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Hereditary pancreatic cancer early surveillance program

Submission date 06/02/2026	**Recruitment status** Recruiting	[X] Prospectively registered [X] Protocol [_] Statistical analysis plan [_] Results [_] Individual participant data [X] Record updated in last year
Registration date 06/02/2026	**Overall study status** Ongoing	
Last Edited 09/02/2026	**Condition category** Cancer	

Plain English summary of protocol

Background and study aims
Pancreatic cancer is often hard to treat because it is usually found at a late stage. Some people have a higher risk because of their family history or inherited genes. This study aims to find people at higher risk and follow them over time so that pancreatic cancer, or early warning signs, can be found as early as possible. The study also aims to improve blood tests and other tools that may help doctors detect pancreatic cancer earlier in the future.

Who can participate?
Adults aged 18 or over may be able to take part if they have a strong family history of pancreatic cancer or carry certain inherited gene changes linked to higher risk. Adults who have been newly diagnosed with pancreatic cancer may also be included to help researchers compare results. People must be able to give informed consent.

What does the study involve?
The study usually starts with an online questionnaire that asks about personal and family health history. If someone appears to be at higher risk, they are invited to a specialist clinic. At the clinic, staff will explain the study and ask for written consent. Some participants will have a genetic test using a blood sample or cheek swab. Those who are eligible will be invited to take part in regular follow-up, usually once a year. This may include an MRI scan of the pancreas and a blood sample. The study does not change normal medical care.

What are the possible benefits and risks of participating?
Possible benefits include closer monitoring for people at higher risk and the chance that any problems are found earlier. Participants also help research that may benefit others in the future. Risks are generally low and may include discomfort or bruising from blood tests, anxiety about genetic results, or stress from regular check-ups. MRI scans are considered safe but may not suit everyone.

Where is the study run from?
The study is run from several hospitals and universities across Europe, including centres in Sweden, Greece, Lithuania, Slovenia, Belgium, Denmark, and Spain.

When is the study starting and how long is it expected to run for?
The study is expected to begin enrolling participants in April 2026. Follow-up will continue until around 2029.

Who is funding the study?
The study is funded by the European Union's Horizon Europe research programme, with additional support from the Swiss State Secretariat for Education, Research and Innovation.

Who is the main contact?
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Study information

Scientific Title

Surveillance of high-risk individuals and early detection of pancreatic cancer to detect pancreatic cancer early in people at higher inherited or family risk

Acronym
PACES

Study objectives
The main objectives of the study are to :
1. Identify people at elevated inherited/familial risk of pancreatic cancer,
2. Follow them longitudinally with structured surveillance to detect disease earlier, and
3. Use the resulting data/samples to validate and develop biomarkers and prediction tools.

Tier 1: Patient Identification, Pre-screening, Genetic evaluation
Primary objective: To perform an initial risk/eligibility assessment through a public-facing digital pre-screening tool (e.g., chatbot/web platform) based on personal and family history (and other relevant risk factors), in order to identify individuals potentially at increased risk of pancreatic cancer and triage/direct those individuals to a participating clinical site for confirmatory eligibility assessment and subsequent germline genetic evaluation and risk stratification.
Secondary objectives: Classify participants by pathogenic/likely pathogenic variants in the targeted gene panel; assess the distribution of genetic syndromes in the referred population; correlate genetic profiles with clinical/demographic risk factors; generate a baseline cohort for longitudinal surveillance.

Tier 2: Surveillance program
Primary objective: Identify pancreatic ductal adenocarcinoma (PDAC) at an early stage in people with hereditary/familial risk using serial imaging and/or biomarker tracking.
Secondary objectives: Support development/training/validation of AI-based risk prediction models; build a harmonized dataset integrating genetics, family history, clinical factors, imaging, and biomarkers; provide a research-ready platform for biomarker discovery/validation; establish and refine evidence-based surveillance protocols.

Tier 3: Validation & Biomarker Discovery
Primary objective: To evaluate the diagnostic/triage accuracy of the public-facing digital pre-screening tool in identifying individuals who are eligible/high-risk, using the participating clinical site eligibility assessment and downstream Tier 1 genetic evaluation outcome as the reference standard.

Updated 09/02/2026:
Primary objective: To leverage SHIELD surveillance biospecimens and linked clinical/imaging data to clinically validate Reccan IA and to discover/verify novel proteomic biomarker signatures, with the aim of improving early detection and diagnosis of PDAC in familial/genetically high risk individuals.

Secondary objectives:
1. To estimate pre-screening sensitivity, specificity, PPV and NPV for identifying individuals who meet Tier 1/Tier 2 eligibility criteria (mirroring the kind of performance metrics already used in Tier 3 for Reccan-IA).
2. To assess acceptance and usability of the pre-screening tool among the public (e.g., completion rate, drop-off rate, time-to-complete, user satisfaction, perceived clarity, and willingness to proceed to clinical evaluation).
3. To quantify operational performance (e.g., proportion successfully routed to a site; proportion attending a site visit after being flagged “at risk”).

