

Demonstration of a potent *RET* transcriptional inhibitor for the treatment of medullary thyroid carcinoma based on an ellipticine derivative

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Abstract. Dominant-activating mutations in the *RET* (rearranged during transfection) proto-oncogene, which encodes a receptor tyrosine kinase, is often associated with the development of medullary thyroid carcinoma (MTC). The proximal promoter region of the *RET* gene consists of a guanine-rich sequence containing five runs of three consecutive guanine residues that serve as the binding site for transcriptional factors. As we have recently shown, this stretch of nucleotides in the promoter region is highly dynamic in nature and tend to form non-B DNA secondary structures called G-quadruplexes, which suppress the transcription of the *RET* gene. In the present study, ellipticine and its derivatives were identified as excellent RET G-quadruplex stabilizing agents. Circular dichroism (CD) spectroscopic studies revealed that the incorporation of a piperidine ring in an ellipticine derivative, NSC311153 improves its binding with the G-quadruplex structure and the stability induced by this compound is more potent than ellipticine. Furthermore, this compound also interfered with the transcriptional mechanism of the *RET* gene in an MTC derived cell line, TT cells and significantly decreased the endogenous RET protein expression. We demonstrated the specificity of NSC311153 by using papillary thyroid carcinoma (PTC) cells, the TPC1 cell line which lacks the G-quadruplex forming sequence in the promoter region due to chromosomal rearrangement. The RET downregulation selectively suppresses cell proliferation by inhibiting the intracellular Raf/MEK/ERK and PI3K/Akt/mTOR signaling pathways in the TT cells. In the present study, we also showed that the systemic administration of a water soluble NSC311153 analog in a mouse MTC xenograft model inhibited the tumor growth through RET downregulation.

Introduction

The *RET* proto-oncogene, which is a key component in the development of enteric nervous system, encodes a transmembrane receptor-type tyrosine kinase (1,2). The domain organization of the RET protein includes a ligand-binding extracellular domain, a transmembrane domain and an intracellular tyrosine kinase domain (3-5). The ligands for RET receptor have been identified as the members of glial cell line derived neurotrophic factor (GDNF) family that activate this protein through the interaction with glycosylphosphatidylinositol linked GFR- α co-receptors (6,7). These co-receptors mediate RET homodimerization that leads to trans-autophosphorylation of the tyrosine residues present in the intracellular kinase domain thereby activating its function (8). Upon activation, the phosphorylated tyrosine residues act as binding sites for many adaptor molecules that trigger a cascade of intracellular signaling pathways (9). The major mitogenic signaling pathways include the Raf/MEK/ERK and PI3K/Akt/mTOR pathways that contribute to cell proliferation and survival (10-12).

Activating *RET* germline mutations have been identified as the key cause for the pathogenesis of medullary thyroid carcinoma (MTC), which is a part of multiple endocrine neoplasia type 2 (MEN2) syndrome (13,14). Patients with MEN2 harbor several mutations in the RET protein that leads to ligand independent phosphorylation and activation of the receptor thereby resulting in the constitutive signaling of intracellular pathways (15,16). Unlike other differentiated thyroid cancers such as papillary thyroid carcinoma (PTC) and follicular thyroid carcinoma (FTC), MTC is poorly-differentiated and hence it metastasizes rapidly to distant organs like bones, lungs and liver (17,18). Moreover, most MTC patients have tumor invasion at the time of diagnosis that hampers the effectiveness of standard therapies such as surgical resection of the thyroid gland and external beam radiation (18). Hence, a systemic targeted therapy has gained considerable clinical interest for the treatment of advanced and progressive MTC (19). Owing to the oncogenic potential of RET in the development of MTC, it has been regarded as an ideal molecular target for therapeutic intervention (19,20). Although several approaches have been developed including the use of kinase inhibitors and small interfering RNA (siRNA) to abrogate the RET kinase

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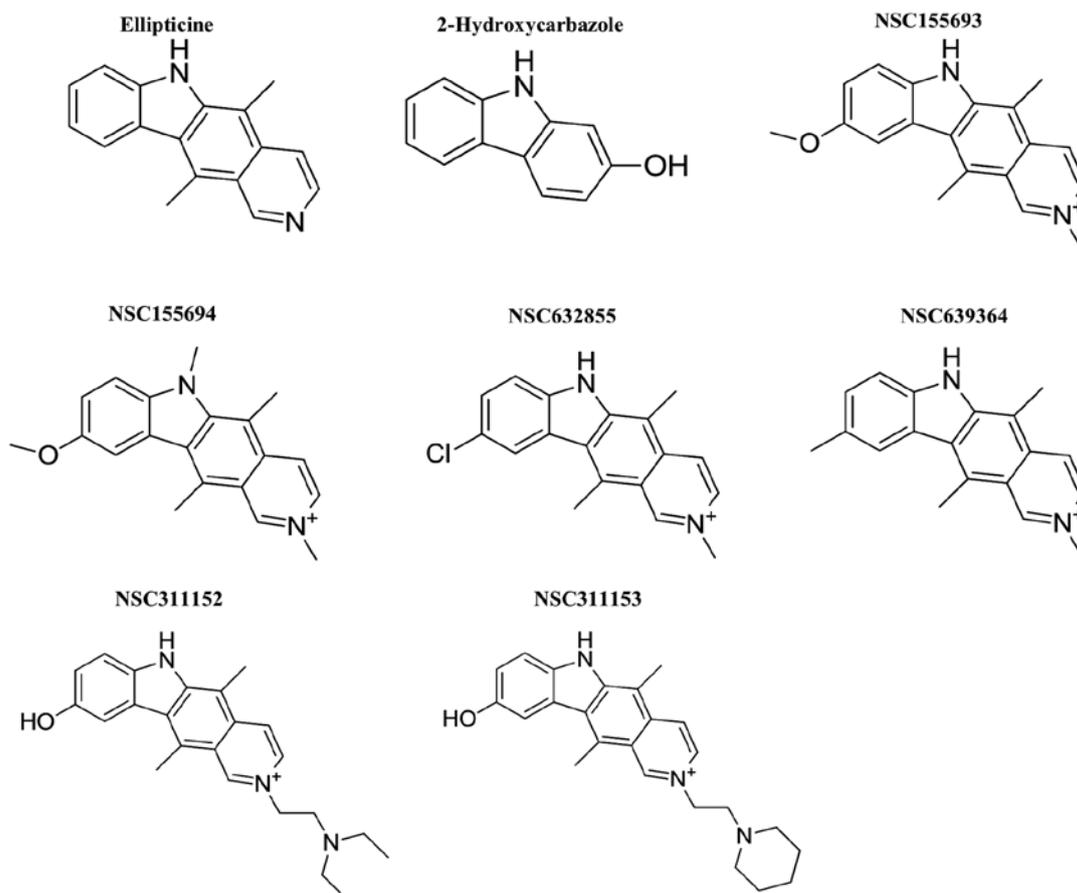


Figure 1. Ellipticine analogs. Chemical structures of ellipticine and its derivatives.

activity and its expression, developing a specific *RET* inhibitor still remains challenging (20-22). Our previous study clearly showed that the transcriptional inhibition of the *RET* gene by targeting its promoter region could be a promising strategy for MTC specific therapy (23,24).

The transcriptional activation of the *RET* gene is regulated by the presence of polypurine (guanine) and polypyrimidine (cytosine) tract in the proximal promoter region (25,26). This upstream core promoter region serves as the binding site for RNA Pol II, Sp1 and other transcriptional factors that are responsible for the basal promoter activity (27). Our previous studies have clearly demonstrated that the G-rich sequences present within the *RET* promoter region are highly dynamic in nature, adopting non-B-DNA conformations such as G-quadruplex structures under negative supercoiling conditions (28-30). These secondary structures are four-stranded intramolecular folding of a single-stranded DNA, which is formed by the stacking of two or more G-tetrads (31). Each G-tetrad comprises of four guanines that are arranged in a square planar conformation and are interconnected through Hoogsteen hydrogen bonding (31,32). The G-quadruplex structure on the promoter region is believed to serve as a silencer element for the *RET* transcription through the sequestration of the transcriptional factor binding sites (23). In our previous study, we have clearly demonstrated that the stabilization of the G-quadruplex structure formed on the *RET* promoter region by a small-molecule, berberine interfered with the binding of

SP1 and RNA Pol II thereby silencing the transcription of this gene (23,24).

