Development of a novel PROTAC using the nucleic acid aptamer as a targeting ligand for tumor-selective degradation of nucleolin

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Abstract: PROteolysis TArgeting Chimeras (PROTACs) induce target protein degradation by hijacking the intracellular ubiquitin proteasome system, thus emerging as a new strategy for drug development. However, most PROTACs generated lack cell-type selectivity, resulting in potential off-tissue on-target toxicity. To address this drawback, we developed a novel PROTAC ZL216 using AS1411 as a targeting ligand for nucleolin. Based on the differential expression of nucleolin, ZL216 could bind to and internalize into breast cancer cells, but not normal breast cells, and induce nucleolin degradation by promoting the formation of a nucleolin-ZL216-VHL ternary complex. Thus, ZL216 inhibited the proliferation and migration of breast cancer cells. These studies demonstrate that in addition to peptides and small molecule compounds, aptamers can also be used to construct PROTACs, which broadens the toolbox constructing PROTACs and provides a promising strategy for the development of tumor-selective PROTACs.

Introduction

PROteolysis Targeting Chimeras (PROTACs) are small molecules with heterobifuntional property, consisting of a ligand for binding to a protein of interest (POI) and the other for recruiting an E3 ubiquitin ligase via a linker connection.[1-2] Such molecules can tether an E3 ligase to POI by forming a ternary complex, thereby triggering proximity-induced ubiquitination and degradation of POI in a catalytic manner.[3] PROTACs have been developed to degrade proteins that play important roles in tumorigenesis and do so with extraordinary efficacy on multiple tumor types, including BRAF mutant V600E for melanoma, [4] BET for prostate cancer,[5] BCL-XL for leukemia[6] and Estrogen Receptor (ER) for breast cancer.[7] Until present, at least 15 targeted protein degraders are expected to be tested in patients at different stages of human clinical trials.[8] However, although PROTACs are highly efficient for protein degradation and, hence, a potential therapeutic strategy for cancer, most PROTACs generated

lack tumor selectivity, one of the main reasons is that the E3 ligases utilized by PROTACs are widely expressed in both normal and tumor tissues. As a result, these PROTACs may produce on-target toxicity if POIs are not tumor-specific. This calls for the development of selective ligands able to restrict the activity of PROTACs to tumor cells, but not normal cells, thus generating tumor-selective PROTACs.

Aptamers are single-stranded DNA or RNA oligonucleotides with a length typically less than 100 nucleotides. [9] Aptamers are generated by an iterative selection process termed systematic evolution of ligands by exponential enrichment (SELEX) from a randomized oligonucleotide library.[10] Similar to antibodies, aptamers bind to their targets with high specificity and affinity by folding into a unique three-dimensional conformation. Compared to protein antibodies, aptamers hold unique characteristics derived from their oligonucleotide properties, such as low immunogenicity and toxicity, easy chemical synthesis and modification, rapid tissue penetration and excellent stability.[11] With the advent of cell-specific aptamers, aptamers have been widely used as tumor recognition ligands for targeted therapy and diagnostics. For example, CD71 ssDNA aptamer was coupled with doxorubicin to specifically target tumor cells and inhibit their proliferation. [12]

AS1411 is a 26-base guanine-rich ssDNA aptamer, which binds to nucleolin with high affinity and specificity. Many studies have indicated that enhanced expression of nucleolin on the cell surface is restricted to tumor cells, but not normal cells, thus conferring a tumor-selective binding behavior to AS1411.[13] Meanwhile, AS1411 can be internalized into tumor cells by nucleolin-dependent macropinocytosis and subsequently exerts antiproliferative activity against a wide range of tumor types, including breast cancer,[14] glioma,[15] renal cell carcinoma[16] and leukemia.[17] Thus, AS1411 potentially acts as both a tumor-targeting element and an anticancer therapeutic agent. Recently, AS1411 was used as a targeted delivery tool, via an ester-disulfide linker to deliver BET-PROTAC into breast cancer cells for targeted release, thereby degrading the BRD 4 protein for tumor therapy. [18]

In this study, we report the first proof-of-concept evidence using nucleic acid aptamer to construct a novel PROTAC. Aptamer AS1411, as a targeting ligand for nucleolin, was conjugated to a small molecule ligand of E3 ligase VHL via a DBCO- azide click reaction, which generated a nucleolin-targeting PROTAC ZL216 with excellent serum stability and water solubility. We demonstrated that ZL216 could recruit E3 ligase VHL to nucleolin in breast cancer cells and potently induce the degradation of nucleolin *in vitro* and *in vivo*. As a result, ZL216 inhibited the proliferation and migration of breast cancer cells. Our work demonstrates the potential use of aptamers in generating PROTACs to achieve selective degradation of target protein in tumor cells and provides a promising strategy for development of tumor-selective PROTACs.

Results

Development of a novel PROTAC ZL216 using aptamer.

By analyzing various cancer types found on the TCGA database using TIMER2.0, we found that the gene expression levels of nucleolin in multiple tumor tissues, including breast cancer tissues, were significantly higher than those of normal tissues (Figure S1A). Consistent with this, the result of the CPTAC proteomics database also showed elevated protein levels of nucleolin in breast cancer tissues compared to corresponding normal tissues (Figure S1B). We further confirmed this finding in cell lines by Western blotting, which showed enhanced expression of nucleolin protein in breast cancer cells (MCF-7 and BT474), but not in immortalized breast epithelial cells (MCF-10A) (Figure S1C). Moreover, a part of nucleolin was distributed at the surface of MCF-7 and BT474 cells, but not the surface of MCF-10A cells (Figure S1D), which is consistent with the notion that the expression of nucleolin on the cell surface is restricted to tumor cells.

