REVIEW



Topoisomerase Induced DNA Damage Coupled Diseases and Therapeutic Potential

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Topoisomerase is an essential enzyme which regulates the topological state of DNA supercoils during replication and transcription. Topoisomerases cleave either one or two DNA strands and then re-join the cleaved strands after passing the intact strand or a double strand through the gap respectively. During relaxation of supercoiled DNA, if topoisomerase is trapped by drugs or alteration of DNA structure, they stabilize topoisomerase-DNA cleavage complex which leads to DNA damage. If Topoisomerase cleavage complex is trapped by any anticancer or others drug, exogenous and endogenous DNA lesion involving mismatches, abasic sites, oxidative damage etc. it may cause DNA damage. DNA damages leads to several diseases such as tumorigenesis, autoimmune disease, Angelman syndrome, SCAN1, SCAR23, Papillary Thyroid Cancer (PTC), cancer therapy-related acute myeloid leukemia. Topoisomerase uses as a potential drug target to manage infectious diseases like leishmaniasis, Chagas disease, pneumococcal, dengue, yellow fever, corona virus, gastrointestinal infection. Here we review the recent information about the topoisomerase mediated DNA damage, related diseases, role of topoisomerase in heterochromatin structure and uses of topoisomerase as drug target in many diseases.

Key words: Camptothecin, etoposide, doxorubicin, xenotoxic, non-Hodgkin's lymphoma

Topoisomerase catalyzes the changes in topological state of DNA by interconverting relaxed the supercoiled DNA (Pommier et al., 2006). Topoisomerases cleave either one or two DNA strands and then re-join the cleaved strands after passing the intact strand or a double strand through the gap respectively. The active site tyrosine residue attacks a phosphodiester bond in the backbone of the target DNA generating a break in the strand and remains attached covalently to the 5' broken end via a phosphotyrosine linkage. The other broken end with terminal OH group is also held tightly by the enzyme. The unbroken strand of DNA duplex is passed through this gap to release one supercoiling (Watson et al., 2013). The topoisomerase then reseals the broken strands by reversing the original reaction. According to number of strand break topoisomerases are of two types - type I topoisomerase which is responsible for single strand break and subsequent release of one negative supercoil in the same DNA duplex and type II topoisomerase is responsible for double strand break and catenation or decatenation (Pommier et al., 2006).

Type I Topoisomerase

Topoisomerase I (Top1) creates a single strand break by formation of phosphotyrosine linkage at the 5' end of the cut end of the target DNA strand. Top1 religates the break by reversing the reaction of phosphotyrosine bond formation. Relaxation of DNA supercoiling is achieved by allowing rotation of the broken strand around the Top1 bound DNA strand (Stewart et al., 1998; Lesher et al., 2002; Staker et al., 2002). Religation of the DNA 5' end requires hydroxyl group to be aligned with the tyrosine DNA phosphoester bond (Pommier et al., 2006). No ATP is required for this reaction rather, the energy from breaking the phosphodiester bond is stored in the phosphotyrosine linkage and is utilized for religation (Stewart et al., 1998; Lesher et al., 2002; Staker et al., 2002). Both the type 1A and 1B are present in Mammalian system. Top1A are of two types such Top3 α and Top3 β . The Top1B is subdivided into Top1 nuclear in nucleus and Top1mt in mitochondria. Top 3α is responsible for resolution of post replicative hemicatenes and recombination intermediates (Wu & Hickson, 2003; Harmon *et al.*, 2003). Top3 β reduces the frequency of chromosomal translocation (Barthelmes, 2000). Top1 Mt couples mitochondrial functions that is translation, mtDNA expansion, ATP generation and biogenesis (Dalla Rosa *et al.*, 2014; Dalla Rosa *et al.*, 2017). Top1 nuclear is responsible for releases of supercoiling during DNA replication and transcription in nucleus (Pommier *et al.*, 2006).

