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# The Assay Matters: ctDNA Assessment in Localized Pancreatic Cancer

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## Introduction

- While circulating tumor DNA, (ctDNA) has emerged as a pancreatic cancer (PDAC) biomarker candidate in other malignancies, its investigation is emerging in localized PDAC.
- Both digital droplet PCR (ddPCR) and next generation sequencing (NGS) are published methods of assessing ctDNA
- The advantages and advantages of ctDNA assessment by ddPCR and NGS in patients with localized PDAC treated with NAC are unclear

## Objectives

**1. To assess detection and prognostic capabilities of PDAC ctDNA assessment by NGS and ddPCR**

**2. To compare and examine the relative advantages of PDAC ctDNA assessment by NGS and ddPCR**

## Methods

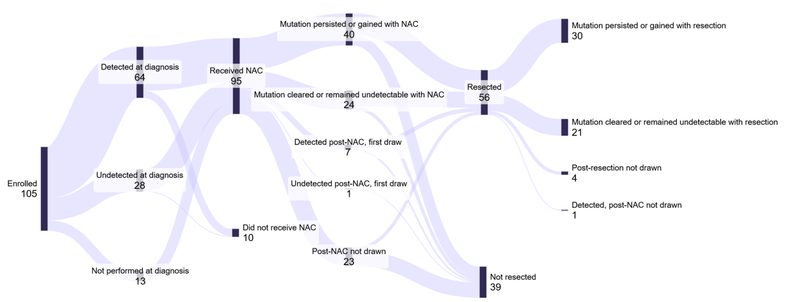
Data source: Prospectively recruited cohort

### Inclusion Criteria

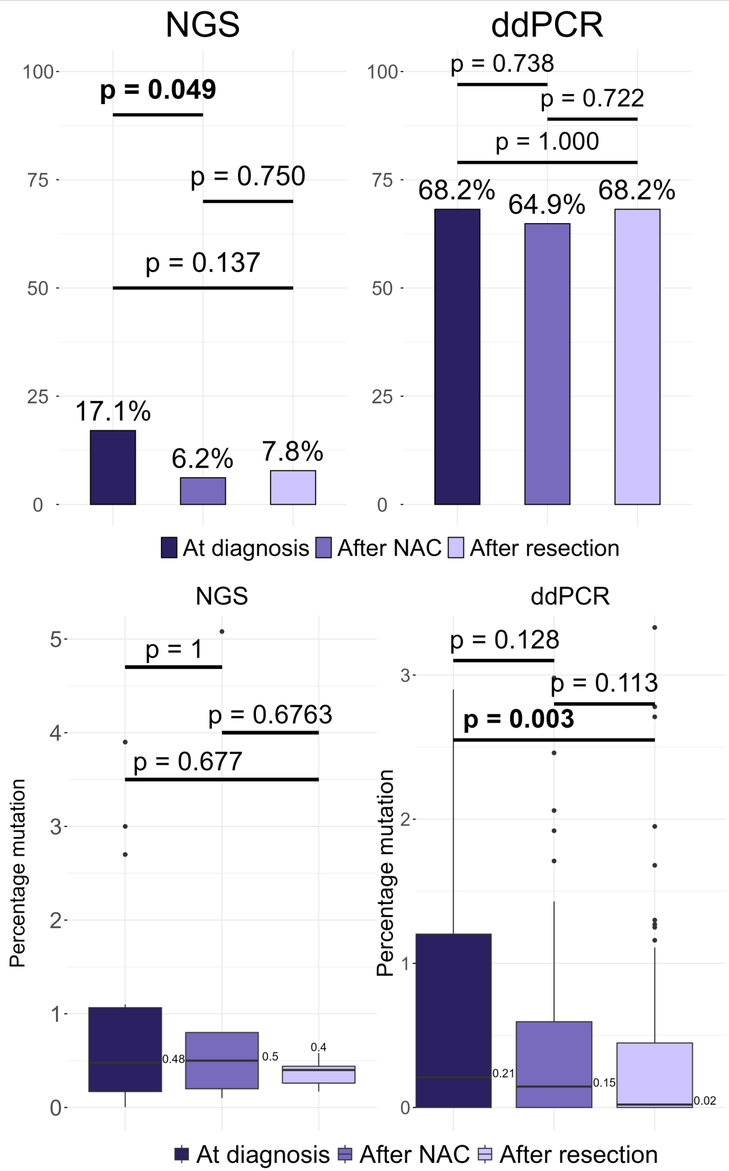
- Newly diagnosed PDAC
- Patients with resectable disease
- Patients planned to undergo NAC

### Sample handling

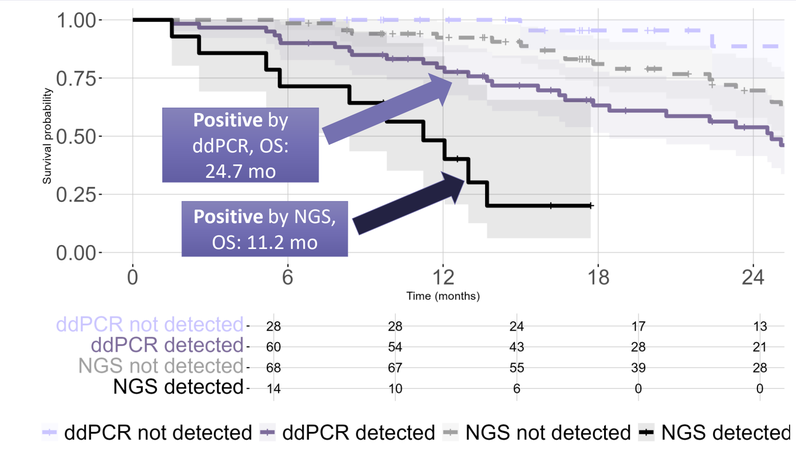
- Peripheral blood samples collected at diagnosis, after NAC, and after resection
- Samples analyzed by ddPCR for mutant *KRAS* G12D, G12V, and G12R




## Results – Descriptive Statistics and Regression




## Results – Kaplan-Meier Estimates




## Conclusions

1. Mutant *KRAS* ctDNA is detectable by NGS and ddPCR throughout treatment in patients with localized PDAC
2. Detection is prognostic
3. ddPCR has higher sensitivity for the detection of smaller ctDNA quantities than NGS
4. The higher ctDNA loads required for detection by NGS implicate clinically more aggressive disease

**Further study by our group using ddPCR in the detection of mutant KRAS ctDNA will include incorporation into adaptive-treatment trial designs such as Alliance A021806**

## Key points

1. The use of ctDNA as a biomarker in PDAC is expanding
2. Both NGS and ddPCR were able to detect ctDNA throughout treatment
3. ddPCR is more sensitive for ctDNA detection than NGS
4. Detection is prognostic
5. Future work will include the investigation of ctDNA dynamics during treatment
6. Future work will also include investigation of the use of ctDNA to inform NAC regimens and optimally select patients for surgical resection