AS1411 functions as an ssDNA aptamer that can bind to nucleolin with high affinity and specificity and that it is quickly internalized into cells following binding to nucleolin.[12] Given the critical role of nucleolin in supporting tumorigenesis and metastasis, we hypothesized that AS1411-constructed PROTAC could achieve targeted antitumor activity through promoting nucleolin degradation specifically in tumor cells (Figure 1A). To test the possibility, DBCO-labeled AS1411, as a targeting element for nucleolin, was conjugated via the click reaction to a VHL E3 ligase-binding ligand, (S, R, S)-AHPC-PEG3-azide (AHPC), to generate a nucleolin degrader ZL216 (Figure 1B), whereas an ssDNA sequence, which has no affinity for nucleolin, was linked to AHPC as a negative control (Figure S2A). In addition, the synthesis and characterization of Cy5-labeled Control and ZL216 were shown in Figure S2B and S2C. To measure the stability of ZL216 in serum, ZL216 and AS1411 were incubated with human serum. We found that ZL216 held an excellent serum stability, similar to that of AS1411, with a half-life is 70.5 hours (Figure 1C). Meanwhile, the water solubility of ZL216 was significantly enhanced compared to that of free VHL E3 ligase-binding ligand AHPC through conjugation with aptamer AS1411 (Figure S3).

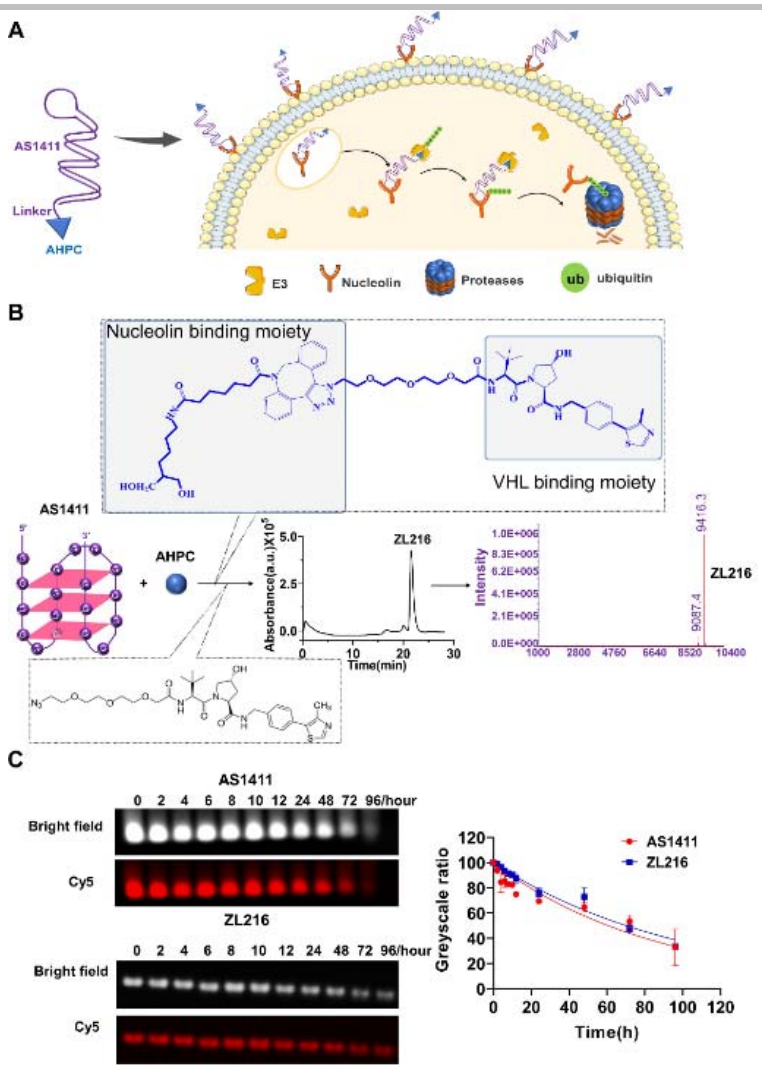

Figure 1. Development of aptamer-based PROTAC ZL216. (A) Presumed mode of action of ZL216 on degradation of nucleolin in cancer cell. (B) Synthetic roadmap and LC-MS analysis of ZL216. (C) Agarose gel electrophoresis and quantitative analysis of AS1411 and ZL216 in human serum. Data are presented as the means ± standard deviation, n = 3.

Selective binding ability of ZL216.

Previous studies have shown that AS1411 can specifically bind to breast cancer cells through recognizing cell-surface nucleolin. [19-20] To assess whether ZL216 still retains the binding specificity to breast cancer cells, cells were incubated with Cy5-labeled AS1411, ZL216 and Controls, respectively. As shown in Figure 2A, 2B and 2C, a significant fluorescence peak

shift was observed from MCF-7 and BT474, but not MCF-10A cells, indicating that ZL216 held its binding specificity to breast cancer cells in a manner similar to that of AS1411. Meanwhile, the selective binding ability of ZL216 was further confirmed by confocal imaging (Figure 2D-F). To identify whether ZL216 has the same binding sites as AS1411, a competitive binding assay was performed by flow cytometry. Different concentrations of unlabeled AS1411 were incubated with Cy5-labeled ZL216. Intriguingly, ZL216 gradually lost its binding to MCF-7 and BT474 cells as the concentration of AS1411 increased, whereas the Control showed no effect from the binding between ZL216 and MCF-7 or BT474 cells, implying that the same binding sites were shared by ZL216 and AS1411(Figure 2G and 2H). Furthermore, the binding affinity assay showed that the K_d of ZL216 for MCF-7 and BT474 cells was 11.92±3.66 nM and 15.27±2.848 nM, while the K_d of AS1411 on MCF-7 and BT474 cells was 13.53±3.576 nM and 30.76±7.019 nM, respectively (Figure 2I and 2J), suggesting that ZL216 had stronger binding ability than AS1411 alone. We speculate that the mechanism underlying this enhanced binding ability might be associated with the role of the conjugate in stabilizing the dynamic binding of AS1411.