Type II topoisomerase

DNA Topoisomerase II (Top2) introduces an enzyme bridged DNA double strand break (DSB) where each 5' end of the cleaved DNA are covalently attached to the enzyme active sites by tyrosine phosphodiester linkage (Swan et al., 2022). This enzyme bridged DSB is induced by nucleophilic attack of the phosphate backbone of DNA by the Top2 active site tyrosine which creates breaks forming covalent 5' phosphotyrosyl linkage between Top2 and the 5' end of the DNA (Swan et al., 2022). Enzyme then passes a second DNA duplex through the DNA break, religates the cut ends and dissociate from the DNA. Topoisomerase II (Top2) requires divalent cation such as Mg2+ and ATP for double strand passage reaction (Osheroff, 1986; Lindsley & Wang, 1993; Osheroff et al., 1983; Lindsley & Wang, 1991). There are three types of Top2 such as, DNA Тор 2α; Mainly implicated in relaxation/decatenation and segregation (Grue et al., 1998) Top2β; Mostly associated to transcription (Ju et. al., 2006) and Spo11; which expression is limited in germ cell (Swan et al., 2022). Primary structure of Top 2α & Top 2β are very similar and divided into three domains based on sequence homology with the bacterial type II enzyme, DNA gyrase (Wang, 1996; Nitiss, 1998; Fortune & Osheroff, 2000; Austin & Marsh, 1998; Berger et al., 1996). The N-terminal domain of Topoisomerase II which is the ATP binding site of the enzyme, homologous to the B subunit of DNA gyrase (Champoux, 2001; Velez-Cruz & Osheroff, 2004; Berger et al., 1998). The central portion of the enzyme contains active site of tyrosine which is homologous to the A subunit of DNA gyrase (Champoux, 2001; Velez-Cruz & Osheroff, 2004; Worland & Wang, 1989). The Cterminal domain is highly variable among species and

between the two human isoforms $top2\alpha$ and $top2\beta$ (McClendon & Osheroff, 2007). Top2 α plays an important role during formation of replication fork and remains tightly associated with chromosome during mitosis. (Nitiss, 1998; Bauman *et al.*, 1997). In contrast Top2 β dissociates from chromosome during mitosis (Nitiss, 1998; Austin & Marsh, 1998; Woessner *et al.*, 1991; Isaacs *et al.*, 1998).

Top1 mediated DNA damage

The key step in the catalytic cycle of Top1 is the formation of a transient covalent bond between the Top1 active site tyrosine and the phosphate group of DNA strand and their by a Top1 DNA cleavage complex (Top1cc) intermediate is formed (Wang, 2002). Under certain conditions before relegation of the DNA strand this intermediate Top1cc is stabilized that triggers a DNA damage response including DNA lesion and single strand breaks (SSBs). Stabilization of Top1cc results from misalignment of the 5' OH end of DNA. These misalignments may be generated by any drug like camptothecin bound at the interface of the enzyme and broken DNA (Pommier & Cherfils, 2005; Pommier & Marchand, 2005). Camptothecin and Top1cc binds reversibly. The ternary drug-enzyme-DNA complex and the dissociated complex establish a rapid equilibrium in pharmacological conditions. Hence, cleavage complex reverse rapidly due to dilution of camptothecin (Covey, 1989). Camptothecin traps only a subset of the existing Top1cc that contain a guanine at the 5' end of the break (+1 position) (Jaxel et al., 1991; Tanizawa et al., 1995). Alternatively, Indenoisoquinolines stabilize those cleavage complexes which contain a cytosine at the 3' end of the breaks (-1 position) (Antony et al., 2003).

Endogenous and frequent DNA lesions such as abasic sites, mismatches, oxidized bases, nicks at carcinogenic DNA adducts may lead to trapping of Top1cc irreversibly (Pommier *et al.*, 2006). DNA modifications due to oxidative damage can produce Top1cc (Pourquier *et al.*, 1999). The abasic site or DNA break causes irreversible misalignments of the 5' end of the DNA and thus the Top1cc induced by such lesions are irreversible (Pourquier *et al.*, 1997; Pourquier *et al.*, 1997a). Reactive oxygen species mediated chromatin modifications have also been reported to trap Top1cc during apoptosis (Pommier *et al.*, 2006). The irreversible Top1cc referred as 'suicide complexes' are composed of DNA lesion where the large Top1 remains covalently bound to the 3' end of the broken DNA (Burgin *et al.*, 1995; Shuman, 1989). The resulting disruption of the DNA backbone may lead to SSB or double strand breaks (DSBS) (Pommier *et al.*, 2006).

