

Data as of September 20th, 2013

Population: CT/OS

Cases: All primary pancreatic adenocarcinoma (ICD-O-2 site code no longer necessary) cases. Definition now includes cases reported as cause of death.

Controls: Participants who did not have a pancreatic cancer event as described above

Table 1. Sample size changes upon application of exclusion criteria

Exclusion Criteria	Aim 2 (DNA)	
	Cases	Controls
Original Sample	836	160972
Exclude participants already selected for Aim 2	253	159807
Exclude all participants w/ history of any cancer (except non-melanoma skin cancer)	177	145034
Exclude all participants with missing matching variable data or no follow-up time	176	144315
Exclude all participants who have both inadequate DNA and are not members of an existing major GWAS ¹	167	142386
Exclude all participants w/ a refusal for genetic studies	167	142370
Total post-exclusion participants	167	142370

¹Major GWAS studies include GARNET, SHARE, WHIMS+, GECCO, BAA 03, and PanScan

A total of 167 cases and 142370 potential controls remained in the matching pool for aim 2.

Matching Phase 4: Additional Participants eligible for Aim 2 only

A total of 167 cases and 142370 controls were put into the matching algorithm. Because these cases are ineligible for the serum component, all serum components of the matching were removed.

Table 2. Final Phase 4 Matching Criteria, maximum distance, and weighting for matching

Criteria	Maximum Distance	Weighting
Age	3 years	45
Ethnicity	Exact	-
WHI randomization date	6 months	1
OS enrollment	Exact	-
HT trial arm	Exact	-
DM trial arm	Exact	-
CaD trial enrollment	Exact	-
Hysterectomy	Exact	-
Randomization/Enrollment Clinic	Exact	-
Core analytes done (set to 'yes' for cases)	1	500
SHARE membership (set to 'yes' for cases)	1	500
PANSCAN membership (set to 'yes' for cases)	1	500
Major GWAS (set to 'yes' for cases)	1	500

Out of a total of 167 cases put into the matching algorithm, 106 successfully matched 2 controls to each case, 16 were able to match 1 control to each case, and 45 were unable to match any controls. For the cases that were unable to get two matches, the matching algorithm was run a second time, removing the criteria to match clinical center and expanding the maximum age difference to 5 years.

For this second round of matching, all 16 cases who had previously matched a control were able to match a second control. Of the 45 cases unable to match controls in the first round of matching, 10 were able to match 2 controls, 35 were unable to match any controls.

Total participants from phase 4 include 132 cases and 264 controls for Aim 2 (DNA).

Table 3. Matching Results – Additional Aim 2 (DNA) Participants

Matching Factor	Sum (weighted) of Absolute Differences	Pancreatic Cancer Cases (n=132)	Pancreatic Cancer Controls (n=264)
	Mean (min, max)	Mean (SD) / n (%)	Mean (SD) / n (%)
Age	1.3 (0.0, 5.0)	66.4 (7.2)	66.1 (6.9)
Ethnicity	0		
White		113 (85.6)	226 (85.6)
African American		9 (6.8)	18 (6.8)
Hispanic		6 (4.6)	12 (4.6)
Native American		0 (0.0)	0 (0.0)
Asian / Pacific Islander		3 (2.3)	6 (2.3)
Unknown		1 (0.8)	2 (0.8)
WHI Randomization / Enrollment Date	60.6 (1.0, 182.0)	10/4/96 (404)	10/10/96 (395)
OS enrollment	0	63 (47.7)	126 (47.7)
HT Intervention Arm	0		
E-Alone Active		8 (6.1)	16 (6.1)
E-Alone Placebo		8 (6.1)	16 (6.1)
E+P Active		8 (6.1)	16 (6.1)
E+P Placebo		7 (5.3)	14 (5.3)
Not randomized		101 (76.5)	202 (76.5)
DM Intervention Arm	0		
Low-fat diet		16 (12.1)	32 (12.1)
Comparison		27 (20.5)	54 (20.5)
Not randomized		89 (67.4)	178 (67.4)
CaD Trial Enrollment	0	36 (27.3)	72 (27.3)
Hysterectomy	0	61 (46.2)	122 (46.2)
Randomization Clinic (% matched to case)	-	-	228 (86.4)
Core analytes done	-	8 (6.1)	42 (15.9)
SHARE membership	-	40 (6.9)	27 (10.2)
PanScan membership	-	0 (0.0)	5 (1.9)
GWAS ¹ Done	-	35 (26.5)	152 (57.6)

¹Major GWAS studies include GARNET, SHARE, WHIMS+, GECCO, BAA 03, and PanScan

The average control follow-up time for cases was 10.0 years, for controls 15.2 years

Total Participants: 396

If participants who are already in a major GWAS do not need additional genetic testing, we have a total of 209 additional participants who need genetic analyses.