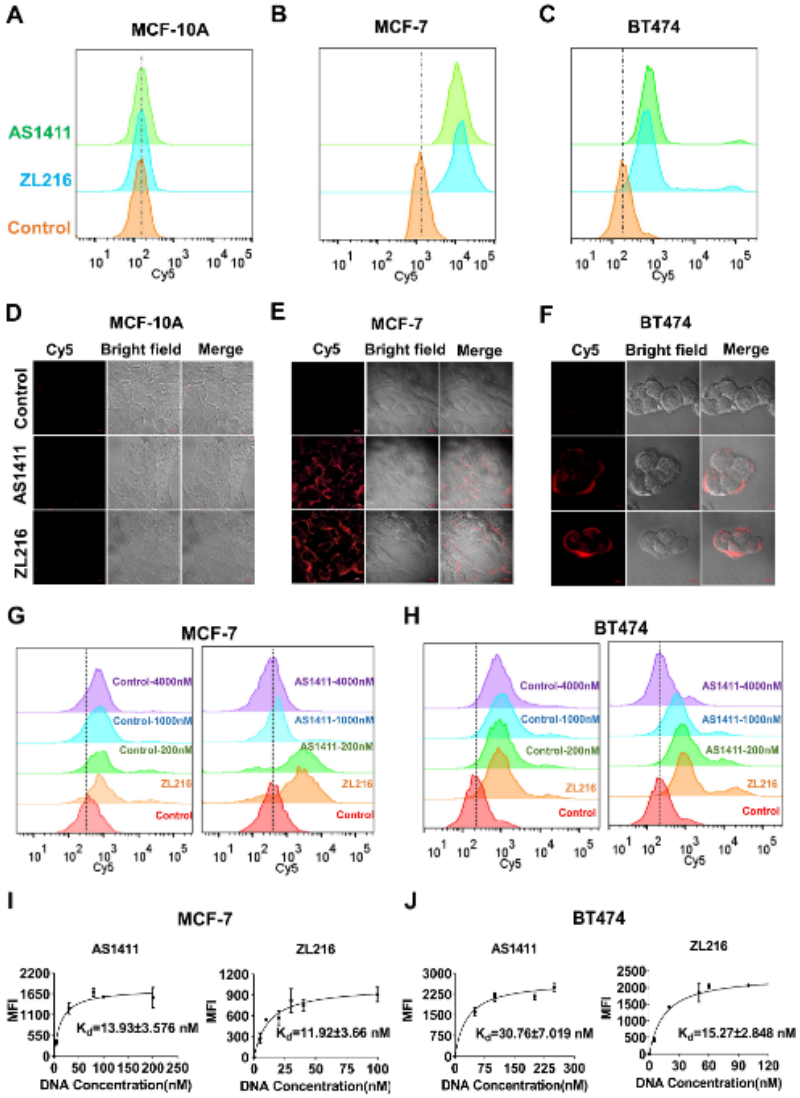

Figure 2. ZL216 selectively binds to breast cancer cells. (A-C) The binding of ZL216 and AS1411 to MCF-10A (A), MCF-7 (B) and BT474 (C) cells was analyzed by flow cytometry. The concentrations of ZL216 were 25 nM in MCF-7 or 50 nM in BT474 and MCF-10A cells. (D-F) MCF-10A (D), MCF-7 (E) and BT474 (F) cells were incubated with Cy5-labeled ZL216 and AS1411. Fluorescence, bright-field, and merged confocal images were shown. (G-H) MCF-7 (G) and BT474 (H) cells were incubated with the indicated concentration of AS1411, followed by treatment with Cy5-ZL216. Competition binding was analyzed by flow cytometry. (I-J) The dissociation constant of AS1411 and ZL216 for MCF-7 (I) and BT474 (J) cells was determined by flow cytometry (Median fluorescence intensity, MFI). Data are presented as the means ± standard deviation, n = 3.

ZL216 specifically attenuates nucleolin of breast cancer cells *in vitro* and *in vivo*.