Ethics approval required
Ethics approval required

Ethics approval(s)
1. Approved 22/12/2025, Komisija Republike Slovenije za medicinsko etiko (Štefanova ulica 5, Ljubljana, 1000, Slovenia; +386 1 478 69 06; kme.mz@gov.si), ref: 0120-650/2025-2711-3

2. Approved 26/10/2025, Comité de ética de investigación clinica (Avda. Montepríncipe, 25., Madrid, 28660, Spain; +34 91 708 99 00, ext. 12588.; Secretaria.ceic@hmhospitales.com), ref: CEIm code 25.10.2611-GHM

3. Submitted 06/01/2026, Nationalt Center for Etik, Råd og Komitéer (Ørestads Boulevard 5, København S, 2300, Denmark; N/A; dketik@dketik.dk), ref: Not Assgined Yet

4. Submitted 02/02/2026, Research Ethics Commitee of the National and Kapodistrian University of Athens (Christou Lada 6, Athens, 10676, Greece; +30 6974006084; diradmin@uoa.gr), ref: Not assigned yet

5. Submitted 18/12/2025, Etikprövningmhyndigheten (Box 2110, Uppsala, 75002, Sweden; +46 10-475 08 00; registrator@etikprovning.se), ref: Not assigned yet

6. Submitted 06/01/2026, Comité d'Éthique Hospitalo-Facultaire Universitaire de Liège (CHU de Liège, Sart Tilman, Liege, 4000, Belgium; +32 4 323 21 58; ethique@chuliege.be), ref: Not assigned yet

7. Submitted 06/01/2026, Vilnius regional biomedical research ethics committee (M. K. Čiurlionio str. 21/27, Vilnius, 01513, Lithuania; + 370 (0)5 2 68 69 98; rbtek@mrvu.lt), ref: Not assigned yet

Primary study design
Observational

Secondary study design
Prospective, multicentre, longitudinal surveillance and sample-collection program

Study type(s)

Health condition(s) or problem(s) studied
Pancreatic ductal adenocarcinoma (PDAC)

Interventions
The study is designed as a prospective, multicentre, non-interventional, longitudinal observational surveillance and sample-collection programme in adults with increased hereditary and/or familial risk of pancreatic ductal adenocarcinoma (PDAC), with additional inclusion of newly diagnosed, treatment-naïve PDAC cases as a reference cohort where applicable. The study is structured in three tiers that support risk identification, longitudinal surveillance, and translational research outputs (biomarker validation and discovery), while clinical care and imaging are delivered according to local standard-of-care pathways.

Tier 1: Identification, pre-screening, genetic evaluation
Potential participants are approached via participating clinical centres/cancer genetics routes

and/or are pre-screened through a public-facing digital eligibility assessment tool (e.g., web platform/chat-based interface) that collects structured personal and family history and other relevant risk factors and triages potentially eligible individuals to a participating clinical site. At the clinical site, eligibility is confirmed and written informed consent is obtained prior to study procedures, after which germline genetic testing is performed using a targeted next-generation sequencing (NGS) panel on buccal swab or whole blood samples, with variant classification and risk stratification used to determine eligibility for surveillance. Post-test counselling and reporting are provided according to local procedures, and participants may be categorised as genetically eligible (pathogenic/likely pathogenic variants), eligible based on familial criteria, or not eligible for surveillance based on the defined criteria.

Tier 2: Longitudinal surveillance observations and tests
Eligible high-risk participants are followed longitudinally with annual surveillance visits that include (i) imaging and (ii) blood sampling, alongside structured clinical data capture. Imaging is performed as MRI within the protocol-defined timing window relative to blood sampling (and EUS may be used when MRI cannot be performed, with deviations documented), and imaging findings are recorded as observational outcomes (e.g., lesions, PDAC, precursor lesions). Blood sampling is performed annually (up to ~20 mL) for biomarker-related analyses and banking; samples are processed locally following standardised procedures and aliquots are shipped to the central SHIELD biobank for approved research use, while clinical/demographic data, family history, and other observations are captured via structured questionnaires and/or electronic health records in harmonised case report forms.

Tier 3: Biomarker validation and exploratory research
Participants enrolled in the surveillance cohort constitute the source population for prospective clinical performance evaluation of the blood-based Reccan-IA test (used with an algorithmic risk score) and for biomarker discovery projects that use the longitudinally collected, consented biospecimens and harmonised data. The Tier 3 validation framework evaluates diagnostic performance metrics (including sensitivity and specificity, and potentially PPV/NPV) relative to clinical diagnosis based on MRI with histopathology confirmation when applicable.