In continuation of our previous study, the main objective of the present study was to discover new drug-like small-molecules that have clinical implications as a potent suppressor of *RET* gene through the stabilization of the promoter G-quadruplex structure. Hence, we repurposed ellipticine and its structural derivatives as potential G-quadruplex stabilizing agents and also exerting transcriptional inhibitory effect on the *RET* gene in medullary thyroid carcinoma (MTC) derived TT cell line. Ellipticine is a natural alkaloid, which has been demonstrated to have therapeutic benefits in different types of cancers (33,34). The anti-neoplastic activity of this molecule has been attributed to its ability to intercalate with DNA and/or to inhibit the topoisomerase II activity (35,36). However, recent studies have revealed that ellipticine also binds and stabilizes the G-quadruplex structures formed on the telomere region and the promoter region of *c-Myc* oncogene *in vivo* (37,38). In order to identify promising lead compounds for the present study, we explored for different structural derivatives of ellipticine from the NCI/DTP open chemical repository (Fig. 1). This led us to the identification of NSC311153 and NSC311152 as lead compounds that silence the *RET* gene expression by targeting the G-quadruplex structure formed on the promoter region of this gene. We also investigated the cellular effects mediated by these compounds in TT cells and its *in vivo* antitumor efficacy using MTC xenograft models to further

understand the therapeutic implications in targeting the *RET* transcription through the promoter G-quadruplex.

Materials and methods

Chemicals. Ellipticine was obtained from Santa Cruz Biotechnology (SC-200878; Santa Cruz, CA, USA). NSC311153 and other structural analogs were kindly provided from the U.S. NCI/DTP Open Chemical Repository. All the compounds were dissolved in dimethyl sulfoxide (DMSO) at a final concentration of 10 mg/ml.

Materials. The 5'-FAM labelled RET-WT (5'-AGCGGGT AGGGGCGGGGCGGGGCGGGGCGG-3') oligonucleotide was purchased from Sigma Genosys (Woodlands, TX, USA). Taq DNA polymerase was purchased from Fermentas (Hanover, MD, USA).

Cell culture and media. The TT cell line was obtained from the American Type Culture Collection (ATCC; Manassas, VA, USA) and maintained in Dulbecco's modified Eagle's medium (DMEM)/F-12 medium (Cellgro, Manassas, VA, USA) supplemented with 15% heat inactivated fetal bovine serum (FBS). The TPC1 cells and another MTC derived cell line, MZ-CRC-1 cells were provided by Dr Rebecca Schweppe (University of Colorado, Denver, CO, USA). These cells were maintained in RPMI-1640 medium supplemented with 9% FBS and DMEM/F-12 medium supplemented with 15% FBS, respectively. The isogenic cell line HEK293-RET, which carries the luciferase reporter gene under the control of *RET* gene promoter was generated as described in our previous study and grown in DMEM medium supplemented with 9% FBS (23). The normal thyroid cell line, Nthy-ori-3-1 was purchased from Sigma Genosys and cultured in RPMI-1640 medium supplemented with 9% FBS. All the cell lines were maintained in a humidified atmosphere containing 5% CO₂ at 37°C. The stocks for all these cell lines were obtained from the cell bank and utilized within 6 months. These cell lines were also tested for mycoplasma contamination and were further authenticated using STR profiling.

CD spectroscopy. The RET-WT oligonucleotide (5 μM) was allowed to form the G-quadruplex structure in the presence of Tris-HCl buffer (20 mM, pH 7.6) and 25 mM KCl by denaturing at 95°C for 5 min and slowly cooled to room temperature. The CD spectra were recorded using a Jasco J-810 spectrophotometer (Jasco, Inc., Easton, MD, USA) using a quartz cell of 1 mm path length and instrument scanning speed of 100 nm/min with a response time of 1 sec over a wavelength range of 230-330 nm as previously described (23). The T_m was determined by monitoring the molar ellipticity vs. temperature profiles at 262 nm at increasing temperature from 20 to 90°C at a gradient of 1°C/min.

Polymerase stop assay. The polymerase stop assay was performed on a DNA template containing the G-quadruplex forming sequence, which is present in the *RET* promoter region as previously described (39). In brief, the template DNA was annealed with a 5'-γ³²P end-labelled primer (P28) and

purified on an 8% non-denaturing polyacrylamide gel. The purified primer-DNA template was used in a primer extension assay in the presence of Taq DNA polymerase.

Dimethyl sulfate (DMS) footprinting. The DMS footprinting was performed on the 5'-FAM labelled RET-WT oligonucleotides as described in our previous studies (23,24). In brief, the oligonucleotides were allowed to form the G-quadruplex structure and were incubated in the absence and presence of NSC311153 (5 equivalents) at room temperature for 1 h. The samples were treated with DMS (0.2%) for 2 min and were resolved on an 8% non-denaturing polyacrylamide gel. Each DNA band was recovered from the gel and treated with piperidine (10%) after ethanol precipitation. The cleaved products were resolved on a 16% denaturing polyacrylamide gel along with purine and pyrimidine specific sequencing markers that were generated according to the published procedure (40). The gel was dried and the fluorescence was read on a Typhoon 8600 scanner (GE Healthcare Life Sciences, Pittsburgh, PA, USA) for analysis.

Semi-quantitative RT-PCR analysis. Total RNA was extracted from the cells using the RNeasy Mini QIAcube kit (Qiagen, Redwood City, CA, USA) according to the manufacturer's protocol. The extracted RNA was subjected to reverse-transcription using the oligo (dT)18 primer with QuantiTect reverse-transcription kit (Qiagen) to generate single-stranded cDNA. The primers used for RT-PCR were as follows: RET forward, (5'-GCAGCATTGTTGGGGGACA-3') and RET reverse, (5'-CACCGGAAGAGGAGTAGCTG-3'); Rpl9 forward, (5'-CTGAAGGGACGCACAGTTAT-3') and Rpl9 reverse, (5'-ACGGTAGCCAGTTCCTTCT-3'). The PCR reactions involved an initial denaturation at 95°C for 3 min followed by 33 and 23 cycles for RET and Rpl9, respectively, at 95°C for 30 sec, 52°C for 30 sec and 72°C for 30 sec on a GeneAmp PCR system 9600 (Perkin-Elmer, Waltham, MA, USA). The PCR products were analyzed on 1.5% agarose gel electrophoresis.

Western blotting. The whole-cell protein extracts were prepared by lysing the cells with 2% CHAPS lysis buffer in the presence of 10 mM Tris-HCl, pH 7.4, 0.15 M NaCl, 5 mM EDTA and Halt Protease Inhibitor Cocktail (Thermo Fisher Scientific, Waltham, MA, USA). The extracted proteins were resolved on a 4-12% polyacrylamide SDS-PAGE, as previously described (23,24). The primary antibodies used were as follows: anti-RET (#3220), anti-RET/PTC1 (#14698), anti-cMYC (#5605), anti-p-mTOR (#2971) and anti-mTOR (#2972) (dilution 1:1,000) were purchased from Cell Signaling Technology (Beverly, MA, USA), anti-Bcl-2 (sc-7382), anti-pERK (sc-7383), anti-ERK (sc-271270), anti-cyclin D1 (sc-20044) and anti-β-actin (sc-47778) (dilution 1:300) were purchased from Santa Cruz Biotechnology. Anti-VEGF antibody was purchased from GeneTex (Irvine, CA, USA; #GTX102643). Mouse and rabbit IgG antibodies tagged with horseradish peroxidase (HRP) (Bio-Rad Laboratories, Hercules, CA, USA) were used as secondary antibodies (dilution 1:1,000). An enhanced chemiluminescence substrate kit (#32106) purchased from Thermo Fischer Scientific was used for detection.