Internalization into cells directly determines whether aptamer-constructed PROTAC can hijack the intracellular ubiquitin proteasome system. To investigate the internalization property of ZL216, intracellular fluorescence signals were detected by flow cytometry after eliminating the fluorescence signals on the cell surface by trypsin or proteinase K. As shown in Figure S4A and S4B, the removal of the fluorescence signals on the cell surface reduced, rather than eliminated, the fluorescence signals from target cells, indicating that a fraction of ZL216 could be internalized into target cells. Next, we evaluated ZL216 for its ability to regulate nucleolin levels. After cells were treated with different concentrations of ZL216, nucleolin abundance was analyzed by Western blotting. We found that ZL216 could effectively downregulate nucleolin levels in MCF-7 and BT474 cells (Figure 3B and 3C). At the 5-h time point, the half-maximal inhibition concentration (DC_{50}) and maximum inhibition (D_{max}) of MCF-7 cells were 13.5 nM and 77%, while those of BT474 cells were 17.8 nM and 87%, respectively. In contrast, ZL216 failed to reduce nucleolin level in MCF-10A cells (Figure 3A). The time dependency of ZL216 on nucleolin showed that maximal reduction of nucleolin was achieved at 48 h for MCF-7 cells (Figure 3E) and 5 h for BT474 cells (Figure 3F). In addition, both AS1411 and an E3 ligase-binding ligand AHPC had no effect on nucleolin levels (Figure S5A and S5B). Furthermore, to deter-mine whether ZL216 retains its recognition ability and reduces nucleolin levels *in vivo*, we generated MCF-7 and BT474 xenografts in mice and then treated the mice with Cy5-labeled ZL216, AS1411 and Control via tail vein injection. As expected, the fluorescence signal was rapidly accumulated at the tumor sites after injecting ZL216 and AS1411, while no significant fluorescence signal was observed at the tumor sites treated with Control, indicating that ZL216 held the same ability to target tumor *in vivo* as that achieved by AS1411 (Figure 3G and 3H). Notably, ZL216 could decrease nucleolin levels in xenografts (Figure 3I and 3J). In contrast, neither AS1411 nor AHPC had any effect on nucleolin levels

(Figure 3K and 3L). This result highlighted that ZL216 not only possessed an ability to target tumors similar to that of AS1411, but also had the added benefit of reducing nucleolin levels, not otherwise achievable by AS1411.

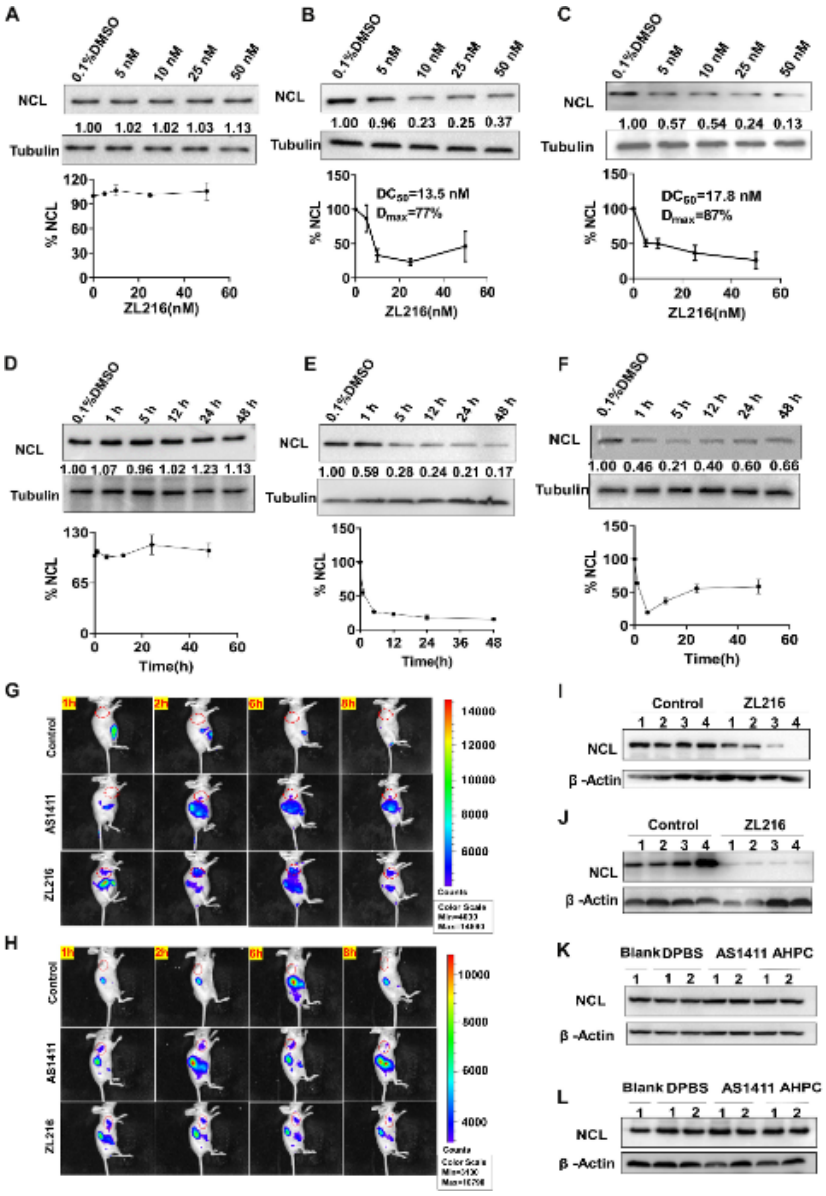

Figure 3. ZL216 downregulates the nucleolin (NCL) of breast cancer cells *in vitro* and *in vivo*. (A-C) MCF-10A (A), MCF-7 (B) and BT474 (C) cells were treated with the indicated concentration of ZL216. Total protein was extracted and subjected to Western blotting using the indicated antibodies. (D-F) ZL216-treated cells at the concentration of 50 nM (MCF-10A) (D), 25 nM (MCF-7) (E) and 50 nM (BT474) (F). Total protein was extracted at the indicated time points and subjected to Western blotting

using the indicated antibodies. (G-H) MCF-7 cells (G) and BT474 cells (H) were injected subcutaneously into nude mice. When tumors grew to desired size, 50 μM Cy5-labeled AS1411, ZL216 or Control was injected intravenously into nude mice. The fluorescence images *in vivo* were shown at the indicated time points. (I-J) MCF-7 (I) and BT474 (J) tumor-bearing mice were injected intravenously with 50 μM ZL216 or Control. Total protein was extracted from tumor tissues and subjected to Western blotting using the indicated antibodies. (K-L) MCF-7 (K) and BT474 (L) tumor-bearing mice were injected intravenously with 50 μM AS1411, AHPC or equivalent DPBS. Total protein was extracted from tumor tissues and subjected to Western blotting using the indicated antibodies.

