- 1 Novel splice-switching oligonucleotide promotes BRCA1 aberrant splicing and susceptibility to
- 2 PARP inhibitor action
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- 12 Author Contributions: L.D.S., M.R., J.P.B., and D.B. designed the research; L.D.S, M.R., J.P.B., and
- 13 D.B., wrote the manuscript; L.D.S., F.L.C., M.R., and M.M. performed the research and analysed the
- data. E.B. provided critical review and suggested experiments.

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- 19 Abbreviations: BRCA1, Breast Cancer Gene 1; SSO, Splice-switching oligonucleotide; DSB, Double
- 20 Strand Break; SSB, Single-strand break; SO, scrambled oligonucleotide; PARP, Poly (ADP-ribose)
- 21 polymerase.
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- Novelty & Impact Statement
- 28 PARP and BRCA1 act in tandem to orchestrate the repair of DNA damage. PARP inhibitors increase
- 29 the potency of chemotherapeutic treatment of BRCA1-deficient breast tumours. However, tumours
- 30 expressing functional BRCA1 are less sensitive to the action of PARP inhibitors, owing to the function
- 31 of BRCA1 in DNA damage repair. We have developed a splice-switching oligonucleotide which
- 32 stimulates BRCA1 exon 11 skipping and show that this treatment induces PARP inhibitor
- 33 susceptibility in BRCA1-functional breast cancer cells.

Abstract

Tumours carrying hereditary mutations in *BRCA1*, which attenuate the BRCA1 DNA damage repair pathway, are more susceptible to dual treatment with PARP inhibitors and DNA damaging therapeutics. Conversely, breast cancer tumours with non-mutated functional BRCA1 are less sensitive to PARP inhibition. We describe a method that triggers susceptibility to PARP inhibition in BRCA1-functional tumour cells. *BRCA1* exon 11 is key for the function of BRCA1 in DNA damage repair. Analysis of the *BRCA1* exon 11 splicing mechanism identified a key region within this exon which, when deleted, induced exon 11 skipping. An RNA splice-switching oligonucleotide (SSO) developed to target this region was shown to artificially stimulate skipping of exon 11 in endogenous *BRCA1* pre-mRNA. SSO transfection rendered wild-type BRCA1 expressing cell lines more susceptible to PARP inhibitor treatment, as demonstrated by a reduction in cell survival at all SSO concentrations tested. Combined SSO and PARP inhibitor treatment increased γH2AX expression indicating that SSO dependent skipping of BRCA1 exon 11 was able to promote DSBs and therefore synthetic lethality. In conclusion, this SSO provides a new potential therapeutic strategy for targeting BRCA1-functional breast cancer by enhancing the effect of PARP inhibitors.

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Fully functioning DNA repair mechanisms are crucial given the natural accumulation of both double-strand and single-strand breaks (DSB/SSB) within cellular DNA¹. Poly (ADP-ribose) polymerase (PARP) binds and modifies DNA SSBs as a prerequisite for SSB repair². PARP inhibition can lead to the accumulation of DNA DSBs, which are usually repaired by homologous-recombination³. DSB repair is executed by an extensive complex in which BRCA1 acts as a vital platform^{4, 5}. The relationship between these two DNA repair proteins makes PARP inhibitor (PARPi) treatment an attractive method of targeting BRCA1-deficient breast tumours⁶⁻⁸. However, only 2-5% of breast cancer cases harbour *BRCA1* mutations⁹ leaving ~95% of cases unable to be successfully targeted with this strategy. Hence, an attractive approach to treat BRCA1-functional breast tumours would be to artificially induce synthetic lethality through dual inhibition of BRCA1 and PARP activity¹⁰.

BRCA1 exon 11 encodes 60% of the BRCA1 protein and skipping of this exon ($BRCA1-\Delta 11$) inhibits BRCA1 mediated DSB repair¹¹. The $BRCA1-\Delta 11$ splice variant has been detected in breast cancer cell lines and tissues^{12, 13}, and has been shown to stimulate the formation of mammary tumours in mouse models¹⁴. Splice-switching oligonucleotides (SSOs) have been highly successful at modifying disease related splicing events *in vivo* to provide therapeutic advantage^{15, 16}. SSOs function by annealing to pre-mRNA sequences which regulate splicing, consequently altering the mRNA isoform produced¹⁷.