Reversible Top1cc may be converted into irreversible strand breaks after the DNA or RNA polymerase collide them on the leading strand during replication and on the transcribed strand during transcription respectively (Bendixen et al., 1990; Wu & Liu, 1997). Thus, both DNA & RNA synthesis convert reversible cleavage complex into permanent DNA damage. In cancer cells replication induced DNA damaged contributes to most of the cytotoxicity at low dose camptothecin while, during transcription higher dose is generally required to induce DNA damage and cytotoxicity (Holm et al., 1989; Hsiang et al., 1989). Camptothecin-induced Top1cc may be readily converted into replication DSBs. The trapped Top1cc may also inhibit transcription by blocking elongation and this is a high probability event considering that Top1 is associated with transcription complexes (Pommier et al., 1998). Single strand breaks accumulate in the DNA due to irreversible cleavage by Top1 adjacent to a misincorporated ribonucleotide (Kim et al., 2011).

Top2 mediated DNA damage

Top2 cuts scissile bonds on the two strands of double helix which is staggered and located across the major groove. Then enzyme form cleaved DNA molecules which contain 4 base single stranded ends at their 5'termini (Liu & Wang, 1983; Sander & Hsieh, 1983). Thus Top2 covalently joins to these newly formed 5'-termini (Worland & Wang, 1989; Liu & Wang, 1983; Zechiedrich et al.,, 1989). This covalently attach enzyme-cleave DNA complex is referred to as "cleavage complex" (Top2cc) (McClendon & Osheroff, 2007). Chemotherapeutic drugs such as etoposide and doxorubicin, Xenotoxic chemicals like benzene, dietary factors (bioflavonoids) and endogenous stressor like base mismatches and apurinic sites are common Top2 poisons (Loike, 1982; Tewey, et al., 1984; Chen & Eastmond, 1995; Frantz et al., 1996; Strick et al., 2000;

Kingma et al., 1997; Sabourin & Osheroff, 2000). These types of Top2 poisons stabilize the Top2cc and generate DSBs formation (Long & Stringfellow, 1988). The Top2 poison separates the DNA broken ends and prevents the relegation of the DNA which is cut by Top2 (Pommier et al., 2015). Many Top2 poisons which are termed as interfacial inhibitors (Marchand & Pommier, 2011) bind at the interface between the enzyme and DNA and then form a drug-enzyme-DNA ternary complex. Anti-tumour drugs such as doxorubicin and etoposide generate high level of Top2 mediated DNA breakage. These drugs target and trap the Top2cc by stacking between the base pairs flanking the scission site and displacing the 5'phophotyrosl group from the 3'-OH group thereby preventing relegation. Thus a drugenzyme-DNA ternary complex is formed leading to DNA damage (Capranico et al., 1990; Marchand & Pommier, 2011; Pommier et al., 1991).

Top2 poisons selectively trap Top2 at different sites like upstream and downstream nucleobase pairs which flank the cleavage sites where the enzymes cleave (Chen *et al.*, 1984; Tewey *et al.*, 1984a; Capranico *et al.*, 1990a; Pommier *et al.*, 1991a; Capranico *et al.*, 1993). In mammalian cells the two isoforms of Top2 areTop2 α & Top2 β . Top2 poisons the anticancer drug such as Idarubicin and Etoposide target both the isoforms and stabilize Top2cc preventing religation of the broken ends. Etoposide, a Top2 poison, stacks between the cytosine at -1 of the break site and guanine at +5 of the break site to trap the Top2 β cc (Marchand & Pommier, 2011).