ZL216 degrades nucleolin in a VHL- and proteasome-dependent manner.

To confirm that ZL216 causes the reduction of nucleolin levels through the expected degradation mechanism via proteasome, we first tested the effect of ZL216 on the expression of nucleolin mRNA by real-time PCR. We found that the levels of nucleolin mRNA were not regulated by ZL216, Control, AHPC or AS1411 (Figure 4A and 4B), indicating that ZL216 did not affect nucleolin expression at the transcriptional level. Furthermore, downregulation of nucleolin caused by ZL216 could be abolished by a proteasome inhibitor, MG132, or a cullin neddylation inhibitor, MLN4924 (Figure 4C and 4D), suggesting that ZL216 decreased nucleolin levels through the proteasome degradation pathway. To further identify whether ZL216 degrades nucleolin via VHL, cells were treated with a high concentration of free AHPC to compete for the binding of ZL216 to VHL. The results showed that an excess amount of AHPC could significantly attenuate the effect of ZL216 on nucleolin in MCF-7 and BT474 cells (Figure 4E and 4F), demonstrating that ZL216-mediated regulation of nucleolin protein levels depended on VHL. Since ZL216 downregulated nucleolin protein levels, we questioned whether ZL216 affected the stability of nucleolin. To this end, cells were treated with cycloheximide (CHX) to inhibit protein biosynthesis, followed by analyzing nucleolin protein at

indicated time points. We found that ZL216 treatment significantly shortened the half-life of nucleolin protein compared with Control treatment (Figure 4G and 4H).

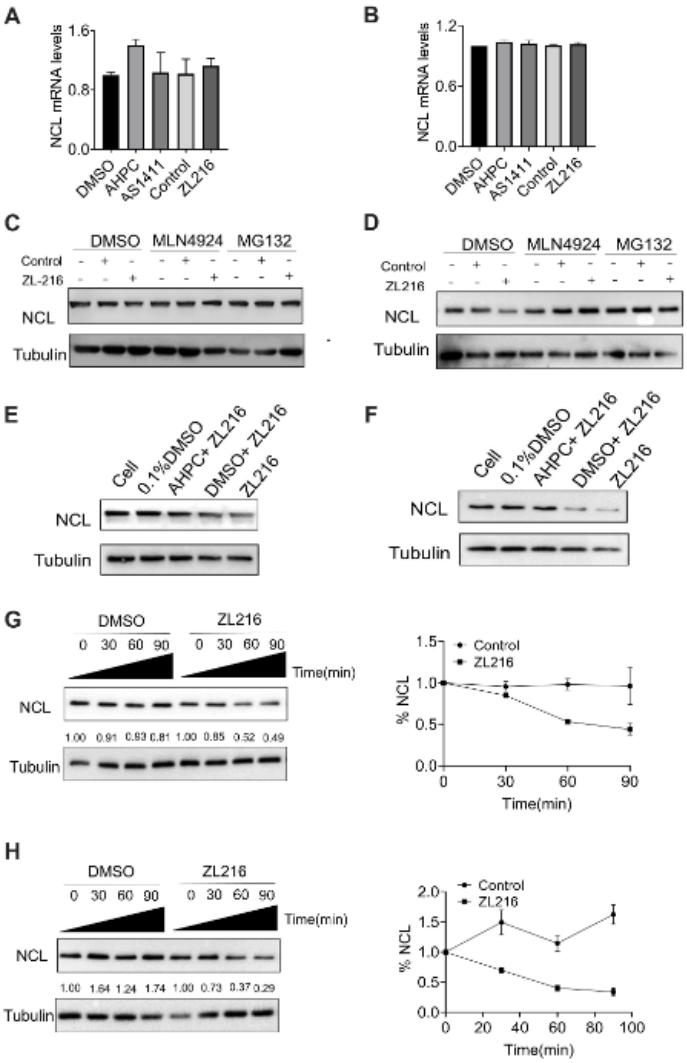

Figure 4. ZL216 redirects E3 ubiquitin ligase VHL to degrade NCL proteins via the proteasomal pathway. (A-B) Total RNA from MCF-7 (A) or BT474 (B) cells treated with Control, AHPC, AS1411 or ZL216 was isolated and subjected to RT-PCR. The error bars represent the SD of triplicate measurements. (C-D) MCF-7 (C) or BT474 (D) cells were pretreated with DMSO, MLN4924 (5 μM) or MG132 (20 μM), followed by ZL216 treatment for 5 h. The indicated proteins were analyzed by Western blotting. (E-F) MCF-7 (E) or BT474 (F) cells were in-cubated with AHPC (1 μM), followed by ZL216 treatment for 5 h. The indicated proteins were analyzed by Western blotting. (G-H) MCF-7 (G) or BT474

(H) cells were incubated with 100 μg·mL^{-1} CHX for 1 h, followed by ZL216 treatment. Total proteins were extracted at the indicated time points and subject-ed to Western blotting using the indicated antibodies. The concentrations of Control, AS1411 or ZL216 were 25 nM or 50 nM respectively in MCF-7 or BT474 cells.

ZL216 induces the formation of nucleolin-ZL216-VHL ternary complex.