Luciferase assay. The isogenic cell line HEK293-RET was exposed to different concentrations of NSC311153 up to 24 h. Luciferase expression level is determined using the ONE-Glo Luciferase Assay system (Promega, Madison, WI, USA) following the manufacturer's instruction.

Cell viability assay. Cells were plated at a concentration of 7,500 cells/well in a 96-well dish and incubated overnight, followed by the treatment with NSC311153 at increasing concentrations up to 96 h. The cell viability was determined by using 0.33 mg/ml MTS dye in the presence of phenazine methosulfate (PMS) (25 μ M) as previously described (41). The absorbance was measured at 590 nm using a Synergy HT multi-detection microplate reader (BioTek Instruments, Inc., Winooski, VT, USA).

Caspase-3 assay. TT cells were treated with different concentrations of NSC311153 up to 48 h and caspase-3 activity was measured using the ApoAlert Caspase Fluorescent Assay kit (Clontech Laboratories, Inc., Mountain View, CA, USA) by following the manufacturer's protocol.

In vivo studies. The *in vivo* antitumor efficacy of the ellipticine derivative was evaluated using 8-10-week old male severe combined immunodeficiency (SCID) mice, xenotransplanted with MTC derived TT cells. Animal experiments were conducted in accordance with the Institutional Animal Care and Use Committee (IACUC). The experiments were performed in the Experimental Mouse Shared Resource (EMSR) Animal Facility Laboratory (University of Arizona), which is accredited by the International Association for Assessment and Accreditation of Laboratory Animal Care (AAALAC). In brief, exponentially growing TT cells (1×10^7) were subcutaneously injected into the flank of the mice and the tumor growth was monitored every week by measuring the tumor diameters using a vernier caliper. Tumor volume was calculated according to the formula $(b^2 \times l)/2$ where *b* and *l* are the shortest and the longest diameters, respectively. Once the tumor volume reaches 100 mm³, the mice are randomly pair matched to vehicle and treated group ($n=8$ /group). The compound was dissolved in 90% phosphate-buffered saline (PBS) and 10% DMSO and administered intraperitoneally (i.p) at a single dose of 4 mg/kg for 5 days/week up to 2 weeks. The antitumor efficacy was assessed based on the percentage inhibition of tumor growth in treated vs. control group. The toxicity of the compound was evaluated based on the loss of average weight of mice. Tumor tissue from vehicle and treated group were explanted at the end of last dosage to examine the effect of the compound on the expression of proteins that contribute to tumor growth.

Results

Interaction of ellipticine with RET G-quadruplex. The molecular structure of ellipticine consists of an aromatic pyridocarbazole ring, which allows the π - π stacking interactions with the planar guanine residues present in the terminal G-tetrad (Fig. 1) (37). Not surprisingly, previous studies have reported that ellipticine stabilizes different G-quadruplex structures formed on the telomere region and on the promoter

region of *c-Myc* oncogene (37,38). Hence, in the present study we investigated whether this compound binds and stabilizes the RET G-quadruplex structure using CD spectroscopic analysis. First, we examined whether ellipticine alters the structural conformation of the RET G-quadruplex by monitoring the CD spectra of RET G4 sequence (5 μ M) in the absence and presence of increasing concentrations of this compound. As shown in Fig. 2A, the positive peak at 262 nm, which corresponds to a parallel G-quadruplex structure (42), was not affected in the presence of ellipticine, suggesting that the parallel configuration of the RET G-quadruplex was not changed in the presence of this molecule. Next, we examined the thermal stability of the G-quadruplex structure by monitoring the CD melting curve in the absence and presence of ellipticine (1 equivalent) at increasing temperatures. As shown in Fig. 2B, the melting temperature (T_m) of the RET G-quadruplex structure in the absence of ellipticine was determined to be 75°C. Based on the melting curves, the binding of ellipticine with the G-quadruplex structure increases its melting temperature up to 85°C and the ΔT_m was found to be 10°C (Fig. 2B). To further understand the structural features required for the interaction of ellipticine with the RET G-quadruplex structure, we examined the binding of 2-hydroxycarbazole with this structure by monitoring the CD melting profiles. As shown in Fig. 2C the T_m of the G-quadruplex structure was not increased even in the presence of 5 equivalents of 2-hydroxycarbazole, suggesting that the presence of pyridine ring in ellipticine allows additional π - π interactions with the guanine residue. Overall these data imply that the pyridocarbazole ring moiety is essential for the stabilization of the RET G-quadruplex structure by ellipticine.

Effect of ellipticine on the RET expression. In our previous studies we have clearly demonstrated that the small-molecule mediated stabilization of the G-quadruplex structure formed on the *RET* promoter region exerts transcriptional inhibitory effect on this gene (23,24). Hence, we determined whether ellipticine downregulates the endogenous *RET* expression in the TT cell line in which the *RET* gene transcription is regulated by the promoter region that contains the G-quadruplex forming sequence. As shown in Fig. 2D, a concentration dependent decrease in the *RET* protein expression was observed in the presence of ellipticine following 48-h exposure. To further confirm that the *RET* downregulation by ellipticine is mediated through the stabilization of the G-quadruplex structure, we determined the effect of 2-hydroxycarbazole on the *RET* expression in this cell line. As shown in Fig. 2E the *RET* protein expression was not decreased in the presence of this compound even at high concentration (5 μ g/ml). These data are consistent with our previous studies that the stabilization of the G-quadruplex structure formed within the *RET* promoter region is responsible for silencing the expression of this gene.

Identification of NSC311153 as RET G-quadruplex binding compound. Although we identified ellipticine as a potent *RET* transcriptional inhibitor, this compound was withdrawn from this study due to its adverse cytotoxic effects in TT cells, which was evaluated by MTS assay. The IC_{50} of ellipticine was calculated to be 0.3 μ g/ml after 96-h treatment of TT cells in the presence of increasing concentration of this compound