In the current study we have used a systematic minigene method to develop an SSO (oligoAB) which successfully stimulates *BRCA1* exon 11 skipping. Furthermore, we have assessed cell survival and DNA damage in two-model breast cancer cell-lines following simultaneous treatment with oligoAB and the PARPi, veliparib.

Materials and Methods

75 Minigenes

- Minigenes were synthesised by two-step overlapping PCR using the pB1-WT minigene established in
- 77 a previous study¹⁸.

Splice-switching Oligonucleotides

- 80 Sequences of morpholino SSOs: OligoAB 5'-ATACTGAACATCATCAACCC-3'; Scrambled control 5'-
- 81 CCTGATGAATTTTCAAATGG-3'¹⁹ (Genetools).

Cell Culture and Transfection

MCF-7 cells (Sigma-Aldrich) were maintained in Dulbecco's Modified Eagle Medium (DMEM) supplemented with 1% penicillin/streptomycin and 10% FBS. Cells were cultured for less than 20 passages in all experiments shown. For minigene transfection experiments 8 x 10^4 cells were seeded 24 hours prior to transfection in 6 well plates. 24 hours following seeding, cells were transfected with either 1 µg of minigene using Fugene6 (Roche) according to manufacturer's instructions or with SSOs using Endoporter-DMSO (Genetools) according to manufacturer's instructions. 48 hrs following transfection RNA was extracted using the RNAeasy kit plus (Quiagen) and *BRCA1* splicing products (*FL*, 11Q and Δ 11) were analysed by RT-PCR using a specific primer combination as described previously¹⁸. The band intensities of *BRCA1-FL*, *BRCA1-11Q* and *BRCA1-\Delta11* were measured using Image J; band intensities of *BRCA1-11Q* and *BRCA1-\Delta11* were normalised to the band intensity of *BRCA1-FL* to account for differences in product length. The percentage of *BRCA1-FL*, *BRCA1-11Q* and *BRCA1-A11* expression at each oligoAB concentration was calculated as a percentage of the normalised *FL+11Q+\Delta11* values. Statistical analysis (one-way ANOVA) was performed using GraphPad Prism software.

Clonogenic Assay

24 hours following SSO transfection cells were trypsinised and 10^3 cells were re-plated in 6 well plates in media supplemented with 1 μ M of veliparib (Enzo Life Sciences). Four days later cells were re-treated with veliparib. Plates were incubated for 11 days before fixing and staining colonies with Giemsa. Colonies were counted manually using the cell counter application in Image J. Percentage oligoAB colony number was calculated relative to scrambled control SSO colony number. Statistical analysis (one-way ANOVA) was performed using GraphPad Prism software.

Immunoblotting

MCF-7 cells were transfected with SSOs with or without 10 μ M veliparib (Enzo Life Sciences) and 8 hours later protein was extracted using RIPA buffer (Sigma), and sonication for H2AX. Proteins were separated on 6 % (BRCA1) and 15 % (H2AX) polyacrylamide gels and transferred onto nitrocellulose membrane (Amersham). Membranes were probed with antibodies against γ H2AX (phosphoSer139; Millipore, 05-636), BRCA1 (Santa cruz, sc-642) and Hsc70 (Santa cruz, Sc-7298). Bands were detected using HRP-linked mouse (Dako, 2021-05) or rabbit (Dako, 2021-08) secondary antibodies plus ECL blotting substrate (pierce, 32106) and visualised using a chemiDoc-it imaging system (UVP). Densitometry of all blots was carried out using image J.