In Top2 α -DNA –drug ternary complex amino acids in the etoposide-binding pocket of Top2 α distinguished from Top2 β by Met 762 and Ser 800 in Top2 α while Gln 778 and Ala 816 in Top2 β (Nitiss & Beck, 1996). This drug stabilized Top2 α cc are reversible, however, their persistence leads to DSB formation (Mao *et al.*, 2001).Top2 mediated DSBs formation in the promoter region of some stimulus responsive genes in a variety of cell types and systems that are induced upon exposure to insulin, estrogen, progesterone etc. have also been reported (Ju *et al.*, 2006).

Human diseases caused by Top1 induced DNA damage

Top1 in tumorigenesis

Negatively supercoiled DNA facilitates RNA: DNA hybrid or R loops formation during transcription. If remains unresolved, the coiling R Loop prevents further RNA transcription & replication, leading to DSB formation (Aguilera & García-Muse, 2012). Top1 interact with RNA polymerase II (RNAPII) localized at transcriptionally active region (TARs) of the genome (Aguilera & García-Muse, 2012; Gilmour et al., 1986). During RNAPII dependent transcription Top1 supresses R loop formation by removing supercoiled DNA. The Top1 holds RNAPII at the promoter proximal P site and RNAPII pauses at initiation (Khobta et al., 2006). Top1 promotes recruitment and assembly of spliceosome at TARs which phosphorylates splicing factor (Tuduri et al., 2009). For coupling of RNA processing factors to TARs is critical for continuous production of full-length mature mRNA. During Topoisomerase reaction with DNA. Top1 covalently link with the 5'phosphate group of DNA and accidentally form Top1cc which generate DNA lesion (Li & Liu, 2016). Presence of these Top1cc may generate DNA damage leading to cell death or mutagenesis which is a precursor for tumorigenesis. Top1 adjoining to a misincorporated ribonucleotide generally form irreversible Top1cc that results into SSBs deposition (Kim et al., 2011). In human cells novel SUMO modification at the lysine residue K391 & K436 supress the topoisomerase activity of Top1 at TARs, thereby reducingTop1 induced DNA damage. Any defect in the SUMOylation on K391 & K436 against Top1 induced DNA damaged during transcription may turn to genome instability, mutagenesis and cancer (Li & Liu, 2016).

Top1 in autoimmune disease

Top1 autoimmune antibodies are most common features of scleroderma and associated with a poor prognosis (Hu *et al.* 2004; Mahler *et al.*, 2010). Sclerodermal disease is hardening of the skin and connective tissue which is caused by production of autoimmune antibodies against nuclear constituents (Li & Liu, 2016). Catalytic domain of α Top1 autoantibodies are highly reactive (Li & Liu, 2016). Patients with

autoimmune antibodies against RNAPII are also frequently positive for α Top1 autoantibodies (Harvey et al., 1996). In many tissues of Scleroderma patients Top1 SUMOylationis increased but Top1 catalytic activity is decreased (Li & Liu, 2016). K391 & K436 residue of SUMOylation supresses the Top1 activity of Transcription associated Top1 while facilitate the Top1-RNAPII interaction. Therefore the Top1 K391/K436 SUMOylation may lead to DNA damage and genome instability (Li & Liu, 2016). Hyper K391/K436 SUMOylation improve the level of Top1-RNAPII complexes in cells which alter the transcriptional stress and increased programmed cell death (Li & Liu, 2016). The increased cell death due to apoptosis is expected to increase presentation of the Top1-RNAPII complex to the immune system resulting into autoimmunity (Li & Liu, 2016).

Top1 in autism

Top1 poisons are shown to alleviate Angelman syndrome, an autism spectrum disorders (ASD) by supressing the exceptionally long antisense RNA transcribed UBE3A-ATS (King et al., 2013). UB3-ATS prevents the expression of its sense gene UB3A that is important for the disease to prevent (King et al., 2013).Top1 recruits spliceosome assembly at TARS to promote efficient transcriptional progression. Top1 Poison (CPT & Topotecan) reduce the expression of exceptionally long and highly transcribed gene with median gene length of 66kb. This Top1 poisons upregulate the expression of shorter gene that are normally expressed at low level. Top1 poison possibly influences the spliceosome assembly to inhibit gene expression in an intron dependent manner (Li & Liu, 2016). Spliceosome represses the R loop in the newly synthesized mRNA (Li & Liu, 2016). Top1 poison spliceosome stabilizes R loop formation and thereby inhibit the expression of UBE3A-ATS (Li & Liu, 2016).