Analyses, monitoring, and data handling
For Tier 1 and Tier 2, analyses are primarily descriptive (e.g., demographics, adherence /retention, frequency of detected lesions/PDAC, and completeness/quality of self-reported data /imaging/genetic/biospecimen data). Comparative analyses (e.g., chi-square/Fisher’s exact tests and logistic regression as appropriate) will be used to explore associations between mutation status and demographic/clinical variables.

Monitoring includes both remote and on-site activities to ensure protocol adherence, data integrity, and participant safety. Remote monitoring reviews CRF data and consent forms, while on-site visits verify source documents and operational records (including sample logs and freezer records), with an initial visit after site initiation and subsequent annual and/or risk-based visits.

Participant data are handled in a GDPR-aligned manner using pseudonymisation. Source data (e. g., genetic test results, clinical observations, imaging, and questionnaire responses) are collected and stored locally at each clinical site in secure, access-controlled environments compliant with applicable national/institutional policies. Data transferred for consortium use will be structured and encrypted, and participants will be coded/pseudonymised. The re-identification key will remain securely stored at the originating clinical site.

Protocol deviations will be documented and explained, with prior approvals required except under emergency circumstances; corrective actions (typically including re-training and, if needed, site termination) will be implemented to prevent recurrence. The protocol allows study suspension/termination for defined reasons including data-privacy concerns (e.g., breaches /unauthorised access/non-compliance) and legal/regulatory issues, with notification to the responsible organisation and ethics alignment. At close-out, monitoring will ensure CRFs are complete and prior findings are resolved, and the local site principal Investigator will notfiy the ethics committee of study closure localy relevant report/format. Principal Investigator of the study will also, when relevant, provide update infromation to the Regisgtration Registry.

Intervention Type
Other

Primary outcome(s)
1. Tier1: Proportion of approached individuals who use the public-facing interfaces and who meet SHIELD high-risk eligibility criteria based on genetic results measured using recruitment funnel metrics captured via platform logs and site screening logs: (1) number approached /invited, (2) number who engage with the public-facing interface (e.g., web/chat), (3) number triaged to a site, (4) number consented and genetically tested, (5) number meeting SHIELD high-risk eligibility based on germline testing and eligibility evaluation; eligibility is determined using targeted NGS results plus predefined criteria recorded in study records/eCRF at continuously, summarised at defined recruitment cut-offs (interim and end of recruitment)

2. Tier2: Longitudinal adherence rate to annual follow-up schedule (e.g., MRI completion and blood sampling) measured using for each scheduled annual surveillance cycle, proportion completing required components (MRI and blood sampling) within protocol-defined windows; MRI is scheduled/performed in relation to the surveillance blood test within the protocol window (no later than 6 months after blood test; coordination guidance also allows alignment with prior/next imaging for those already in surveillance) at annual follow-up visit (12-month intervals) and cumulatively across follow-up until study end/withdrawal/diagnosis

3. Tier2: Completeness and quality of the surveillance dataset (clinical, imaging, genetic, biospecimen data) measured using data completeness/quality indicators derived from eCRF and supporting records: completeness of required fields and visit forms, availability/quality of imaging reports, completeness of biospecimen chain-of-custody (collection, processing, aliquoting, shipment/biobank receipt), and documentation of deviations at At each surveillance visit and cumulatively at data cut and study close-out

4. Tier 3: Sensitivity measured using proportion of true PDAC cases correctly identified by the Reccan-IA test against the clinical reference standard at when participant’s blood sample is collected for the test and when the corresponding clinical disease status is established by MRI (and histopathology when applicable)

5. Tier3: Specificity measured using proportion of non-PDAC individuals correctly identified by the Reccan-IA test against the clinical reference standard at when participant’s blood sample is collected for the test and when the corresponding clinical disease status is established by MRI (and histopathology when applicable)

Key secondary outcome(s)

1. Frequency of pathogenic or likely pathogenic variants measured using Proportion and distribution of participants with pathogenic/likely pathogenic variants in the targeted panel; measured from germline testing results (targeted NGS panel) and variant classification recorded in study records at Once per participant when genetic results are available;

2. Proportion of genetically high-risk individuals enrolled into the clinical validation of Reccan-IA measured using Proportion: numerator = participants classified as genetically high-risk who enrol into the downstream validation component; denominator = all participants classified as genetically high-risk; measured from eligibility categorisation and Tier 3 enrolment records at cumulative, from the point of genetic eligibility determination through end of enrolment into Tier 3

3. Incidence of PDAC or high-grade precursor lesions detected during surveillance measured using rate of PDAC and/or high-grade precursor lesions detected; determined through surveillance imaging (annual MRI; EUS if MRI cannot be performed) and clinical outcome documentation, with histopathology confirmation when applicable at longitudinally during annual follow-up until diagnosis, withdrawal, or programme closure