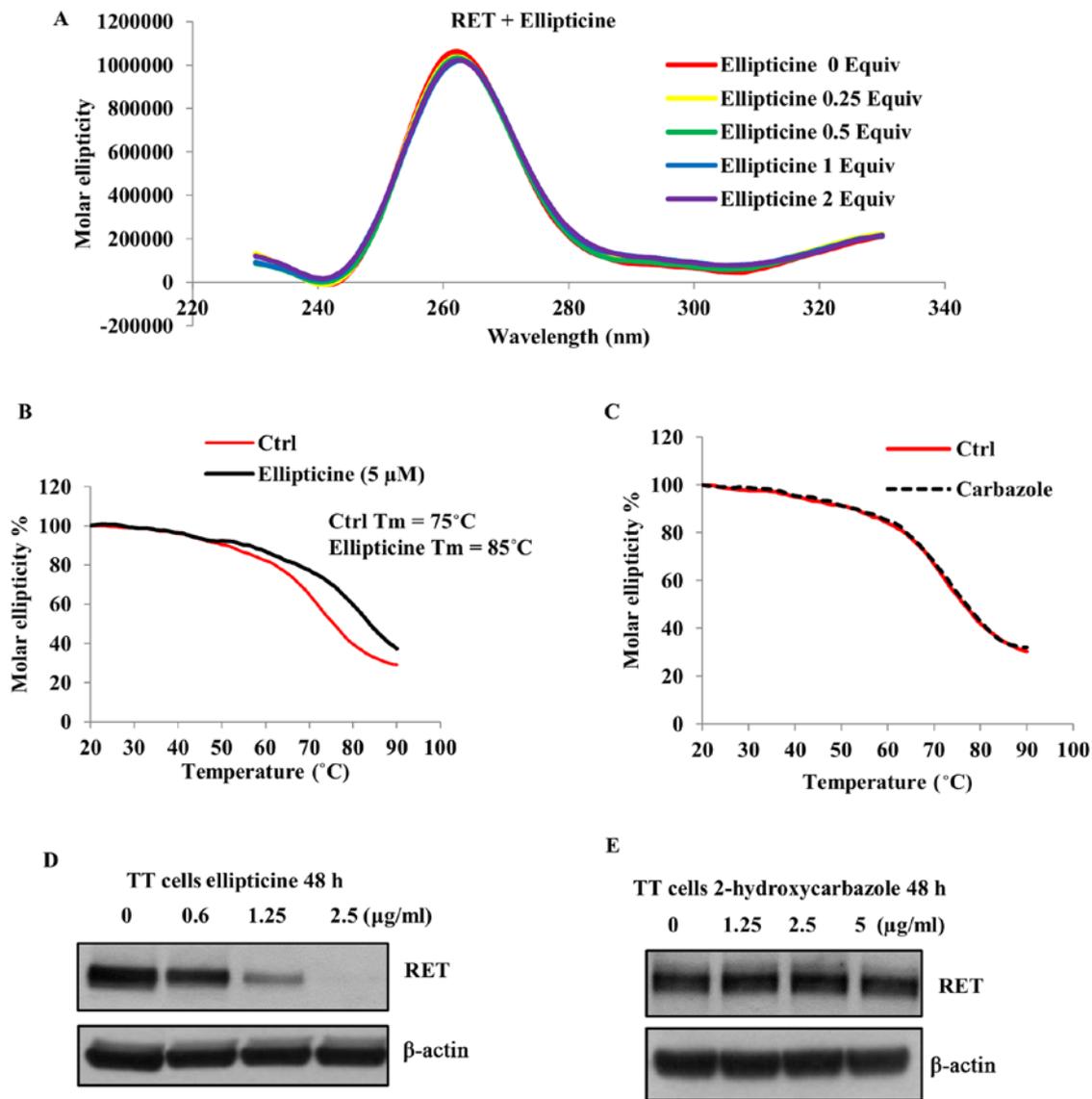


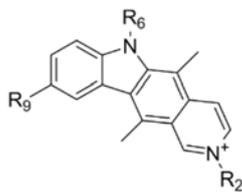
Figure 2. Evaluation of ellipticine as a potential RET G-quadruplex stabilizing agent. (A) CD titration spectra for the RET-WT ($5 \mu\text{M}$) in the absence and presence of increasing concentrations of ellipticine. x-axes and y-axes represent the wavelength of the spectral scan and molar ellipticity of the G-quadruplex structure, respectively. (B) Melting curve of the RET-WT G-quadruplex in the absence and presence of ellipticine (1 equivalent). (C) Melting curve of the RET-WT G-quadruplex in the absence and in the presence of 2-hydroxycarbazole (5 equivalents). x-axes and y-axes represent the temperature and relative molar ellipticity of the G-quadruplex structure, respectively. (D) Western blot analysis to determine the effect of ellipticine on RET protein expression in TT cells after 48-h incubation. (E) Effect of 2-hydroxycarbazole on RET expression in TT cells at various concentrations.

(Fig. 3A). Hence, we attempted to identify other structural analogs of ellipticine from the NCI/DPT open chemicals repository that could suppress the *RET* gene transcription at non-toxic concentrations without affecting their ability to stabilize the RET G-quadruplex structure (Figs. 1 and 3A). Based on the CD melting curves the ΔT_m was calculated individually for the ellipticine analogs and the IC_{50} values for these compounds were also determined by MTS assay (Fig. 3A). The ellipticine derivatives, which have different substituents such as methoxy, chloride and methyl groups at position C-9 of the pyridocarbazole ring stabilizes the RET G-quadruplex structure by increasing the $T_m > 10^\circ\text{C}$ (Fig. 3A). These compounds also possess RET inhibitory effects in TT cells, which is comparable to their parent molecule, ellipticine (Fig. 3B). However, the structural modifications in these compounds did not improve the cytotoxicity in TT cells as

compared to ellipticine (Fig. 3A). Notably, one of the ellipticine analogs, NSC311153, which carries a hydroxyl group and a 2-piperidin-1-ylethy moiety at positions C-9 and N-2, respectively showed an increased binding ability with the RET G-quadruplex structure with an estimated ΔT_m as 15°C (Fig. 3A). The IC_{50} value of this compound was also estimated to be $2.5 \mu\text{g/ml}$ after 96 h of exposure, which is significantly higher than that of ellipticine (Fig. 3A). Based on these data, we selected NSC311153 as a lead compound to further proceed with the *in vitro* studies.

Validation of NSC311153 as RET G4 stabilizing agent. To further validate that NSC311153 stabilizes the RET G-quadruplex structure formed on the promoter region of this gene, a DNA polymerase stop assay was performed as previously described (23). In this assay, the ligand mediated

A
Cellular Toxicity & ΔT_m of ellipticine analogs as determined by MTS assay and CD spectroscopy respectively



Compounds	R2	R6	R9	Cellular toxicity IC ₅₀ (μg/ml)	Melting temperature (ΔT_m °C)
Ellipticine		H	H	0.3	10
NSC155693	CH ₃	H	OCH ₃	0.8	11
NSC155694	CH ₃	CH ₃	OCH ₃	0.5	12
NSC632855	CH ₃	H	Cl	0.6	11
NSC639364	CH ₃	H	CH ₃	1.0	12
NSC311153		H	OH	2.5	15
NSC311152		H	OH	2.63	15

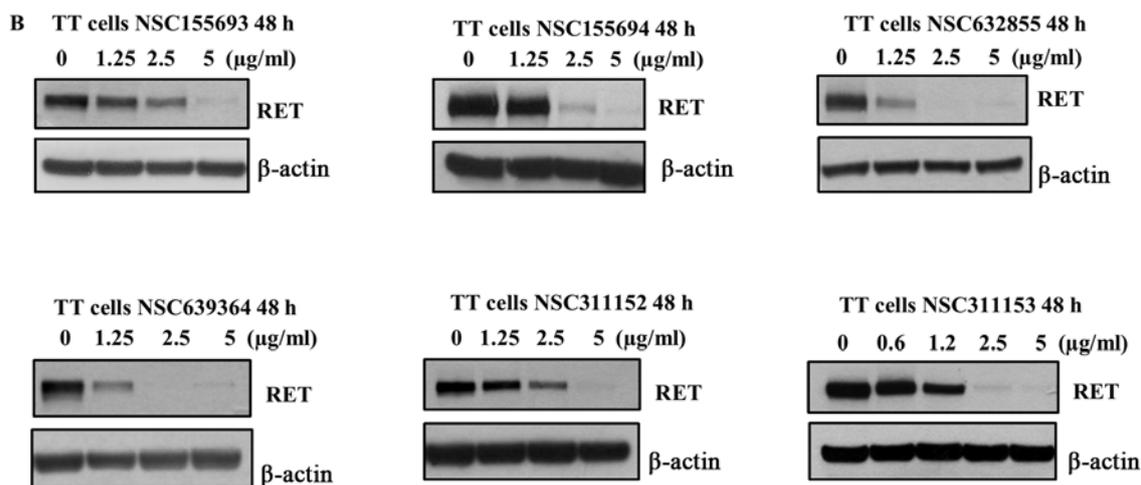


Figure 3. Effect of ellipticine and its structural derivatives on the RET expression in TT cells. (A) Ellipticine derivatives with different functional groups at positions C-9, N-2 and N-6. The IC₅₀ values of the ellipticine derivatives in TT cells and the increase in G-quadruplex T_m in the presence of these compounds were determined by MTS assay and CD spectroscopic analysis, respectively. (B) Evaluation of the RET inhibitory effects of all the ellipticine analogs in TT cells after 48-h treatment.

stabilization of the G-quadruplex structure that arises on the DNA template prevents the progression of the Taq DNA polymerase during primer extension. As shown in Fig. 4A, in the presence of NSC311153 at increasing concentrations, a dose-dependent increase in the amount of arrested product was observed, indicating the potential stabilization of the G-quadruplex structure by this compound.