TOP1cc in Ataxia with Axonal Neuropathy

Accumulation of Top1cc can contribute to the development of Spinocerebellar ataxia with axonal neuropathy (SCAN1) (Takashima *et al.*, 2002; El-Khamisy *et al.*, 2005; El-Khamisy *et al.*, 2007; Walton *et al.*, 2010). SCAN1 is a neurodegenerative disease (Takashima *et al.*, 2002). A particular mutation (H493R)

in TDP1 has been identified to be the underlying cause of SCAN1 (Takashima et al., 2002; Interthal et al., 2001; Katyal et al., 2007). This mutated TDP1 was observed to be unable to resolve endogenous TOP1ccs and as a result SCAN1 cells accumulate Top1ccs. The mutation in TDP1 actually inhibits the second step of TDP1 mediated DNA damage repair pathway leading to accumulation of TDP1-DNA catalytic intermediate or TDP1cc in addition to Top1cc. The accumulation of TDP1cc may block the alternative mechanisms for resolution of DNA lesions that typically respond to Top1cc formation (Interthal et al., 2005; He et al., 2007). Endogenous accumulation of Top1cc in TDP1 deficient cell is prevented by treatment with transcription inhibitor (Katyal et al. 2014). Therefore transcription and oxidative stress are major contributors to steady state levels of Top1cc that become pathological in SCAN1.

Disease caused by Topoisomerase II induced DNA damage

Cancer therapy-related acute myeloid leukemia

Top2 poisons, used in cancer treatment, induces apoptosis of the cancer cells by the DNA fork collapsing and unresolved DSBs. The DSBs produced may cause mutations that promote to secondary malignancies, such as therapy-related acute myeloid leukemia (t-AML). Breast cancer and non-Hodgkin's lymphoma (NHL) patients treated with the Top2 poisons like daunorubicin, etoposide, and doxorubicin, have the highest risk of being diagnosed with t-AML (Beadle et al., 2009; Morton et al., 2013; Leone, et al., 2002). The majority of t-AML cases have been diagnosed with mutation due to translocation at chromosome 11 specifically the KMT2A or MLL gene (Pedersen-Bjergaard & Philip 1991; Broeker, et al., 1996; Felix, 1998; Meyer et al., 2018). It has been observed that the MLL gene fuse with either AF9, ENL, ELL, or AF4 (Meyer et al., 2018). Some work on human hematopoietic stem cell and progenitor cells (HSPCs) demonstrated that treatment with low-dose, non-cytotoxic levels of etoposide and doxorubicin increase DNA break frequency within the therapyrelated breakpoint cluster region (BCR) of MLL gene (Thys et al., 2015). It has also been reported that the Top2 poison etoposide may induce chromosome breakage and translocations involving MLL, AF9, AF4,

AF6, and ENL in human HSPCs and lymphoblastoid cells (Gothe *et al.*, 2019). Altogether, the Top2 and its poisons may facilitate the mutagenic process which leads to t-AML in breast cancer and NHL patients.

Papillary Thyroid Cancer (PTC)

