer
Liposomes [139]	Mainly systemic	1. Delivery efficiency affected by lipid components	Gene and drug delivery to many cancers such as melanoma, glioma, etc
Polymer-based 1. Micelle [140]	Mainly systemic	1. Smaller than liposome and efficient accumulation in tumor	1. Drug delivery to some cancers such as colon, gastric, pancreas, etc.; dependent on the drug
2. Atelocollagen [141]		2. In vivo use only	2. -- 5. Not clinically tested
3. Gelatin [142]	Mainly topical	3. Slow release of therapeutic molecules	
4. Chitosan [143]	Mainly systemic	4. 5. More suitable for gene	
5. PEI[144]	Topical	and siRNA delivery	
Physical 1. Electroporation[145]	Topical	1. High gene expression	1. Gene transfer to melanoma
2. Sonoporation [146]		2. Less invasive than electroporation	2. Not clinically tested
3. Hydrodynamic [147]		3. Limited use for gene delivery	3. Vaccination (melanoma)
4. Gene-gun [148]		4. Gene transfer to the tissue surface	4. Tumor cell vaccine (melanoma, sarcoma)
Virosome [149] 1. HVJ-E [150]	Mainly topical	1. Fusion-mediated delivery, tumor-specific killing, activation of tumor-specific immunity	1. Melanoma treatment using empty vector*
2. HBV [151]	Systemic	2. Hepatocyte-specific delivery	2. Not clinically tested

Table 2. Comparison of different delivery systems

knock out or introduce particular DNA segments within a cell or organism. Early gene-editing relied on an inefficient homologous recombination targeting technique prone to off-target consequences. Zinc Finger Nuclease (ZNF), Transcription activator-like effector nuclease (TALEN), and clustered regularly interspaced short palindromic repeats (CRISPR)-associated are the three main types of CRISPRs used for genome editing [152, 153].

Zinc finger proteins (ZNFs)

These are discovered as DNA-binding domains in eukaryotes. These are made up of 30-amino acid modules organized in the shape of an array of Cys2-His2 DNA-binding zinc fingers. These modules are utilized to create a nuclease domain of FokI. The modules consist of 3-6 zinc fingers that detect nucleotide triplets. The FokI nuclease works only as dimers. Thus, a pair of zinc finger nucleases are required to target any site in the genome. One ZFN will identify the sequence upstream of the genomic area to be changed, and the other will identify the downstream sequence [154]. These arrays attach to adjacent DNA sequences in the opposite strands to cause a double-stranded break in the particular location. The fractures are subsequently repaired in various ways that may produce diverse alterations in the particular area, such as point mutations, indels, or translocations. The ZNFs are specially built to identify all conceivable nucleotides and any particular section of DNA [155, 156].

Coupled to nucleases (TALENs)

TALENs, like ZnF-Ns, have nucleic acid- (DNA or RNA) binding domains on a single polypeptide chain coupled to an endonuclease. TALENs are proteins identified in Gram-negative plant pathogenic bacteria of the genus Xanthomonas. To aid in the infection process, Xanthomonas secretes TALENs into plant host cells through the type III secretion system [157]. Ralstoniasolanacearum and Burkholderiarhizoxhinica, two plant pathogenic Gramnegative bacteria, were subsequently found to possess them[158]. They have minimal structural similarity to ZnF domains. TALENs have the potential to target complicated cancer genes. It cleaves the target gene sequence by dimerizing the TALEN's FokI nuclease cleavage domain. Because it can target any gene in the genome, this gene-editing method may be used to successfully treat cancer cell lines [155, 159].

CRISPR-CAS9 system is a potent tool for cancer genome editing

CRISPR stands for Clustered regularly interspaced palindromic sequences and is a potent genome-editing technique [159]. This ground-breaking technology enables researchers to manipulate every gene (DNA sequence) in any organism's whole genome in vitro or even directly in the genome. It aids in the elucidation of the functional structure of the genome at the systems level, as well as the detection of random genetic variants. The use of technology is critical in early cancer diagnosis [160].

CRISPR-Cas9 mechanism in cancer treatment

CRISPR-Cas9 system has been developed as an immunological response against foreign bacteriophage or plasmid invasion. A repeat-spacer array is integrated into CRISPR to identify and record exogenous DNA or RNA fragments. Transcription and processing of the CRISPR precursor result in mature CRISP-derived RNA (Fig. 5) [161]. CRISPR-cas9 is a valuable technique for identifying genes that might be used as therapeutic targets for cancer. Cancer cells addicted to oncogenes are more susceptible to treatments that target specific driver genes, such as CRISPR and other cutting-edge techniques. A comprehensive library of potential cancer treatment targets has been developed using genome-scale CRISPR-CAS9 screening in 324 cancer cell lines from 30 cancer types [162]. CRISPR-Cas9 is more efficient against tumors with single-gene changes, and it is typically administered in vitro to a specific area. Two different repair methods are used to repair double-stranded breaks or nicks in particular areas. NHEJ is a clumsy repair method that connects damaged ends, resulting in hete-rogeneousindels (insertions and deletions). HDR is a precise repair method using homologous donor template DNA to repair DNA damage [163].

The benefits of CRISPR over traditional methods

The CRISPR target design process is simpler because it relies on ribonucleotide complexes rather than DNA recognition. The method is much less expensive than nu-

cleases since it does not need separate proteins for each target and avoids time-consuming cloning procedures [164]. This method may be used to any sequence in the genome. It outperforms ZFNs and TALENs in terms of efficiency. The RNA encoding Cas protein may be directly injected to change the host genome. Compared to traditional techniques, it is a much quicker and simpler approach [165]. It does not cause DNA methylation sensitivity. Therefore it may be utilized at GC-rich target sites. Using a vast number of gRNAs, multiple genes may be altered simultaneously.

Conclusion and future perspectives

Molecular biology has advanced faster in the last decade than ever before. Various cancer therapy methods are being developed and are proving to be effective. Any sequence in the genome, including several genes, may be targeted by scientists. This may be very beneficial in treating diseases such as cancer [166]. Vectors that are efficient and minimally intrusive are often regarded as a perfect drug delivery system (DDS). However, in the case of cancer, DDS with anticancer properties might be a viable treatment option. Multiple therapeutic routes may be improved by combining medicinal compounds with DDS with anticancer properties [167]. However, some new methods have a great potential to treat cancer, such as epigenetics [168]. Epigenetics studies dynamic and heritable changes to the genome that occur regardless of DNA sequence. It necessitates cooperative interactions with a variety of enzymes and other chemical components. The inappropriate beginning of genetic expressions and cancer may be caused by erroneous epigenetic changes. Because epigenetic modifiers are reversible and vulnerable to external influences, they become interesting targets in various cancer treatment methods. Several epi-drugs have recently been created and tested in clinical trials. Epi-drugs have demonstrated promising results, whether alone or in conjunction with chemotherapy or immunotherapy, including enhanced antitumor effects, drug resistance, and stimulation of the host immune response [169, 170].

Footnotes

Authors' Contribution: All authors have the same contribution.

Conflict of Interests: The authors declare no conflict of interest.

Ethical Approval: This manuscript was approved by the Ethics Committee of Mohaghegh Ardabili University.

Funding/Support: This manuscript did not receive any funds.

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