Results

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Minigene analysis of BRCA1 exon 11 splicing

In order to develop a BRCA1-Δ11 stimulating SSO, splicing regulatory regions suitable for SSO targeting were identified by analysis of the exon 11 splicing mechanism using minigenes mimicking BRCA1 exon 11 splicing. Our previous work¹⁸ identified a 41 nucleotide region (D2) within exon 11 which, when deleted in the BRCA1 exon 11 minigene system (pB1-D2), induced the expression of the BRCA1-Δ11 splicing isoform (Fig. 1a) when transfected in to MCF-7 cells. In the current study we used in silico analysis of RNA protein binding motifs to predict key targetable regions within BRCA1 region D2 for SSO development^{20, 21} (data not shown). Three regions within D2 were predicted to bind splicing regulatory proteins which could affect exon 11 splicing. Deletions in these regions were made in the previously described minigene containing BRCA1 exon 11 (pB1-WT)¹⁸ generating minigenes pB1-D2A, pB1-D2B and pB1-D2C (deleted regions are shown in Fig. 1b). This minigene was also designed to study the expression of BRCA1 exon 11 splicing variant, BRCA1-11Q, which contains a shortened exon 11 (Fig. 1a) and has been linked to PARP inhibitor resistance²². pB1 minigenes containing targeted deletions were transfected into MCF-7 cells and the effect of each deletion on exon 11 splicing analysed. As reported previously 18, the pB1-D2 minigene showed predominant BRCA1- Δ 11 expression (Fig. 1c). Both pB1-D2A and pB1-D2C showed enhanced BRCA1- Δ 11 expression in comparison to that seen with pB1-WT, and pB1-D2B stimulated BRCA1-11Q expression with almost no detectable BRCA1-Δ11 expression (Fig. 1c). None of these shorter deletions were able to fully recapitulate the splicing pattern observed with deletion of the entire 41 nucleotide D2 region. Further in silico analysis identified a putative regulatory region 5' of region D2, which was consequently deleted in conjunction with region D2A and the first 3 nucleotides of D2B to create minigene pB1-D2AB' (deleted region D2AB' is shown underlined in Fig. 1b). Analysis of the pB1-D2AB' splicing pattern identified that this combination of deletions induced a comparable splicing pattern to that of pB1-D2, stimulating BRCA1- Δ 11 and reducing BRCA1-FL and BRCA1-11Q expression (Fig. 1d).

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Development of a BRCA1 exon 11 splice-switching oligonucleotide

A morpholino SSO, oligoAB, was designed to bind the RNA sequence corresponding to region D2AB' in *BRCA1* exon 11 (Fig. 1b and d). At each concentration tested, oligoAB treatment reduced endogenous *BRCA1-FL* and *BRCA1-11Q* expression and simultaneously increased *BRCA1-\Delta11* expression in MCF-7 (Fig. 2a and c) and MDA-MB-231 (Fig. 2b and c) cells compared to the control SSO. For instance, 10 μ M oligoAB treatment reduced *BRCA1-FL* expression by 1.7-fold (p=0.02) and 2.3-fold (p=0.04), and *BRCA1-11Q* expression by 6.6-fold and 10.6-fold in MCF-7 and MDA-MB-231

cells respectively (Fig. 2c). Furthermore, MCF-7 and MDA-MB-231 cells treated with 10 μ M oligoAB had a 12-fold (p=0.02) and 61-fold (p=0.02) increase in BRCA1- Δ 11 expression respectively, compared with cells treated with 10 μ M control SSO (Fig. 2c). OligoAB dependent decreases in BRCA1-FL and BRCA1-11Q expression, and simultaneous increases in BRCA1- Δ 11 expression show that oligoAB actively switched BRCA1 splicing rather than specifically degraded certain BRCA1 isoform pre-mRNAs.

In addition to inducing changes in mRNA expression, oligoAB treatment also stimulated changes in BRCA1-FL and BRCA1-11Q protein expression (Fig. 2d). BRCA1-FL and BRCA1-11Q proteins were assigned based on previous studies^{22, 23}. Treatment of MCF-7 cells with oligoAB (5 μ M) resulted in a loss of BRCA1-FL and BRCA1-11Q protein expression and an increase in the expression of smaller BRCA1- Δ 11 associated protein isoforms (Fig. 2d). OligoAB treatment stimulated the expression of two BRCA1- Δ 11 associated protein isoforms, which maybe the result of oligoAB acting alongside other BRCA1 alternative splicing events²⁴ to generate unique BRCA1- Δ 11 isoforms.