Some evidence suggests that the TOP2 also facilitates the formation of oncogenic translocations in solid tumours. According to the National Cancer Institute's Surveillance, Epidemiology, and End Results (SEER) database Papillary thyroid cancer (PTC) increased dramatically since the 1970s (Chen et al., 2005; Davies & Welch, 2006; Enewold et al., 2009). PTC is increased by exposure of environmental chemicals and chemotherapeutic agents. Sporadic rearrangement-positive PTC cases are predominantly due to chemical exposure which possess the RET/PTC1 rearrangement (Nikiforov et al., 1997; Finn et al., 2003; Fenton et al., 2000). The genes RET, CCDC6, and NCOA4 involved in the RET/PTC1 and RET/PTC3 rearrangements are located within known fragile sites indicating that they are more prone to DNA breaks than non-fragile sites of the genome (Burrow et al., 2009). The chemical exposure-associated PTC cases have been found to be triggered by the benzene and/or chemotherapeutic agents, like Top1 and Top2 inhibitors/poisons. Benzene is a carcinogen consisting of anti-Top2 properties which is found in cigarette smoke, gasoline, and industrial emissions (National Toxicology Program, 2011; Eastmond et al., 2005). For fragile site induction, low-dose exposure from these sources is sufficient (National Toxicology Program, 2011; Yunis et al., 1987; Dillon et al., 2012). PTC has been reported in some secondary cancer patients treated with fragile siteinducing chemotherapeutic agents for cancers such as Hodgkin's lymphoma, osteosarcoma, pediatric rhabdomyosarcoma, and others (Boffetta & Kaldor, 1994, Swerdlow et al., 1992; Goto et al., 1996; Jimenez et al., 1995; Tsuchiya et al., 1991; Verneris et al., 2001; Yen et al., 1993; Venkitaraman et al., 2008; De Vathaire et al., 1999; Gow et al., 2003; Froelich-Ammon et al., 1994; Jonstrup et al., 2008). HTori-3 cells when treated with low-dose, non-cytotoxic level of benzene, etoposide, and doxorubicin a significant increase of the frequency of DNA breaks within the RET-BCR in intron

11 was observed (Lehman *et al.*, 2017). This suggests translocation process of PTC is regulated by Top2. Further studies shown that HTori-3 cells treated with fragile site-inducing chemicals or Top1/Top2 poisons generate DNA breaks within RET intron 11 which are predominantly distributed around predicted Top1 and Top2 cleavage sites (Dillon *et al.*, 2013). As topoisomerase enzymatic activity is enhanced by DNA secondary structures, the fragility associated with RET intron 11 increase by activity of topoisomerases at the DNA secondary structures (Froelich-Ammon *et al.*, 1994; Jonstrup *et al.*, 2008; Mills *et al.*, 2018).

Spinocerebellar Ataxia Autosomal Recessive23 (SCAR23)

The deficiency of DSB repair lead to the development of neurological abnormalities like SCAR23 (Alt & Schwer, 2018). This indicated that topoisomerase induced DNA damaged may be an important relevant lesion for neurological abnormalities. SCAR23 is an autosomal recessive syndrome that is characterized by treatment resistant epilepsy, progressive ataxia, and cerebellar degeneration (Gómez-Herreros et al., 2013; Gómez-Herreros et al., 2014). SCAR23 is also a degenerative rather than developmental disorder because SCAR23 patients also display a later age onset than other inherited ataxias, with symptoms which increases during older age (Gómez-Herreros et al., 2013; Gómez-Herreros et al., 2014). The cause of SCAR23 are mutations with TDP2 and SCAR23 cells are deficient for the resolution within TDP2. SCAR23 cells are insufficient for resolve the stalled Top2cc and are hypersensitive to ETP (epipolythiodioxopiperazine are a class of secondary metabolic toxin) (Gómez-Herreros et al., 2014). TDP2 mutation results in shortened mRNA expression and nonsense mediated (Gómez-Herreros et al., decay 2014). During transcription Top2cc is resolved by TDP2 when TDP2 insufficient in neurons show significant delay in recovery of transcription with treatment of ETP (Gómez-Herreros et al., 2014). Wide expression of Genome profiling show over 100 genes which `are regulated in TDP2 deficient neurons than WT neurons and half of these genes are known to be epilepsy, ataxia and cognitive development (Gómez-Herreros et al., 2014). Different expressions of long genes in TDP2 insufficient cells specify inhibition of topoisomerase which result in a length dependent impairment in gene expression in post mitotic stage neurons (Zylka *et al.*, 2015).