Nucleolin is not the intracellular natural substrate of the E3 ligase VHL. We hypothesized that ZL216 may mediate the degradation of nucleolin through the formation of a nucleolin-ZL216-VHL ternary complex. To address this, Flag-VHL and Myc-NCL plasmid were transfected into MCF-7 cells, and coimmunoprecipitation was conducted using anti-Flag or anti-Myc antibody. The results indicated that Myc-nucleolin was present in Flag-VHL immunoprecipitates after cells were treated with 25 nM ZL216 and vice versa (Figure 5A and 5B). Conversely, treatment with Control, which lacks nucleolin binding, failed to detect the expected protein in Flag-VHL or Myc-nucleolin immunoprecipitates. Immunofluorescence staining further revealed that ZL216, but not Control treatment, caused the colocalization of nucleolin and VHL (Figure 5C). Because the E3 ligase catalyzes proximity-induced ubiquitination of substrate, we questioned whether the formation of ternary complex induced by ZL216 contributed to nucleolin ubiquitination. To this end, the ubiquitination levels of nucleolin were measured. As expected, ZL216 significantly increased the ubiquitination levels of nucleolin, whereas DMSO and Control exhibited no effect on nucleolin ubiquitination (Figure 5D and 5E). Collectively, these results suggest that ZL216 promotes nucleolin ubiquitination by inducing nucleolin-ZL216-VHL ternary complex formation.

To investigate the molecular basis of nucleolin-ZL216-VHL ternary complex formation, molecular docking and dynamics simulation were performed. A total of 100 conformations were extracted and ranked by docking energy value. Since low-energy conformations help reveal detailed intermolecular interaction and stable bonding interface, conformations with the lowest

binding energy were chosen to predict the binding spots. The result showed that the binding mode between nucleolin and AS1411 was mainly dependent on hydrophobic bonds with the binding energy of -123 kcal/mol, whereas the binding between VHL and AHPC appeared to be maintained by the formation of polar hydrogen bonds with docking energy of -7.99 Kcal /mol (Figure 5F). The above results implied that ZL216 could interact with nucleolin and VHL with high binding affinity.

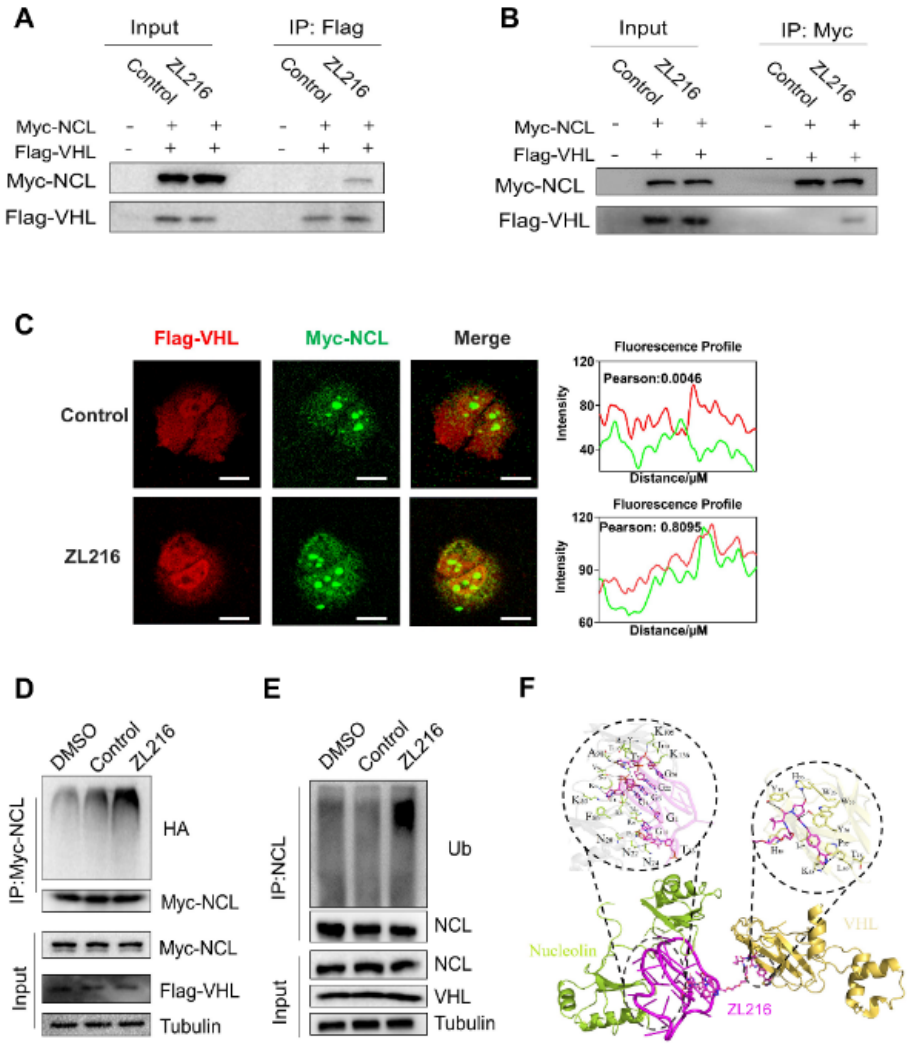

Figure 5. ZL216 mediates nucleolin-ZL216-VHL ternary com-plex formation. (A-B) MCF-7 cells transfected with plasmids expressing Flag-VHL and Myc-NCL were treated by 25 nM ZL216 or Control treatment for 5 h. Total cell lysates were subjected to immunoprecipitation with anti-Flag (A) or anti-Myc