Functional effect of SSO dependent exon 11 skipping

Studies have shown that antagonising BRCA1 expression induces synthetic lethality in combination with PARP1i action⁷. To assess whether oligoAB could recapitulate this effect we performed clonogenic assays in BRCA1-functional cell lines, MCF-7 and MDA-MB-231. Cells were treated with a combination of oligoAB and the PARP1/2i, veliparib, and the effect on colony survival determined. Transfection of oligoAB (5 and 10 μ M) into MCF-7 or MDA-MB-231 plus treatment with veliparib (1 μ M) significantly (p<0.01) reduced colony number compared with control SSO and veliparib treatment (Fig. 3a and b). More specifically, combined veliparib and oligoAB (10 μ M) treatment induced a 15-fold reduction in colony number in MCF-7 cells (p=0.01) and a 2.1-fold reduction in colony number in MDA-MB-231 cells (p=0.0001) (Fig. 3a and b). These results show that oligoAB augments the inhibitory effect of veliparib on cell survival and proliferation in BRCA1-functional cell lines.

To assess whether this effect was due to dual inhibition of the DNA SSB and DSB repair pathways by veliparib and oligoAB respectively, we next investigated whether oligoAB was functionally disrupting the DSB repair mechanism of BRCA1. When DNA DSBs occur γ H2AX is rapidly phosphorylated and recruited to these sites²⁵. γ H2AX functions to recruit BRCA1 along with other DNA repair molecules to carry out DSB repair at these regions²⁶. Functional BRCA1 and PARP are both required for attenuation of γ H2AX expression following completion of DSB repair^{10, 27}. As we had shown that

oligoAB treatment inhibited the expression of in BRCA1-FL and BRCA1-11Q, we next investigated
γ H2AX expression following oligoAB treatment with or without Veliparib. Dual treatment of MCF-7
cells with oligoAB (10 $\mu\text{M})$ and veliparib (10 $\mu\text{M})$ increased γH2AX expression by 2.3-fold compared
to control SSO and veliparib treatment (Fig. 3c). These results show that oligoAB disrupted the
functional role of BRCA1 in DNA DSB repair, thereby enhancing the effect of veliparib.

Discussion

It has been shown that domains within *BRCA1* exon 11 are crucial for the function of BRCA1 in DNA DSB repair^{4, 5}, and that impairment of BRCA1's role in this promotes cellular susceptibility to PARPi^{7, 8, 10, 28}. Studies have shown that inhibition of BRCA1 in otherwise BRCA1-functional breast cancer cells results in susceptibility to PARP inhibition^{7, 8}. However, there has been limited investigation in to the translation of this finding into an effective therapeutic option for patients.

SSO target sequences within a pre-mRNA region of interest can be identified through *in silico* analysis of splicing regulatory protein binding^{20, 21}. This analysis allows assumptions to be made as to how splicing could be controlled and consequently where SSOs should be targeted to. However, this method provides no evidence as to whether SSOs designed to these predicted regulatory regions would be functional. Due to this either the antisense walk or minigene method, the latter detailed in this study, must be employed to identify the most effective SSO target site. The antisense walk²⁹ method requires the synthesis and testing of a number of overlapping SSOs targeted to the region of interest. Therefore, unless in-house facilities for SSO synthesis are available, this puts a financial burden on SSO development. Importantly, the current study shows how minigenes can be used to economically design SSOs without the need for an extensive antisense walk.

Our study is the first to identify an SSO (oligoAB) capable of altering BRCA1 pre-mRNA splicing through the increase of *BRCA1* exon 11 skipping and simultaneous reduction of *BRCA1-FL* and *BRCA1-11Q* expression. Changes in mRNA expression were also mirrored by changes in protein expression, with oligoAB treatment inhibiting the expression of functional BRCA1 proteins, BRCA1-FL and BRCA1-11Q. Clonogenic assays combining oligoAB and PARPi treatment showed that *BRCA1* exon 11 skipping enhanced the effect of PARPi on cell proliferation and survival in BRCA1 wild-type cells. There were fewer colonies present in wells combing oligoAB and veliparib than in those with either oligoAB alone, or the control SSO with or without veliparib. However, there was a discrepancy between the response of the two cell-lines to the oligoAB-veliparib combination. MCF-7 cells had a more pronounced reduction in colony number both with and without veliparib than MDA-MB-231 cells. This effect had been previously reported in a study which identified that veliparib was more effective at reducing colony number in MCF-7 than MDA-MB-231 cells³⁰. However, in the current study, the overriding effect of combined oligoAB-veliparib treatment on the induction of synthetic lethality was consistent between the two model cell lines.