Topoisomerase in Heterochromatin, aging and disease

Role of Top1 in Heterochromatin

Heterochromatin plays critical role in transcriptional silencing of transposons (SanMiguel et al., 1996; Lander et al., 2001; Waterston et al., 2002). Aging and premature aging syndrome is caused by loss of heterochromatin (Villeponteau, 1997). Loss of heterochromatin and alteration of heterochromatin structure leads to cancer risk and neurological disease respectively (Feinberg et al., 2016; Janssen et al., 2018; Tenreiro et al., 2014). Top1 plays important role for heterochromatin structure and histone modification. Heterochromatin in Trypanosoma cruzi is unpacked by Top1 inhibitors, camptothecin (CPT) and rebeccamycin (Zuma et al., 2011). Decompression of heterochromatin with altered histone modifications is induced by the CPT treatment of human HCT16 cells (Baranello et al., 2010). Inactivation of Top1 disrupts transcriptional silencing of transposons (Dinh et al., 2015). Excess RNA-DNA hybrid or R-loop formation in heterochromatin domains was observed in Top1 depleted HEK293 cells. This observation indicate important role of Top1 in regulating R-loop homeostasis in heterochromatin (Manzo et al., 2018).

Role of Top2 in heterochromatin

Transcriptional silencing in heterochromatinis regulated by Top2 as displacement of Top2 from satellite III in heterochromatin or chemical inhibition of Top2 activity which can disrupt heterochromatic silencing of a reporter gene (Blattes et al., 2006). Top2 and chromatin remodelling complexes such as BAF (multisubunit of chromatin remodelers) which make accessorv heterochromatin more accessible to transcription factors (Miller et al., 2017). BAF complexes are ATP dependent chromatin remodelling complexes that modify chromatin structure and make the DNA more accessible to machinery of transcription, replication, repair (Clapier & Cairns, 2009; Kadoch et al., 2013; Kadoch et al., 2017). DNA entanglement during mitosis is prevented by BAF complex associated with Top2a (Kadoch et al., 2013; Kadoch et al., 2017). Top2α is identified by chromatin indicator assay (CIA) during BAF mediated chromatin remodelling of facultative heterochromatin. This process is specifically dependent on Top2 α because it resolves the topological state of catenated facultative heterochromatin (Lee & Wang, 2019). Decatenation of DNA by Top2α makes the facultative heterochromatin more accessible for chromatin remodelers as well as transcription factors (Miller et al., 2017).

Topoisomerase as target for treatment of diseases

By binding Topoisomerase with DNA strand create a break and passing another DNA strand through the break and releasing DNA. During cleavage process a covalent bond formed between the tyrosine residue of topoisomerase and phosphate group of breaking end of the DNA strand. Topoisomerase cleaves one or both strand of the DNA double helix. The Top1cc is a vulnerable intermediate that can lead to cell death if trapped by any anticancer drug or biomolecule (Seddek *et al.*, 2021). This property of topoisomerase may be utilizing for treatment of both infectious and noninfectious diseases (Seddek *et al.*, 2021).

Rationale for targeting Topoisomerase as drug target

Topoisomerases being a major factor for impacting cell viability, have widely been targeted for clinical treatment of cancer and infectious disease. According to mechanism Topoisomerase inhibitors are classified as poison inhibitors and catalytic inhibitors (Pommier et al., 2010). Poison inhibitors stabilize the topoisomerase covalent complex which forms during catalysis. Catalytic inhibitors interfere with the catalytic cycle of the enzyme inhibiting initial substrate binding of the cleavage complexes. In current clinical studies poison inhibitors against Top1B and Top2αare being used as Topoisomerase targeting drugs (Pommier et al., 2010; Liu, 1989; Pham & Ziora, 2019). Topoisomerase poison inhibitors cause loss of cellular viability through accumulation of breaks in chromosome and thereby triggering apoptosis in cancer cells (Solary, et al., 1994).

