



CID-078, a first-in-class oral cyclin A/B-RxL inhibitor, elicits anti-tumor activity in breast cancer patient-derived xenograft models

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1. BACKGROUND

- Cell cycle progression is regulated by cyclins and cyclin-dependent kinases (CDKs), along with various substrates and regulators. E2F activity relies on the interaction of its RxL motif and the hydrophobic patch (HP) on cyclin A. Disrupting this cyclin A/E2F RxL interaction leads to hyperactivation of E2F and synthetic lethality in E2F-driven tumors.
- CID-078 is a novel, orally bioavailable, passively cell-permeable, potent, and selective macrocycle that binds to the HP of cyclins A and B blocking the RxL motif-mediated binding of E2F to cyclin A-CDK2 and Myt1 to cyclin B1-**CDK1.** CID-078 induces cell cycle arrest at the G2/M phase, leading to apoptotic tumor cell death.
- Triple negative breast cancer (TNBC) has previously been shown to have higher expression of E2F targets and sensitivity to CID-078 compared to non-TNBC cancer cell lines¹.
- Some ER+/HER2- breast cancer tumors that progress on CDK4/6i may have elevated E2F activity due to alterations in the CDK/RB/E2F pathway².
- In lung cancer tumor models, CID-078 treatment induced tumor regression and **increased phosphorylation of separase (ESPL1)**—a mitosis-specific protein and direct substrate of Cyclin B1-Cdk1^{1,3}.



2. AIM

- 1. Evaluate the anti-tumor efficacy of CID-078 in 8 patient-derived xenografts (PDX) models of breast cancer, including TNBC and ER+/HER2-subtypes.
- 2. Perform pharmacodynamic evaluation to identify and analyze additional biomarkers associated with response to CID-078.

3. METHODOLOGY Genomic Transcriptomic Protein PDX model level level level (🕿 establishmen \rightarrow MSK-**BC** patients RNA-seq **IMPACT[™]** BC subtype Prior and posterior treatments Test CID-078 efficacy Selecting PDX models with Molecular characterization varied E2F/G2M hallmark Created in https://BioRender.com This presentation is the intellectual property of the author/presenter. Copies of this poster obtained through Quick Response (QR) Code are for personal use only and may not be

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4. RESULTS



Figure 1. Heatmap of hallmark pathway scores to select PDX models to test CID-078. A heatmap of hallmark pathway scores was generated for 71 breast cancer patient-derived xenograft (PDX) models, using the GSVA method with the MSigDb Hallmark collection^{4,5}. PDX098, PDX124, PDX473B, PDX127, PDX479, PDX600.1, PDX474.7 and PDX490, models which have varied E2F targets and G2M checkpoint hallmark scores, were selected for *in vivo* evaluation.

CID-078 exhibits robust single dose-dependent agent activity in TNBC and post-CDK4/6i ER+/HER2- BC PDX models



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Figure 2. NMRI-Foxn1nu/nu mice were implanted in the lower flank with tumor fragments of PDX098 (TNBC) (A) or PDX474.7 (ER+/HER2-BC) (B). Upon tumor outgrowth (150-250 mm3), mice were treated with CID-078 at indicated doses. Cisplatin was used in both models and endocrine therapy plus a CDK4/6 inhibitor was used for PDX474.7 as a standard-of-care control for comparison. All treatment regimens were tolerated as assessed by body weight measurements (not shown). Patient clinical history for PDX474.7

PO, orally; IV, intravenously: QD, once daily; BID, twice daily; TID, three times daily; Q2W, once every

PD 4 months



with sensitivity to CID-078



Treatment with CID-078 induces a robust activation of E2F targets and DNA repair pathways in responders



Figure 5. Gene set enrichment analysis (GSEA) of differentially expressed genes sets between vehicle (n=3-4) and CID-078 treatment (n=3reveals distinct gene set 4) enrichment patterns in nonresponders (PDX127 and PDX490, left) and responders (PDX098 and PDX474.7, right). Red and blue lines represent gene sets upregulated and downregulated, respectively, with dot size proportional to the number of enriched genes. All gene sets are significantly enriched in the responder group *p<0.05

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Figure 4. Baseline tumor expression levels of ESPL1, *E2F1*, and *E2F2*, as measured by RNA-seq, correlate with CID-078 antitumor activity. Statistical significance was determined by Welch's Two Sample t-test.

Figure 6. Tumor response biomarker modulation observed upon CID-078 treatment in the PDX098 breast cancer model. Representative immunofluorescence (IF) images and quantification of IF results of PDX098 tumors treated with CID-078 show a significant increase in the mean fluorescence intensity (MFI) of pSeparase (S1126) in cyan (A) and (B) and pATM (S1981) in orange (C) and (D) compared to treatment with vehicle. MFI was quantified using HaLo and normalized to vehicle-treated controls. Statistical significance was determined by Welch's Two Sample t-test.

5. CONCLUSIONS

- The selective cyclin A/B RxL macrocycle CID-078 exhibits potent antitumor activity in the TNBC and ER+/HER2- breast cancer preclinical models tested, consistent with the proposed mechanism of action and correlating with E2F1 and ESPL1 expression.
- Treatment with CID-078 increases phosphorylation of separase (ESPL1) in sensitive breast cancer PDX models.
- Given these results, CID-078 may be a new treatment option for patients with TNBC or ER+/HER2- breast cancer having progressed through CDK4/6i therapy.
- A multi-center phase 1 clinical trial (NCT06577987) is currently enrolling patients.

6. REFERENCES

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Treatment with CID-078 in PDX098 increases mitosis specific biomarker pSeparase (S1126) and DNA damage marker pATM (S1981)