We next showed that oligoAB disrupted the DSB repair function of BRCA1 by identifying a greater accumulation of yH2AX following oligoAB-veliparib treatment compared to control SSO-veliparib treatment. The inhibitory effect of oligoAB on DSB repair may be mediated by an oligoAB dependent reduction in *BRCA1-FL* mRNA expression and so disruption of BRCA1-FL DSB repair function^{4, 5}. Additionally, BRCA1-11Q has been shown to have partial DSB repair function and be able to compensate for loss of BRCA1-FL activity in BRCA1-mutated breast cancer cases²². Moreover, this isoform has been shown to promote resistance to PARPi action²², which suggests that oligoAB may be able to re-sensitise resistant tumours to PARPi treatment though BRCA1-11Q depletion.

A number of methods have been employed to target BRCA1 function and enhance susceptibility to PARPi treatment. For instance, PI3K³¹ and BRCT³² small molecule inhibitors have been shown to enhance the activity of PARP inhibitors in BRCA1 wild-type cells. Studies have also shown that small molecule modulators of splicing, such as spliceostatin³³ ³⁴, could provide a new avenue for cancer therapy, including breast cancer ³⁵. However, the development of resistance to small molecule cancer treatments is an on-going problem. In light of this, it is important to explore novel treatment options and SSOs provide an attractive avenue given that they act on endogenous RNA sequences which limit the target cells ability to develop resistance. Furthermore, small molecule modulators of splicing will trigger global splicing alterations and the effect of changing splicing on such a scale is still not well understood. Therefore, it is important to note that oligoAB will specifically target *BRCA1* splicing and will not interfere with other splicing events which may themselves be tumorigenic.

Regardless of efficacy of oligoAB *in vitro*, it is also important to note factors which limit the use of SSOs as therapeutics and identify how these hurdles could be overcome. One limitation is that the transfection efficiency of oligoAB into model cell lines versus tumour tissue *in vivo* will vary. For oligoAB to be clinically adequate tumour specific ligands to enable delivery and uptake would need to be identified to reduce exposure of surrounding tissue. This is vital for *in vivo* use of oligoAB as this SSO could universally stimulate *BRCA1* exon 11 skipping which would not be beneficial to the patient. It has been shown previously that SSOs can be successfully delivered to their target tissue through use of tissue-specific ligands, which allows for localised treatment and reduces SSO toxicity and dose³⁶. Therefore, the development of such SSO-ligand conjugates for oligoAB delivery is a realistic possibility and requires future research.

In conclusion, this study highlights a novel BRCA1 SSO capable inducing synthetic lethality in combination with PARPi treatment in BRCA1-functional breast cancer. Moreover our data presents a

- simple method for the design of SSOs, as well as showcasing them as a versatile method of achieving
- 257 functional phenotypic changes for the treatment of cancer.

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Figure Legends

Figure 1.

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(a) Schematic diagrams showing un-spliced BRCA1 pre-mRNA and splicing isoforms: Full length (FL), 11Q and $\Delta 11$. Boxes represent exons, lines represent introns. Splice sites = 'SS. (b) The BRCA1 exon 11 sequence from the 3'splice site of BRCA1 exon 11 to the 11Q 5'splice site. The key region, D2, is shown above the exon sequence by a solid line. Deletions = bold text. Deletion D2AB' = italics/underlined. (c and d) Minigenes carrying deletions D2, D2A, D2B, D2C and D2AB' shown in (b) were transfected into MCF-7 cells and their subsequent effect on BRCA1-FL, BRCA1-11Q and BRCA1- $\Delta 11$ expression, in comparison to the wild-type (WT) minigene, was assessed by semi-quantitative PCR. BRCA1-FL, BRCA1-11Q and BRCA1- $\Delta 11$ are labelled to the right of the panels. Quantification was performed using image J and mean values \pm s.d. (n = 2) are shown graphically below each

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376 Figure 2.

representative gel image.