Bacterial Top1A as target for novel antibiotics

In thermophilic bacteria Top1 & Top3 are found (Seddek et al., 2021). During transcription Top1 is responsible for relaxation of negative supercoiling and Top3 helps in resolving replication and recombination intermediates (Terekhova et al., 2012; Terekhova et al., 2014). Endogenous inhibitors of Top1 such as, overexpressed Tn5 transposase, T4 gp55.2 and toxin YJhX have been reported to inhibit cell growth and loss of viability of bacterial cell (Seddek et al., 2021). Top1A poison inhibitors generate DNA lesion in bacteria and thereby exhibit bactericidal property (Seddek et al., 2021). The mutated bacterial Top1including mutations in the conserved sequence D111, D113 and E115 triad that bind Mg²⁺ required for DNA relegation are unable to re-join the DNA (Cheng et al., 2009). Effect of these Top1 mutations is expected to mimic the action of Top1A poison inhibitors. Overexpression of YjhX in E. coli leads to death even through YjhX has been shown to have no poison inhibitory effect of Top1. Some such bacterial pathogens as Mycobacterium tuberculosis (Ravishankar et al., 2015) Streptococcus pneumoniae (Liu et al., 2017), P. aeruginosa (Yan et al., 2019) need Top1 for cellular viability. Bacteria have only Top1A to overcome DNA topological barrier during cellular processes and thus it is important for their survival. Catalytic inhibitors of Top1 have antibacterial adequacy of the mechanism of topoisomerase inhibition. Hence bacterial Top1A represents a valid target for novel antibiotics to overcome antimicrobial resistance (Wang, 2002).

Eukaryotic Top1A as potential target for infectious disease treatment

Top3 has two isoforms Top3 α and Top3 β (Forterre & Gadelle, 2009). In mice embryo development Top3 α plays an important role. Top3 β knockout mice have been reported to develop maturity but with shorter life span (Kwan & Wang, 2001). Both DNA and RNA Topoisomerase activities are found in human Top3 β (Stoll *et al.*, 2013). During transcription it relaxes negatively supercoiled DNA and prevents R loop accumulation (Zhang *et al.*, 2019). Tudor domain containing 3 protein (TDRD3) stabilize Human Top3 β which identified as a host protein needed for replication

of Flavivirus such as dengue and yellow fever virus (Barrows *et al.*, 2019). Study on role of TDRD3 in viral replication have revealed that Top3 β is essential for replication of all single stranded DNA virus and TDRD3 helps in stabilization of Top3 β (Prasanth *et al.*, 2020). Therefore inhibitors specific to Top3 β could be used successfully as broad spectrum antiviral drugs for management of flavivirus and corona virus including SARS-COV2 infections (Prasanth *et al.*, 2020).

Topoisomerase as a drug target in protozoa

Camptothecin is a Top1 poison which stabilizes the DNA-enzyme complex and induces slow religation (Das, 2004). Camptothecin inhibits the enzyme action in kinetoplast of L. donovani, T. cruzi, T. bruci. Camptothecin also induces programmed cell death of amastigote and promastigote stage of Leishmania. Camptothecin induces oxidative stress decrease the GSH level and increased the lipid peroxidation which leads to calcium elevation from intracellular or extracellular sources (Sen et al., 2004, 2004a). The elevated Ca²⁺ loss of membrane potential mitochondria of the Leishmania cells. Decrease in transmembrane K⁺ level of the cell leads to apoptosis (Sen et al., 2004, 2004a). Loss of cell membrane potential, release of cytochrome c and activation of caspase-like proteases result in apoptosis and death of parasites (Kosec et al., 2006).

CONCLUSION

Topoisomerases play an important role in maintaining the topological structure of DNA in all the organisms that used DNA as hereditary material. Any malfunctioning of topoisomerase results into DNA topoisomerase covalent cleavage complex, DSB and SSB which in turn causes mutations in DNA. This mutations lead to pathogenic conditions. Topoisomerase induced changes in DNA are localized in different tissues that trigger disease condition. So far the diseases reported the malfunctioning of topoisomerase has been reviewed here. However, it seems many diseases caused by topoisomerase are yet to be discovered. The topoisomerase induced DNA damaged may be a potential tool to kill harmful pathogens.

Therefore attempts are being made to design drugs targeting topoisomerase of pathogens. The probability of inducing topoisomerase mediated cytotoxicity in cancers cells are also being explored by different researchers.

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CONFLICTS OF INTEREST

The authors declare that they have no potential conflicts of interest.

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