Next, we investigated whether the interaction of NSC311153 with the parallel RET G-quadruplex structure changes the guanine residues that are involved in the G-tetrad formation using dimethyl sulfate (DMS) footprinting. DMS footprinting is a well-established technique to determine the guanine nucleotides that are involved in the formation of G-quadruplex structures (40,43). The N7 position of each of the guanine residues that are involved in Hoogsteen base pairing to form G-tetrads is inaccessible to methylation by DMS, which attacks

this position. As shown in Fig. 4B, the pattern of N7-guanine methylation produced by the RETG4 sequence in the presence of 100 mM K⁺ is consistent with two parallel G-quadruplexes (lane C) in which either the guanines (G19-G21) or (G20-G22) is involved in the G-tetrad formation (Fig. 4C, models 1 and 2). As shown in Fig. 4B, the binding of NSC311153 (5 equivalents) changes the pattern of N7 guanine methylation (lane D) in which the guanines (G14-G16) or (G15-G17) is involved in the G-tetrad formation (Fig. 4C, models 1 and 3). The change in the G-quadruplex structure in the presence of this compound clearly suggest that NSC311153 binds with this secondary structure.

Effect of NSC311153 on the promoter activity of RET gene. Since in our previous studies we reported that the G-quadruplex structure formed on the promoter region of

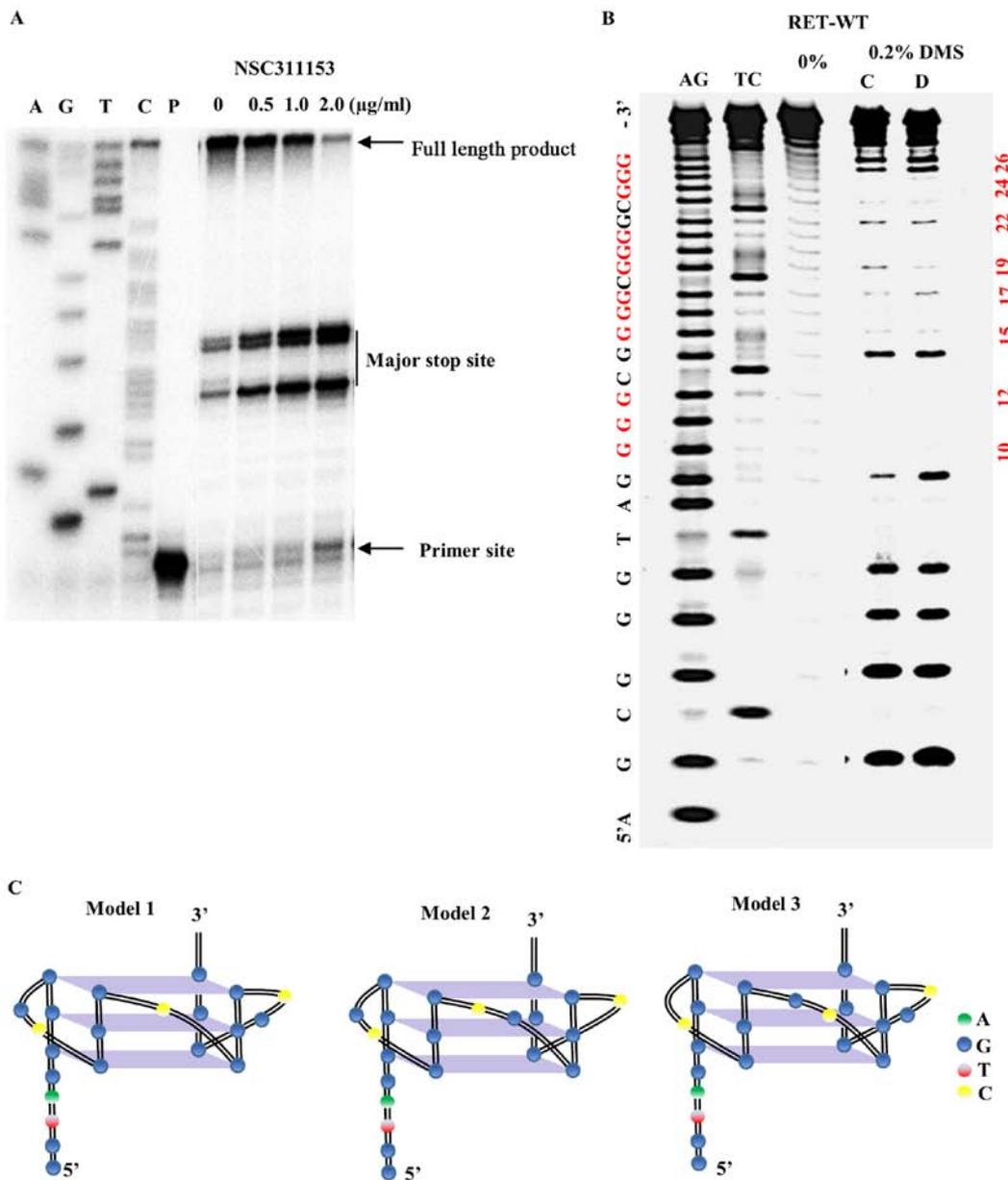


Figure 4. Taq DNA polymerase assay and DMS footprinting to validate the stabilization of RET G-quadruplex by NSC311153. (A) DNA polymerase stop assay at increasing concentrations of NSC311153. Lanes A, G, T and C represent the di-deoxy sequencing reactions with the same template, which serve as the marker to locate the exact stop site. Lane P represents the position of the free primer on the gel. (B) DMS footprinting on the RET-WT G-quadruplex forming sequence in the absence and presence of NSC311153 (5 equivalents) following 0.2% DMS treatment (lanes C and D, respectively). Purine and pyrimidine sequencing act as single base ladders to identify the protected and cleaved guanines after piperidine treatment (lanes AG and TC, respectively). (C) Schematic models for the parallel G-quadruplexes formed by RET-WT sequence in the absence and presence of NSC311153.

RET gene acts as transcriptional silencer element, we next examined whether the stabilization of RET G-quadruplex structure by NSC311153 interferes with the transcriptional activation of this gene in TT cell line. As shown in Fig. 5A, NSC311153 decreased the *RET* mRNA expression by >50 and 90% at a non-toxic concentration of 2.5 µg/ml following the exposure up to 24 and 48 h, respectively. We also utilized the MZ-CRC-1 cell line, which harbors an M918T mutation in the tyrosine kinase domain of the RET protein. Moreover, the *RET* gene expression in this cell line is regulated by the same promoter region as found in the TT cells, which harbors the G-quadruplex forming motif (44). As shown in Fig. 5B, a dose-dependent decrease in the RET protein

expression was observed in the presence of NSC311153 after 48-h incubation.

To determine whether the decrease in RET mRNA expression by NSC311153 is a direct effect of the promoter-specific transcriptional inhibition of this gene, a bioluminescent reporter gene assay was performed using an isogenic cell line HEK293-RET in which the luciferase expression is under the control of the *RET* promoter region as described in our previous study (23). As shown in Fig. 5C, in the presence of NSC311153 a dose-dependent decrease in the basal luciferase expression was observed in the HEK293-RET cell line following 48-h incubation. To further demonstrate that the mechanism of action of NSC311153 is through stabilizing the G-quadruplex

