Non-ductal pancreatic tumor classification by whole genome DNA methylation profiling

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# Statement of translational relevance (120-150)

# Abstract (250)

**Background and aim:** Histopathological diagnosis of acinar cell carcinoma’s (ACC), solid pseudopapillary neoplasm (SPN) and pancreatic neuroendocrine neoplasms (PanNETs) may be challenging in daily clinical practice. As the cancer methylome harbors characteristics reflecting the cell of origin allowing identification of tumor origin, here we build a methylation profiling based classifier in order to facilitate differentiation between ACC, SPN and PanNETs.  
**Methods:  
Results:  
Conclusion:**

# Introduction (361)

Around 90% of pancreatic cancers are pancreatic ductal adenocarcinomas (PDACs), while the remainder (10%) is derived from non-ductal structures. The latter include acinar cell carcinoma (ACC), solid pseudopapillary neoplasms (SPN) and pancreatic neuroendocrine tumors (PanNETs) and comprise 1%, 2% and 5% of all non-ductal pancreatic neoplasms in adults respectively (1, 2).

Behavior varies widely: while SPNs are with an 95% 5-year overall survival predominantly indolent, PanNETs and ACCs have respectively a 5-years overall survival of 59% and 45% come close to the aggressiveness of PDACs (3-6). With regard to histomorphology and immunophenotype ACCs, SPNs and PanNETs are similar (1, 2). Immunohistochemistry and molecular genetics have contributed to an improved classification of these tumors. Still, differentiation sometimes remains challenging while it is crucial for therapeutic decision making.

Whole genome methylation-based tumor classification is increasingly used for tumor classification, and the WHO recommends the routine application in tumor of the central nervous system (7). DNA methylation is a covalent modification of cytosine residues and is involved in gene expression regulation. Hypermethylation of specific gene promotor regions can lead to transcriptional inactivation, including tumor suppressor genes (8, 9). Besides somatically acquired DNA methylation changes, the cancer methylome harbors characteristics reflecting the cell of origin (10). This tissue specificity is what makes DNA methylation profiling well suited for the identification of tumor origin (10, 11). Furthermore, archival formalin-fixed, paraffin embedded (FFPE) tissues can be used for DNA methylation analysis. Based on this rationale numerous classifiers have been developed for cancer classification and some are routinely used in daily practice (11-16). Similarly, Hackeng et al. developed a classifier for distinguishing neuroendocrine tumors from different locations, including pancreatic NETs (17). Previous studies including Jäkel et al. and Benhamida et al., showed methylation profiles of pancreatic tumors are well suited for the differentiation of these tumors (18, 19). Together, these data suggest potential applicability of methylation profiling for classification of non-ductal pancreatic tumors.

To facilitate diagnosis within non-ductal pancreatic tumors ACC, SPN and PanNET, here we have built a methylation-based prediction model. We evaluated random forest classifiers, neural networks and gradient boosting machines and present an approach to distinguish between non-ductal pancreatic cancers with almost perfect accuracy.

# Materials and methods

**Study design**We build a diagnostic classifier able to distinguish PanNETs, ACCs, SPNs and PDACs based on their DNA methylation profiles. DNA methylation array data from PanNETs (n= 87), ACCs (n=37), SPNs (n= 13) and PDACs (n=..) that where publicly available was split into a training (76 primaries) and test cohort (139 primaries and metastases). We trained three machine learning algorithms (Random Forest (RF), artificial neural network (ANN), gradient boosting machines (xgBoost) on the training cohort. The three classifiers were evaluated using the test cohort. The three algorithms were compared and the best performing method was chosen for further analysis. We further validated our classifier on a clinical cohort compiled of DNA methylation array data obtained from FFPE tissue from PanNETs (n= 87), ACCs (n=37) and SPNs (n= 13) primaries and metastases obtained from the University Medical Center Utrecht and Radboud Medical Center pathological archives.

**Patients and samples**The University Medical Center Utrecht (UMCU) Biobank Research Ethics Committee approved the use of archival material for this study. Data used for the test and training cohort were retrieved from previously published datasets GSE117852 and GSE155353 from Gene Expression Omnibus (GEO) (20, 21), E-MTAB-7924 from EMBL-EBI (22), EGAD00010001298 from European Genome-Phenome Archive (EGA) (19), and SPN methylation data used in Selenica et al.(23) was requested by the authors. The clinical cohort included previously published data from dataset EGAS00001004878 from European Genome-Phenome Archive (EGA) (17), and additional cases selected from the University Medical Center Utrecht and Radboud Medical Center pathological archives. These methylation data have been deposited at the EGA, which is hosted by the European Bioinformatics Institute (EBI) and the Centre for Genomic Regulation (CRG), under accession number EGA…..

**Whole genome DNA methylation analysis**On cases selected from our pathology archives, DNA extraction, bisulfite conversion and array processing were performed in-house at our core facility as previously described(17). For DNA extraction the DNA Methylation Bead-Chip manufacturer (Illumina) was used, formalin fixation–induced DNA damage was restored using the FFPE Restore Kit (Illumina) and DNA methylation data was obtained using the Infinium Methylation EPIC BeadChip (Illumina), according to protocols supplied by the manufacturer.

**Data analysis***Preprocessing* All analyses were performed using R version … (R Core Team. R: a language and environment for statistical computing. Available from: <https://www.R-project.org/>.). Raw 450K and EPIC data from all cohorts were separately imported using the minfi package (24) and data was normalized using ssNoob normalization (25). Failed probes with a detection P value >0.01 (n= 83712 (450K), 45443(EPIC)), probes targeting the sex chromosomes were removed (n= (450K), (EPIC)), probes containing a single-nucleotide polymorphism (dbSNP132 Common) within five base pairs of and including the targeted CpG site (n= (450K), (EPIC))/ SNP containing (n= (450K), (EPIC)) and cross reacting probes (n= (450K), (EPIC)) were removed. Betas values were obtained and both normalized 450K and EPIC beta values were merged resulting in … common probes.

*Batch effect* Batch effect was evaluated analyzing tissue types that occurred in two or more studies, these included normal tissue PanNET tissue. Average methylation values were compared, and unsupervised analysis (t-SNE and heatmaps) were made .

*Probe selection and unsupervised analysis*

5000 variable probes were selected for unsupervised analysis.

*Classifier development*

*Classifier validation*

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