4. PPV and NPV of Reccan-IA measured using Positive predictive value and negative predictive value against the clinical reference standard at after results and reference standard status are available for the relevant participants

5. Performance in different high-risk subgroups (familial high-risk, genetic high-risk, and NOD) measured using performance metrics (at minimum sensitivity/specificity; PPV/NPV if planned) computed within subgroup definitions captured in the dataset at when subgroup classification and reference standard outcomes are available

6. Sensitivity for early-stage PDAC measured using Sensitivity specifically for early-stage PDAC (stage I–II) versus reference standard (MRI ± histopathology when applicable) at after staging and reference standard diagnosis are confirmed

Completion date
30/04/2029

Eligibility

Key inclusion criteria
Tier 1 - eligibility assessment
1. Ability to sign the eConsent
2. Age >= 18

Tier 1 - genetic evaluation
3. Individuals with a personal or family history suggestive of heritable pancreatic cancer syndromes, age 40+ (or 10 years younger than the youngest affected family member’s age at onset, per the protocol text).
4. Family-history patterns that can qualify include (examples listed in the protocol): 1 first-degree relative (FDR) with PDAC (with additional qualifiers/limits), 1 FDR plus other cancers/risk factors (e.g., NOD, pancreatitis, IPMN), 2 second-degree relatives (SDR), or meeting CAPS criteria (Annex referenced).
5. Individuals with newly diagnosed pancreatic cancer (age ≥18) are eligible to enter Tier 2 directly per the Tier 1 synopsis.

Tier 2 - Surveillance program & sample collection
1. Written informed consent and adult age ≥18 years.
2. Either: treatment-naïve, confirmed PDAC (with preferred stage distribution targets/limits noted in the protocol), included to build a reference cohort.
3. Or: “overall healthy” individuals with familial/hereditary risk, including any of the following high-risk categories: familial clustering patterns (e.g., ≥2 relatives with PDAC with at least one FDR; or two affected FDRs), or carriers of specific pathogenic/likely pathogenic variants with required family history and age thresholds (e.g., BRCA1/2, PALB2, ATM with an affected FDR /SDR; CDKN2A/FAMMM; STK11/Peutz-Jeghers; Lynch genes with affected FDR/SDR; PRSS1 hereditary pancreatitis with pancreatitis history).

Tier 3 - Validation & Biomarker Discovery
1. Participants enrolled in the SHIELD surveillance program constitute the cohort for the clinical performance validation of ReccanIA and the biomarker discovery

Healthy volunteers allowed
Yes

Age group
Mixed

Lower age limit
18 Years

Upper age limit
80 Years

Sex
All

Total final enrolment
0

Key exclusion criteria
Tier 1 - eligibility assessment:
1. Refusal of consent.

Tier 1 - genetic evaluation:
2. Refusal of consent.
3. Mental or other disabilities that prevent understanding and providing informed consent.

Tier 2 surveillance program & sample collection:
1. Individuals receiving treatment that could affect biomarker levels.
2. Acute inflammation that could interfere with biomarker analysis (the protocol notes leaving a minimum 3month window after end of treatment).
3. Chronic inflammation/infection, except chronic pancreatitis.
4. Prior treatment for PDAC (prior resection, radiotherapy, or chemotherapy).
5. Current immunosuppressive treatment (e.g., systemic steroid therapy or chemotherapy).
6. Systemic treatment for cancer within the last 3 months (because it could affect biomarker levels being measured).

Tier 3 Validation & Biomarker Discovery
No additional exclusion criteria, beyond Tier 1 and Tier 2

Date of first enrolment
30/04/2026

Date of final enrolment
30/11/2028

Locations

Countries of recruitment
Belgium

Denmark

Greece

Lithuania

Slovenia

Spain

Sweden

Sponsor information

Organisation
Univerzitetni klinicni center Maribor

Organisation
Lund University

ROR
https://ror.org/012a77v79

Organisation
Ethniko kai Kapodistriako Panepistimio Athinon

Organisation
Vilnius University

Organisation
Centre Hospitalier Universitaire de Liège

ROR
https://ror.org/044s61914

Organisation
Region Syddanmark

Organisation
Hospital Universitario HM Sanchinarro / Fundación de Investigación HM Hospitales

Funder(s)

Funder type

Funder Name
European Union’s Horizon Europe Research and Innovation Programme, Grant Agreement No 101214779

Funder Name
Swiss State Secretariat for Education, Research and Innovation, Grant Agreement No 101214779

Results and Publications

Individual participant data (IPD) sharing plan

IPD sharing plan summary
Not expected to be made available

Study outputs

Output type	Details	Date created	Date added	Peer reviewed?	Patient-facing?
Participant information sheet			06/02/2026	No	Yes
Protocol file			06/02/2026	No	No