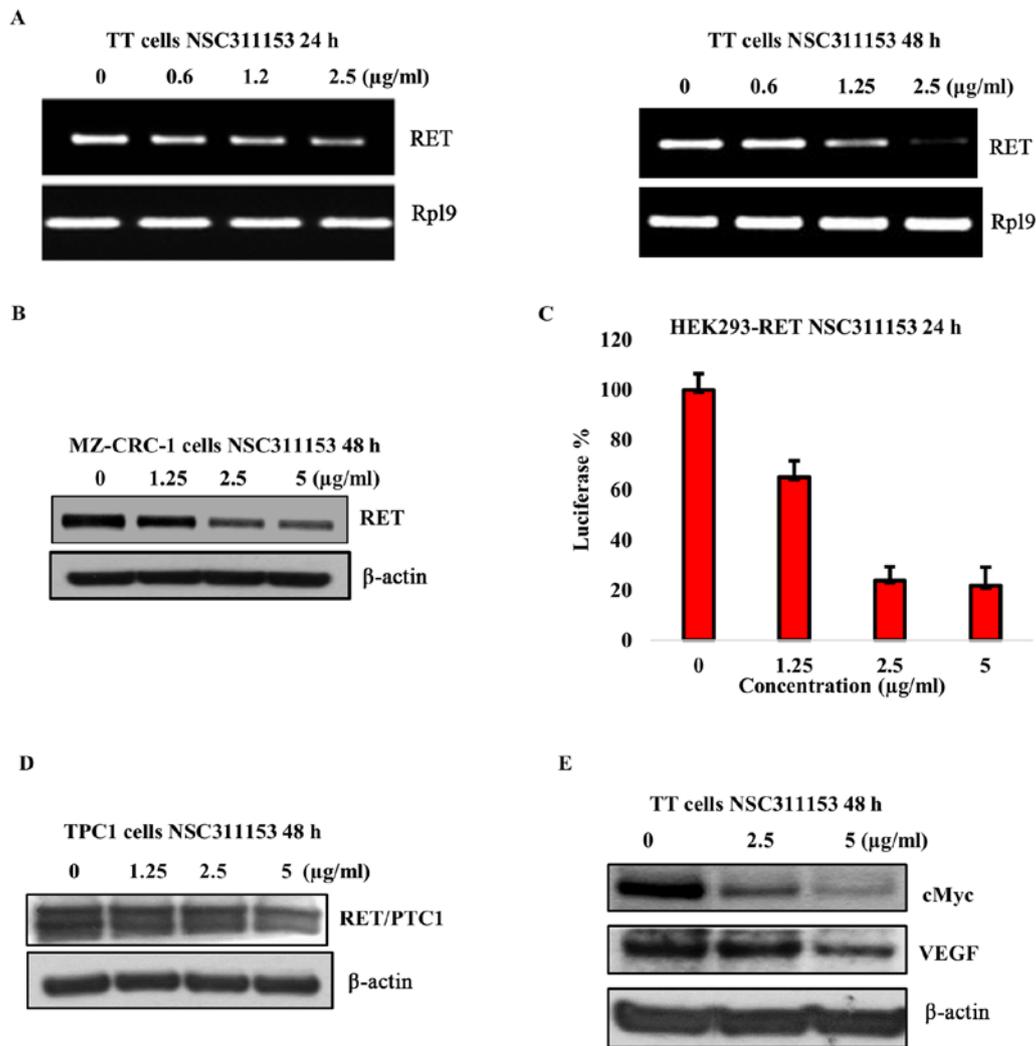


Figure 5. Inhibitory effect of NSC311153 on the promoter activity of *RET* gene. (A) Effect of NSC311153 on the *RET* mRNA expression in TT cells after 24- and 48-h treatments at various concentrations. (B) Effect of NSC311153 on the *RET* expression in MZ-CRC-1 cell line was determined by western blotting following 48-h incubation with this compound. (C) Luciferase expression in HEK293-*RET* cell line following the treatment with NSC311153 up to 24 h. Luciferase activity in cell lysates was measured as relative luminescence units (RLU) and normalized to the total protein content. x-axis and y-axis represent the concentration of NSC311153 and the relative luciferase activity in HEK293-*RET* cell line, respectively. Data are mean \pm SEM of three different experiments. (D) Effect of NSC311153 on the *RET/PTC1* expression in TPC1 cells was determined following 48-h exposure with various concentrations of this compound. (E) Western blot analyses for the expression of c-Myc and VEGF in TT cell line in the presence of different concentrations of NSC311153.

structure present on the *RET* promoter region, we utilized PTC1 derived TPC1 cells as a control. Chromosomal rearrangement between the *RET* kinase domain coding region and the *CCD6* gene results in a chimeric *RET/PTC1* expression, whose transcriptional activation is controlled by the *CCD6* promoter region that lacks the G-quadruplex forming motif (45-49). Notably, NSC311153 did not suppress the *RET/PTC1* expression in this cell line even after 48-h incubation (Fig. 5D). Overall, these data provide clear evidence to support that NSC311153 intervenes in the transcription mechanism of *RET* gene by targeting the intracellular G-quadruplex structure formed on its promoter region.

Cellular effects mediated by NSC311153 due to RET down-regulation. The oncogenic *RET* activation is mainly involved in mediating the cell proliferation and survival and hence the effect of NSC311153 on the viability of TT cell line was determined using the MTS assay. As shown in Fig. 6A

the proliferation of the TT cells decreased with increasing concentrations of NSC311153 and the IC_{50} was found to be ~ 2.5 $\mu\text{g/ml}$ after 96-h exposure. The TPC1 cell line in which the *RET/PTC1* expression was not inhibited by NSC311153 was less sensitive to this compound and the IC_{50} was 10-fold more than the TT cells (Fig. 6A). This clearly shows that the inhibition of cell growth by NSC311153 is mediated through the downregulation of the *RET* gene. To further determine whether the anti-proliferative effect of NSC311153 is cancer cell-specific, we included a normal thyroid cell line, Nthy-ori-3-1 in the present study. Based on the MTS data, the IC_{50} of NSC311153 in the Nthy-ori-3-1 cell line was estimated to be 10 $\mu\text{g/ml}$ (Fig. 6A), which is 4-fold higher than that of TT cells, suggesting that this compound is selectively sensitive to the mutant *RET* driven thyroid cancer.

To further characterize the mechanism through which NSC311153 suppresses the TT cell proliferation, we investigated whether this compound inhibits the *RET* mediated

