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Introduction

Pancreatic Ductal Adenocarcinoma (PDAC) is the **most aggressive gastrointestinal cancer**, with a **97.8% mortality rate in Pakistan** (Ali et al., 2021).

Standard treatments include gemcitabine, FOLFIRINOX, and capecitabine (Ali et al., 2021). The **gut microbiota** significantly contributes to chemoresistance against gemcitabine in PDAC.

Bacterial cytidine deaminase isoform has **higher affinity for gemcitabine** than the human CDA enzyme, converting the drug before it can reach the tumor microenvironment (Geller et al., 2017). This **microbial interaction limits chemotherapy effectiveness in PDAC**.

Objective

To identify compounds and drugs that could reverse gene signatures associated with Gemcitabine Resistant PDAC

Methodology



Literature review

Data collection

Gene conversion

Drug identification

Drug Data

Venn diagram

Results

Volcano Plot

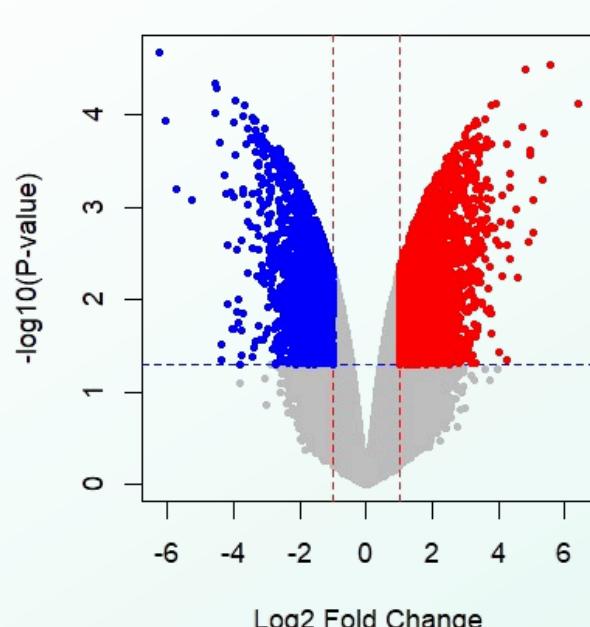


Figure 1. DGE plot for Resistant PDAC

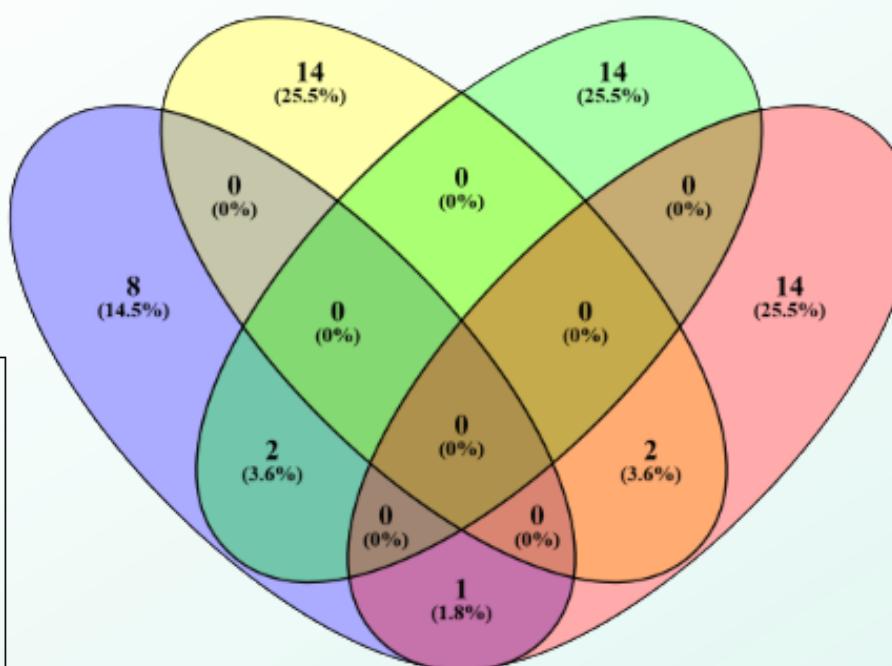


Figure 2. Drug overlap

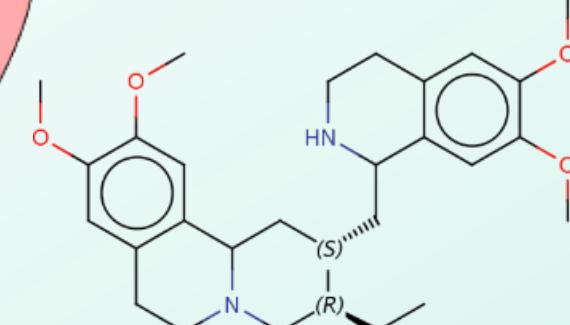


Figure 3. Structure of Emetine

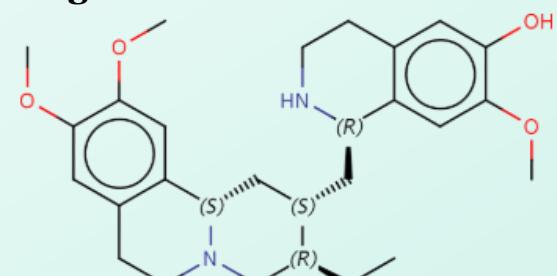


Figure 4. Structure of Cephaline

Conclusion

A panel of **eight drugs and compounds** was identified that effectively reverse gene signatures associated with gemcitabine-resistant pancreatic ductal adenocarcinoma (PDAC). The drugs rediscovered include **Anisomycin, Cephaline, Emetine, QL-X-138, STK17AKO, Navitoclax, Kinetinriboside, and Bortezomib**.

References

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- Geller LT, Barzily-Rokni M, Danino T, et al. Potential role of intratumor bacteria in mediating tumor resistance to the chemotherapeutic drug gemcitabine. *Science*. 2017;357(6356):1156-60.
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Way forward

Integrate meta-omic analysis.
Replicate study for **FOLFIRINOX, Capecitabine** regimens.
validation on PDAC patient cohort

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