The effect of oligoAB or control SSO (SO) on the expression of BRCA1- $Full\ length\ (FL)$, BRCA1-11Q and BRCA1- $\Delta11$ in (a) MCF-7 cells and (b) MDA-MB-231 cells was evaluated (representative RT-PCR shown) and quantified for (c). BRCA1-FL, BRCA1-11Q and BRCA1- $\Delta11$ are labelled to the right of the representative gel panels. Data representative of three independent experiments. Mean values \pm s.d. (n = 2) are provided. One-way anova analysis shown; * $p \le 0.05$; ** $p \le 0.01$; *** $p \le 0.001$. (d) MCF-7 cells were treated with oligoAB or control SSO (SO) and the expression of BRCA1-FL, BRC1-11Q and BRCA1- $\Delta11$ analysed by immunoblotting.

- Figure 3.
- 386 (a) The effect of oligoAB on survival of MCF-7 and MDA-MB-231 cells was assessed by clonogenic 387 assay. Representative images show cells treated with 10 μM oligoAB or control SSO (SO) with or 388 without 1 μM veliparib. Clonogenic assays at each concentration were quantified for (b). Data 389 representative of three independent experiments. Mean values \pm s.d. (n = 3) are provided; One-way 390 anova analysis shown *p<0.05; **p<0.01; ***p<0.001. (e) MCF-7 cells were treated with 10 μM 391 oligoAB or control SSO (scram) with or without 10 μM veliparib and γH2AX expression assessed. Data 392 representative of two independent experiments.

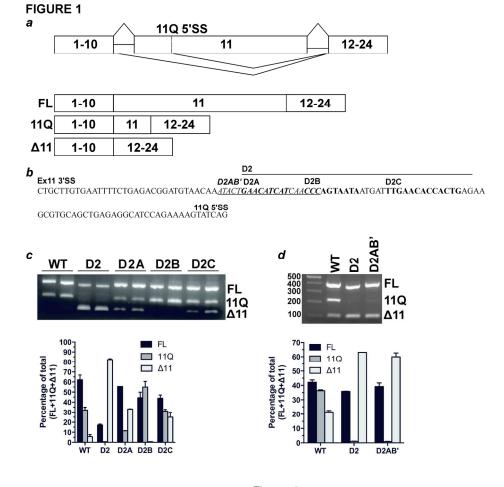


Figure 1 159x147mm (300 x 300 DPI)

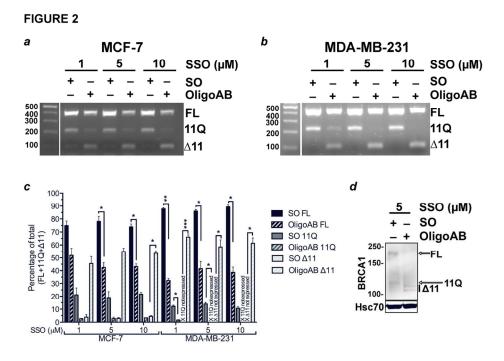


figure 1 119x80mm (300 x 300 DPI)

FIGURE 3

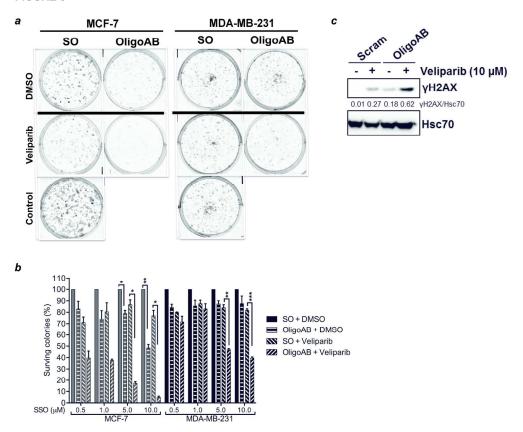


Figure 3 167x145mm (300 x 300 DPI)