(B) antibody. The immunoprecipitates were then analyzed by Western blotting using the indicated antibodies. (C) MCF-7 cells transfected with the indicated plasmids were treated with 25 nM ZL216 or Control for 5 h. The subcellular localization of VHL and nucleolin was visualized using immunofluorescence with the indicated antibodies. (D) MCF-7 cells transfected with plasmids expressing Myc-NCL and HA-Ub were incubated with MG132 (20 μM) for 1 h, followed by treatment with DMSO, 25 nM Control or ZL216 for 5 h. Myc-NCL was immunoprecipitated with anti-Myc antibody, and the immunoprecipitates were probed with the indicated antibodies. (E) MCF7 cells were incubated with MG132 (20 μM) for 1 h, followed by treatment with DMSO, 25 nM Control or ZL216 for 5 h. Nucleolin was immunoprecipitated with an anti-nucleolin antibody, and the immunoprecipitates were probed with the indicated antibodies. (F) Predicting optimal conformation of NCL: ZL216: VHL ternary complex. Light green dashes indicate the NCL structure, and blue cartoons are VHL E3 ligase. Magenta dashes represent ZL216. Scale bars in overlay images represent 20 μm.

ZL216 inhibits the proliferation and migration of breast cancer cells via VHL binding.

To address whether the ZL216-induced degradation of nucleolin affects the proliferation and migration of breast cancer cells, we performed a cell proliferation and migration assay in MCF-10A and MCF-7 cells. The results showed that ZL216 treatment dramatically inhibited the proliferation of MCF-7 cells, but had no effect on MCF-10A cells (Figure 6A and 6B). A wound healing assay demonstrated that ZL216 treatment significantly reduced the migration of MCF-7, but not MCF-10A cells (Figure 6C and 6D). Consistently, a similar result was observed in transwell assay, and MCF-7, but not MCF-10A, cells in lower layer after ZL216 treatment were notably fewer in number compared to Control treatment (Figure S6 and S7). The selective effect was consistent with the specific degradation of nucleolin induced by ZL216 in breast cancer cells. Interestingly, the effect of ZL216 on MCF-7 cells could be abolished by pretreatment with 1 μM AHPC (Figure 6 and Figure S7-8), implying that the anti-proliferation and anti-migration activities of ZL216 were dependent on VHL binding. Of note, although previous studies showed that AS1411 retained its functional activity against breast cancer, we

found that AS1411 treatment failed to show any effect on MCF-7 cells. This might be explained by the lower concentration of AS1411 treatment.

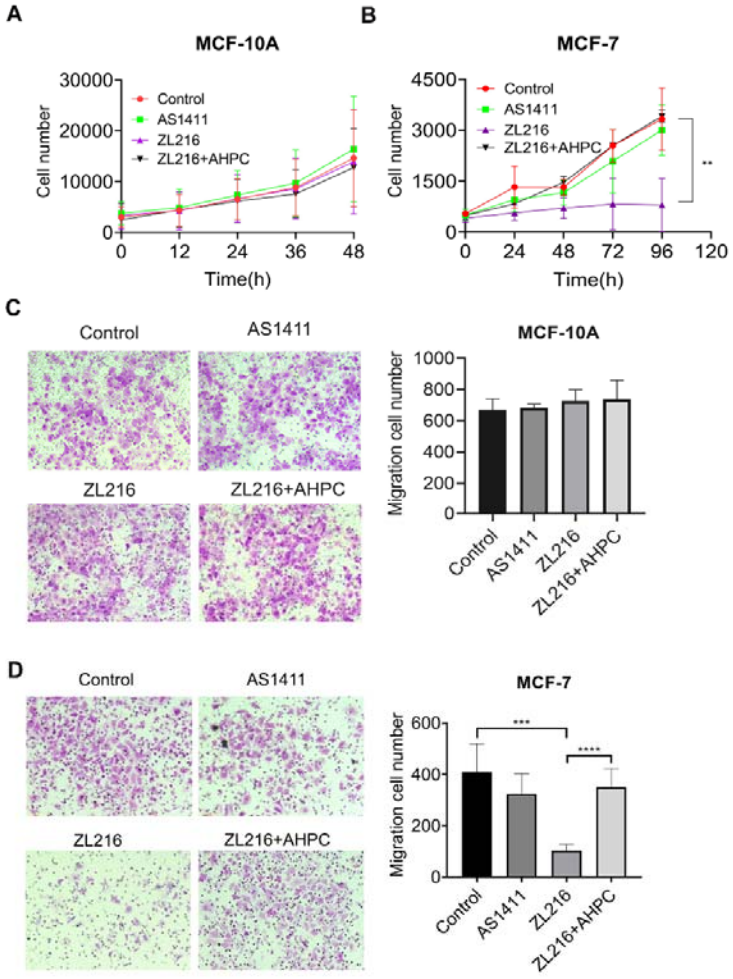

Figure 6. ZL216 inhibits the proliferation and migration of breast cancer cells. (A-B) MCF-10A (A) or MCF-7 (B) cells were incubated, or not, with 1 μM AHPC for 1 h, followed by the treatment with ZL216, AS1411 or Control. Cell number was calculated at the indicated time points. (C-D) MCF-10A (C) or MCF-7 (D) cells were incubated, or not, with 1 μM AHPC for 1 h, followed by treatment with ZL216, AS1411 or Control. The cells that had migrated though the pores were stained and quantified by counting five independent visual fields. (*P<0.05, **P<0.01, ***P<0.001, ****P<0.0001). Data are presented as the means ± standard deviation, n = 3. The concentrations of Control, AS1411 or ZL216 were 25 nM or 50 nM respectively in MCF-7 or MCF-10A cells.