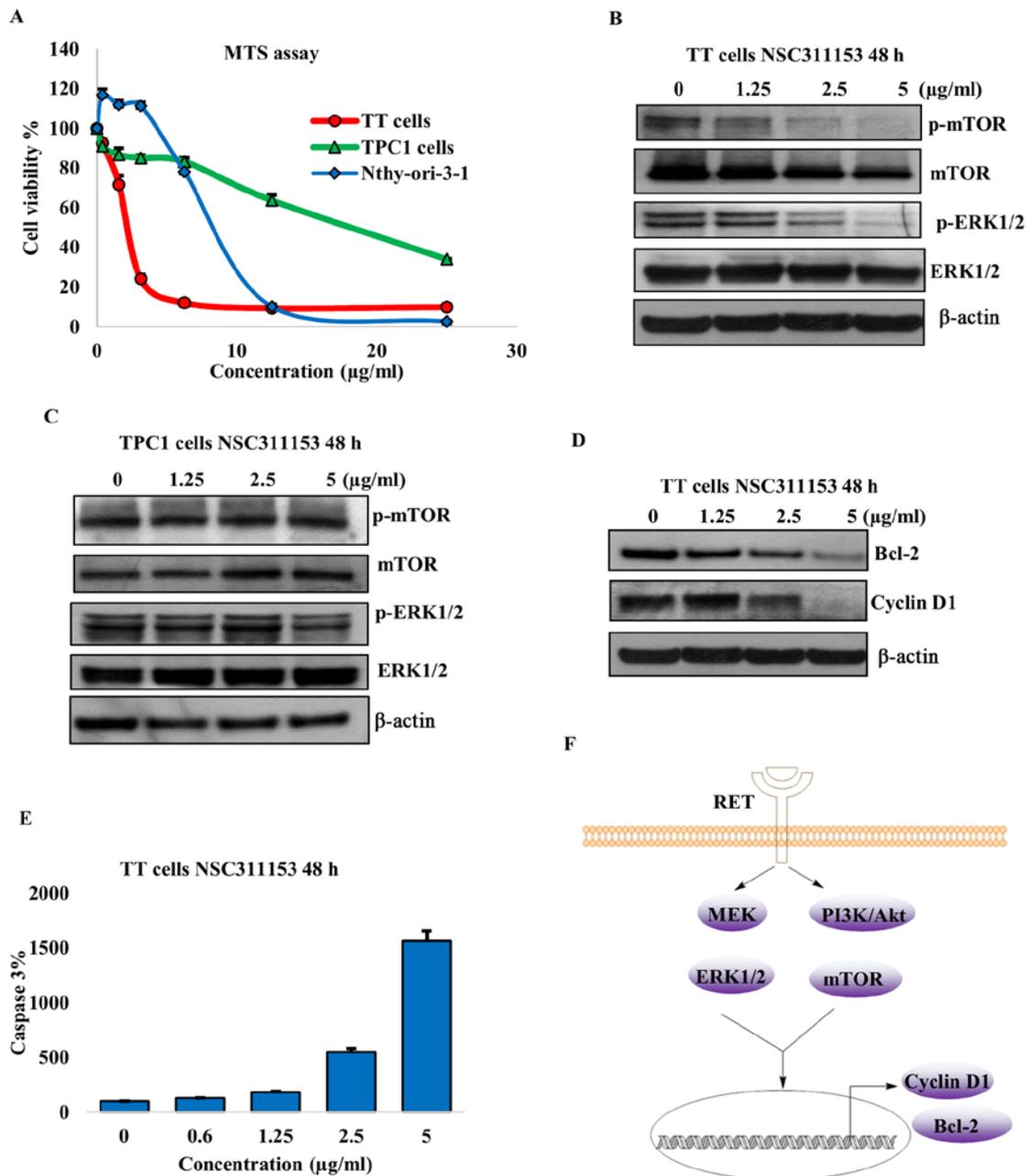


Figure 6. Cellular effects mediated by RET downregulation. (A) MTS assay for TT, TPC1 and Nthy-ori-3-1 cells treated with an increasing concentration of NSC311153 for 96 h to determine the cell viability. x-axes and y-axes represent the concentration of NSC311153 and the relative cell viability, respectively. Data are mean \pm SEM of three separate experiments. (B) The phosphorylation status of mTOR and ERK1/2 were determined in TT and TPC1 cells following the exposure with different concentrations of NSC311153. (C) Western blot analysis to determine the effect of NSC311153 on the phosphorylation of ERK1/2 and mTOR in TPC1 cells. (D) The Bcl-2 and cyclin D1 protein expressions in TT cells were determined by western blotting. (E) Caspase-3 activity was determined in TT cells in the presence of NSC311153. x-axes and y-axes represent the concentration of NSC311153 and the relative caspase-3 activity respectively. Data are mean \pm SEM of three separate experiments. (F) Schematic representation of the signaling pathways that are regulated by oncogenic activation of RET kinase (10).

downstream signal transduction pathways. Previous studies have revealed that RET activates the Raf/MEK and PI3K/Akt downstream signaling pathways, which in turn phosphorylate and activate ERK1/2 and mammalian target of rapamycin (mTOR) proteins, respectively (10-12). As shown in Fig. 6B, the phosphorylation status of ERK1/2 and mTOR were decreased in a dose-dependent manner following the exposure of TT cells in the presence of NSC311153 up to 48 h. However, in TPC1 cells the phosphorylation levels of these proteins were not altered by NSC311153 (Fig. 6C). These data clearly suggest

that the inhibitory effect of NSC311153 on this pathway is a consequence of RET downregulation.

The Raf/MEK/ERK and PI3K/Akt/mTOR pathways are known to promote cancer cell survival through the activation of cyclin D1 and Bcl-2, which are involved in enhancing cell-cycle progression and inhibiting the apoptosis mechanism, respectively (50-52). As shown in Fig. 6D, NSC311153 also decreased the expression of cyclin D1 and Bcl-2 in TT cells in a concentration-dependent manner. Furthermore, the downregulation of Bcl-2 by NSC311153 is further accompanied by

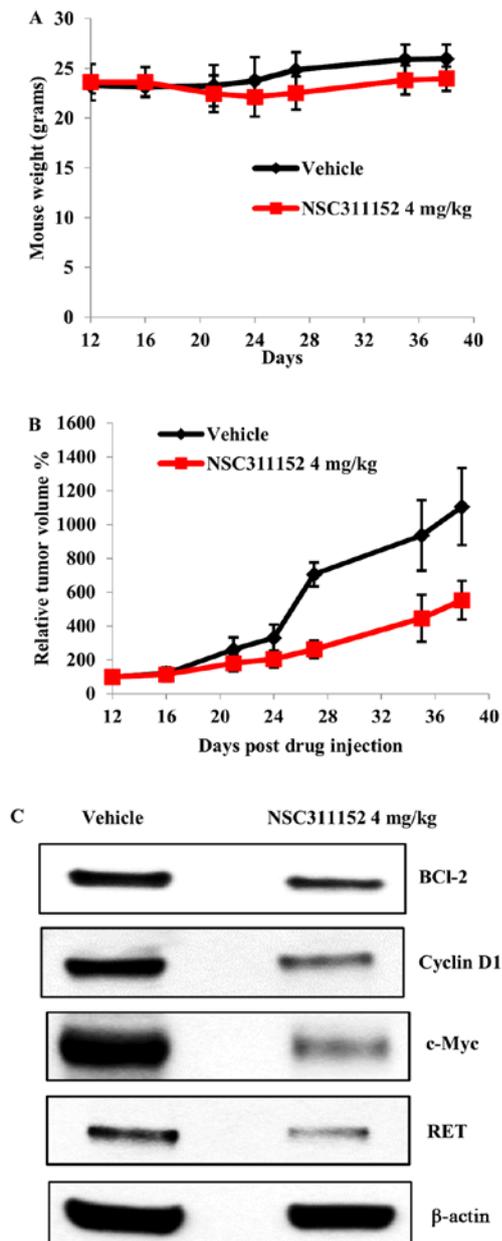


Figure 7. Effect of ellipticine derivative, NSC311152 on the MTC tumor growth *in vivo*. (A) Average weight of mice in vehicle treated group and NSC311152 (4 mg/kg) treated group. x- and y-axes represent the number of days after drug administration and the average mouse weight, respectively. (B) MTC tumor growth curves of the vehicle treated group and NSC311152 (4 mg/kg) treated group. x-axes and y-axes represent the number of days after drug administration and the average tumor volume, respectively. Data are mean \pm SEM of 6 different mice. (C) Western blot analysis to determine the expression of RET, cMyc, Bcl-2 and cyclin D1 on the tumor tissues extracted from the drug treated and vehicle treated mice.

the increase in the caspase-3 activity, which is also a known indicator of apoptosis (Fig. 6E).

In vivo antitumor activity of ellipticine derivative. In the final step of the present study, we evaluated the *in vivo* effect of the ellipticine derivative on the tumor growth of MTC xenografts through subcutaneous injection of the TT cells into SCID mice. Although NSC311153 showed potential anti-proliferative effects in TT cells *in vitro*, the poor solubility of this compound hindered its *in vivo* antitumor examination.

However, a previous study reported that a water soluble ellipticine analog, NSC311152 (datelliptium) was well tolerated in different cancer patients in a phase-I clinical trial (53). As shown in Fig. 1, the structure of NSC311152 is very similar to NSC311153 with the presence of a diethylaminoethyl-moiety at position N-2 that improves the solubility of this compound compared to that of NSC311153. Based on our preliminary data, the inhibitory effect of NSC311152 on RET expression and its IC_{50} value is the same as that of NSC311153, suggesting that the slight structural modification does not alter the efficacy of this compound. Hence, we decided to pursue with NSC311152 to test the *in vivo* antitumor activity. Dosing regimen and treatment schedules were determined based on our preliminary dose optimization studies. Upon systemic administration via i.p, NSC311152 (4 mg/kg) was well tolerated without any significant decrease in the average body weight (Fig. 7A). As shown in Fig. 7B, ~60% inhibition of the tumor growth was observed in mice treated with NSC311152 compared to the vehicle treated group. To further validate whether the inhibition of tumor growth by NSC311152 *in vivo* is mediated through target specific effect, we determined the RET expression in tumor tissues of vehicle- and NSC311152-treated mice using western blotting. As shown in Fig. 7C, the RET protein expression was decreased in the presence of NSC311152 compared to that of vehicle. Furthermore, NSC311152 reduced the expression of other proteins such as c-Myc, Bcl-2 and cyclin D1 that contribute to cell proliferation, which is in accordance with the *in vitro* studies. Overall, these data suggest that NSC311152 possesses potent *in vivo* antitumor activity through RET downregulation.