Discussion

PROTAC function as a designed heterobifunctional molecule to induce the degradation of unwanted protein by hijacking the intracellular ubiquitin-proteasome system. Early PROTACs were developed based on bifunctional peptides that recruited E3 ligases to degrade target proteins.[21-22] However, peptide-based PROTACs suffered from low cell permeability and, hence, poor cellular activity, hindering the broad applicability of PROTACs.[23] Subsequently, owing to the identification of small molecule-based E3 ligase ligands, such as nutlin-3a for MDM2,[24] thalidomide for CRBN[25] and VH032 for VHL,[26] a series of small molecule-based PROTACs were developed, which represents a significant advancement in PROTAC technology. In this study, we further developed the first aptamer-constructed PROTAC ZL216 through conjugating ssDNA aptamer AS1411 with a small-molecule ligand of VHL, which demonstrate that in addition to peptides and small molecule compounds, the nucleic acid aptamers can also be used to construct PROTACs.

Unlike the recently reported aptamer-conjugated PROTAC using aptamer as targeted delivery tool for PROTAC in specific cell types, [18] ZL216 functioned as a novel PROTAC to promote the formation of nucleolin-ZL216-VHL ternary complex by using AS1411 as a ligand for binding to nucleolin, which potently induced the degradation of nucleolin in breast cancer cells *in vitro* and *in vivo*. Currently, few aptamers that specifically bind to E3 ligases are available; therefore, we only utilized the aptamer as a protein of interest (POI) ligand to construct PROTAC. With the development of specific aptamers for E3 ligases in the future, it will contribute to the generation of heterobifunctional aptamers to achieve the function of PROTACs.

It is estimated that the human genome encodes more than 600 E3 ligases.[27] However, the number of E3 ligases currently used for PROTAC development is still very small, mainly including VHL, CRBN, MDM2 and cIAP1.[23] Previous studies show that PROTACs based each of these E3 ligases hold different characteristics, such as specificity, efficacy, or toxicity. For

example, despite using the same BCR-ABL ligand as a warhead, the CRBN-based PROTACs destroyed both BCR-ABL and c-ABL, while the VHL-based PROTACs only had an effect on c-ABL.[28] In this study, we developed a VHL-recruiting PROTAC Z216 using aptamer AS1411 as a nucleolin ligand. We demonstrated that ZL216 induced nucleolin degradation via the ubiquitin proteasome pathway in a VHL-dependent manner. Nevertheless, it is worth investigating if AS1411 can be conjugated with other E3 ligases to obtain similar effects. PROTACs promote the ubiquitination and degradation of target protein by inducing spatial proximity between an E3 ligase and target protein via the formation of a ternary complex. The spatial distance between E3 ligase and targeted protein is critical to the efficacy of PROTACs. Of note, aptamers have a length ranging from approximately 20 to 80 nucleotides. Whether aptamer length affects the formation and stability of ternary complex and the ability of a PROTAC to degrade its target are questions that need further clarification in the future.

The water solubility of PROTACs is critical to its cell permeability and efficacy. AS1411 is a synthetic 26-base guanine-rich ssDNA oligonucleotide. Previous studies have shown that the water solubility of paclitaxel could be improved by conjugating AS1411 and paclitaxel.[29] Consistent with this, although the small molecule E3 ligase ligand APHC exhibited poor water solubility, AS1411-AHPC conjugate ZL216 showed a significant enhancement in water solubility, implying that a hydrophilic nucleic acid aptamer integrated into PROTACs can improve their water solubility.

AS1411 binds to nucleolin with high affinity and specificity. Many studies have indicated that enhanced expression of nucleolin on the cell surface is restricted to tumor cells, but not normal cells, which confers a tumor-selective binding behavior to AS1411.[13] Our results showed that the aptamer-constructed PROTAC ZL216 using AS1411 as a targeting element for nucleolin still retained the same tumor-selective property as free AS1411. Previous studies have shown that AS1411 exhibited antitumor activity. Unexpectedly, a weak activity of AS1411was observed in our studies. This phenomenon may be explained in their different

modes of action. ZL216 functions as a PROTAC to promote nucleolin degradation, whereas AS1411 does not affect nucleolin levels, but rather regulates the function of nucleolin. Meanwhile, the concentration range we set, was based on the activity of ZL216, which is in nanomolar range. However, AS1411 has been reported to inhibit the growth of cancer cells in micromolar range.[30-31] This finding is consistent with previous studies that PROTACs generally achieve a desired pharmacological effect at significantly lower concentration owing to its catalytic mode of action.[32-33] In addition, although we demonstrated that ZL216 could effectively degrade nucleolin *in vitro* and *in vivo* and inhibited the proliferation and migration of breast cancer cells *in vitro*, the therapeutical potential and the pharmacokinetic properties of ZL216 *in vivo* still need further evaluate.

Conclusion

In summary, we developed a novel PROTAC ZL216 using aptamer AS1411 as a targeting ligand for nucleolin, which potently induced the degradation of nucleolin *in vitro* and *in vivo* by promoting the formation of a nucleolin-ZL216-VHL ternary complex in breast cancer cells, but not in normal breast cells. As a result, ZL216 inhibited the proliferation and migration of breast cancer cells. Our work proves that in addition to peptides and small molecule compounds, nucleic acid aptamers can be used to construct PROTACs and provides a promising strategy for development of tumor-selective PROTACs.

Acknowledgements

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Conflict of interest

The authors declare no competing financial interest.

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