Discussion

RET was previously described as a regulator of several intracellular signaling events that contribute to the well-recognized biological processes such as cell survival, proliferation, migration and invasion (54). Hence, it is easy to understand why the constitutive activation of this protein due to point mutations in the functional domains is mainly involved in the progression of MTC. The clinical responses to standard chemotherapy and radiation therapy in patients with MTC have been shown to be less effective thereby representing MTC as a promising disease for the field of targeted drug therapy (55-57). Therapeutic approaches that target the RET kinase activity using small-molecule kinase inhibitors such as vandetanib and cabozantinib have proved to be clinically valuable in MTC (58,59). However, these kinase inhibitors possess potential inhibitory effects on other tyrosine-kinase receptors like VEGFR, EGFR, MET and hence the development of a specific inhibitor for RET still remains challenging (60,61). Moreover, a previous study demonstrated that the RET kinase carrying a substitution mutation of V804 to a bulky hydrophobic leucine or methionine amino-acids at the gatekeeper region in ATP binding pocket confers resistance to the kinase inhibitors (62). Hence, these gatekeeper mutations will likely emerge as one of the obstacles in the long-term use of vandetanib and cabozantinib in the treatment of patients with advanced MTC.

Another possible approach for the treatment of RET associated MTC involves the use of small interfering RNAs (siRNAs) to silence the *RET* gene expression. In a previous

investigation the transfection of TT cell line with RET siRNA exerted anti-proliferative effects on this cell line and also inhibited the growth of tumor xenografts *in vivo* (63). However, the development of siRNAs as drug-like molecules possesses several pitfalls that mainly include difficulty in delivering these molecules into target cells and their extracellular instability (64,65). The siRNAs are large and negatively charged molecules that greatly affect their permeability into plasma membrane and prevent intracellular accumulation at their site of action. Furthermore, siRNAs are highly susceptible to degradation by many extracellular enzymes that undermine the clinical implications of these molecules (65). To overcome these challenges, this study mainly focuses in targeting the transcription of the *RET* proto-oncogene using small molecules.

In our previous studies we have clearly demonstrated that the polypurine/polypyrimidine tract within the *RET* gene promoter region has a propensity to undergo strand separation that leads to conformational transition between duplex DNA and G-quadruplex structures (28,29). Moreover, we have also shown that the stabilization of these structures using small molecules emerged as potential transcriptional repressors of *RET* gene (23,24). The present study is based on a previous report, which revealed the interaction of a putative anticancer agent, ellipticine with the G-quadruplex structure formed by the human telomeric sequence (37). However, due to the adverse cytotoxic effects of ellipticine, we investigated the interaction of other ellipticine analogs with the RET G-quadruplex structure using *in vitro* biochemical assays. Notably, we identified an ellipticine derivative, NSC311153, which has a 2-piperidin-1-ylethyl moiety at position N-2 as a potent stabilizer of the RET G-quadruplex structure. The structure activity relationship (SAR) analysis clearly revealed that the presence of 1-ethylpiperidine at the N-2 position improves the binding of NSC311153 with the RET G-quadruplex and also significantly decreases the cellular toxicity compared to its parent molecule, ellipticine. The stabilization of the G-quadruplex structure by NSC311153 also exerted inhibitory effects on the RET promoter activity, which was confirmed using bioluminescent reporter assay in which the luciferase gene expression is driven by the *RET* promoter region. This compound further inhibited the RET mRNA and protein expression in TT cells, which harbor a MEN2A-type mutation. The transcriptional inhibitory effect of NSC311153 on other oncogenes like *VEGF* and *c-MYC* that also harbor the G-quadruplex forming sequences on their promoter regions was also investigated (66,67). As shown in Fig. 5E, the *c-MYC* expression showed a dose-dependent decrease in the presence of NSC311153, which is consistent with a previous study (37). Moreover, the VEGF expression was also partially inhibited by this compound suggesting that the G-quadruplex structure could be a potential intra-cellular target for NSC311153 (Fig. 5E).

In the present study, we also addressed that NSC311153 inhibited the proliferation of TT cells through the down-regulation of RET expression. The oncogenic RET activation promotes cell growth and survival by transducing a cascade of intracellular signaling pathways. In a previous study by Drosten *et al* (10) the RET associated downstream signaling pathways that are required for tumor maintenance and progression were well characterized in the TT cell line. In their study,

they used adenoviral vector expressing the dominant negative truncated RET protein, which lacks the entire intracellular tyrosine kinase domain to disrupt the phosphorylation and activation of RET protein in TT cells. This resulted in the downregulation of Raf/MEK/ERK and PI3K/Akt/mTOR pathways suggesting that these two pathways are mainly involved in RET mediated transformation (10). Consistent with this study, we also observed that the suppression of *RET* expression by NSC311153 inhibited the phosphorylation of ERK and mTOR and further decreased the expression of cyclin D1 and Bcl-2 that are tightly regulated by Raf/MEK/ERK and PI3K/Akt/mTOR pathways (Fig. 6F). Notably, we also observed that the normal thyroid cells, Nthy-ori-3-1 showed significant resistance to NSC311153 with an IC₅₀ of 10 µg/ml suggesting that this compound is more selective to mutant RET driven thyroid cancer.

To validate the drug-target selectivity, we utilized TPC1 cell line in this study, which is more robust and direct in demonstrating the RET G4-targeted activity of NSC311153. The chromosomal rearrangement between the RET tyrosine kinase domain coding region with the 5' terminal region of the coiled-coil domain containing gene 6 (*CCD6*) at chromosome 10q11.2 is a common genetic alteration identified in TPC1 cell line (46). This results in a chimeric fusion protein RET/PTC1, which is capable of ligand independent homodimerization due to the dimerization domain present in the *CCD6* gene thereby resulting in the constitutive activation of this protein (47). Due to chromosomal inversion the transcription of the *RET/PTC1* gene is regulated by the *CCD6* gene promoter region in TPC1 cells, which does not have the GC box region and thus is unable to form the G-quadruplex structure (49). In the present study, the RET/PTC1 expression was not decreased in the presence of NSC311153, suggesting that the presence of G-quadruplex structure on the promoter region of *RET* gene is essential to mediate the inhibitory effect of this compound. Based on the MTS data, the IC₅₀ of this compound in TPC1 cell line was 10-fold higher than that in TT cells, which clearly suggest that the anti-proliferative effect of NSC311153 is specifically mediated through RET downregulation.

In the present study, we also reported the *in vivo* antitumor activity of a water soluble NSC311153 analog, NSC311152 (datelliptium) in MTC xenograft mouse models. A phase I clinical study has been previously carried out using NSC311152 in patients with metastatic breast, ovarian, gastric and colorectal cancers (53). Based on that study, the maximum tolerated dose in humans was determined to be 9 mg/kg with minimal side-effects such as nausea, mild diarrhea, dry mouth and fatigue (53). Since NSC311152 has been investigated in clinical trial, repurposing this compound as a potent anticancer agent for MTC therapy has better advantages in terms of safety and other pharmacokinetic parameters compared to NSC311153. Moreover, the structural modification in NSC311152 did not affect the potency of this molecule in downregulating the RET expression *in vitro*. Hence, in this study we attempted to examine the *in vivo* effects of NSC311152.

Overall, the present study supports the notion that the G-quadruplex mediated RET transcriptional inhibition may be a valid therapeutic approach for the treatment of advanced and metastatic MTC. The identified RET transcriptional inhibitors could also be used in combination with other clinically avail-

able kinase inhibitors to improve their therapeutic efficacy in MTC patients.

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