Article title: Genetic predisposition scores for dyslipidaemia influence plasma lipid concentrations at baseline, but not the changes after controlled intake of n-3 polyunsaturated fatty acids
Journal name: Genes and Nutrition
Author names: Aseel AlSaleh, Zoitsa Maniou, Fiona J Lewis, Wendy L Hall, Thomas A B Sanders and Sandra D O'Dell.
Affiliation and e-mail address of the corresponding author: Dr Sandra O'Dell, King's College London, School of Medicine, Diabetes and Nutritional Sciences Division.
E-mail: sandra.o'dell@kcl.ac.uk.

Online Resource 1 SNP associations with plasma lipids in previous GWAS studies

Genome-wide significant associations for TC

GWAS SNP[a]	Chromosome	Position[b]	Gene(s)[c]	Alleles (maj/min)	Risk allele[d]	Risk allele freq.	Sample *n*[e]	Beta (SE) risk-allele[f,g,h]	*P*-value*	Reference
rs3764261	16q.13	56993324	*CETP*	G,T	T	0.32	94472	1.67 (0.23) mg/dL	6.67E-14	Teslovich TM et al. (2010)[f]
rs1532085	15q21.3	58683366	*LIPC*	G,A	A	0.39	98656	1.54 (0.20) mg/dL	8.83E-20	Teslovich TM et al. (2010)[f]
rs1367117	2p24.1	21263900	*APOB*	G,A	A	0.30	100176	4.16 (0.22) mg/dL	4.08E-96	Teslovich TM et al. (2010)[f]
rs4299376	2p21	44072576	*ABCG5,ABCG8*	T,G	G	0.30	95992	3.01 (0.22) mg/dL	4.03E-45	Teslovich TM et al. (2010)[f]
rs6882076	5q33.3	156390297	*TIMD4,HAVCR1*	C,T	C	0.65	100184	1.98 (0.20) mg/dL	7.46E-28	Teslovich TM et al. (2010)[f]
rs1260326	2p23.3	27730940	*GCKR*	C,T	T	0.41	100176	1.91 (0.19) mg/dL	7.31E-27	Teslovich TM et al. (2010)[f]
rs2954022	8q24.13	126482621	*TRIB1*	C,A	C	0.54	100184	2.30 (0.19) mg/dL	5.02E-36	Teslovich TM et al. (2010)[f]
rs3850634	1p31.3	63050598	*ANGPTL3,DOCK7*	T,G	T	0.68	97148	2.60 (0.20) mg/dL	4.9E-41	Teslovich TM et al. (2010)[f]
rs1167998	1p31.3	62931632	*ANGPTL3,DOCK7*	A,C	A	0.67	17346	0.073 (0.012) SD	6.39E-10	Aulchenko et al. (2009)
rs174550	11q12.2	61571478	*FADS1,FADS2,FADS3*	T,C	T	0.66	100184	1.78 (0.20) mg/dL	2.08E-22	Teslovich TM et al. (2010)[f]

Genome-wide significant associations for HDL-C

GWAS SNP[a]	Chromosome	Position[b]	Gene(s)[c]	Alleles (maj/min)	Risk allele[d]	Risk allele freq.	Sample *n*[e]	Beta (SE) risk-allele[f,g,h]	*P*-value*	Reference
rs3764261	16q.13	56993324	*CETP*	G,T	G	0.68	94225	-3.39 (0.09) mg/dL	7.10E-380	Teslovich TM et al. (2010)[f]
rs3764261	16q.13	56993324	*CETP*	G,T	G	0.69	16728	-3.47 (NR) mg/dL	2.3E-57	Willer et al. (2008)[g]
rs3764261	16q.13	56993324	*CETP*	G,T	G	0.72	4527	-0.092 (0.008) SD	6.97E-29	Sabatti et al. (2009)[h]
rs3764261	16q.13	56993324	*CETP*	G,T	G	0.68	16253	-0.245 (0.012) SD	2.59E-89	Aulchenko et al. (2009)
rs1532085	15q21.3	58683366	*LIPC*	G,A	G	0.61	98409	-1.45 (0.08) mg/dL	2.92E-96	Teslovich TM et al. (2010)[f]
rs1532085	15q21.3	58683366	*LIPC*	G,A	G	0.56	4529	-0.047 (0.0074) SD	1.77E-10	Sabatti et al. (2009)[h]
rs1532085	15q21.3	58683366	*LIPC*	G,A	G	0.59	19736	-0.130 (0.010) SD	9.72E-36	Aulchenko et al. (2009)
rs4846914	1q42.13	230295691	*GALNT2*	A,G	G	0.40	99881	-0.61 (0.07) mg/dL	3.66E-21	Teslovich TM et al. (2010)[f]
rs4846914	1q42.13	230295691	*GALNT2*	A,G	G	0.40	21312	-0.07 (0.01) SD	2E-13	Kathiresan et al. (2009)[h]
rs4149268	9q31.1	107647220	*ABCA1*	C,T	C	0.64	19983	-0.82 (NR) mg/dL	1.2E-10	Willer et al. (2008)[g]
rs10808546	8q24.13	126495818	*TRIB1*	C,T	C	0.56	99900	-0.61 (0.07) mg/dL	6.35E-19	Teslovich TM et al. (2010)[f]
rs174547	11q12.2	61570783	*FADS1,FADS2,FADS3*	T,C	C	0.36	40330	-0.09 (0.02) SD	2E-12	Kathiresan et al. (2009)[h]

Genome-wide significant associations for LDL-C

GWAS SNP[a]	Chromosome	Position[b]	Gene(s)[c]	Alleles (maj/min)	Risk allele[d]	Risk allele freq.	Sample *n*[e]	Beta (SE) risk-allele[f,g,h]	*P*-value*	Reference
rs247616	16q.13	56989590	*CETP*	C,T	C	0.68	89838	1.45 (0.20) mg/dL	9.25E-13	Teslovich TM et al. (2010)[f]
rs1367117	2p24.1	21263900	*APOB*	G,A	A	0.30	95446	4.05 (0.19) mg/dL	4.5E-114	Teslovich TM et al. (2010)[f]
rs4299376	2p21	44072576	*ABCG5,ABCG8*	T,G	G	0.30	91285	2.75 (0.20) mg/dL	1.73E-47	Teslovich TM et al. (2010)[f]

rs6882076	5q33.3	156390297	*TIMD4,HAVCR1*	C,T	C	0.65	95454	1.67 (0.19) mg/dL	1.89E-22	Teslovich TM et al. (2010)[f]
rs1501908	5q33.3	156398169	*TIMD4,HAVCR1*	C,G	C	0.63	27280	0.07 (0.02) SD	1.00E-11	Kathiresan et al. (2009)[h]
rs2954022	8q24.13	126482621	*TRIB1*	C,A	C	0.54	95454	1.84 (0.17) SD	2.59E-29	Teslovich TM et al. (2010)[f]
rs3850634	1p31.3	63050598	*ANGPTL3,DOCK7*	T,G	T	0.68	92503	1.59 (0.19) mg/dL	2.63E-18	Teslovich TM et al. (2010)[f]
rs174546	11q12.2	61569830	*FADS1,FADS2,FADS3*	C,T	C	0.56	4268	0.096 (0.018) SD	1.30E-07	Sabatti et al. (2009)[h]
rs174583	11q12.2	61609750	*FADS1,FADS2,FADS3*	C,T	C	0.65	95443	1.71 (0.19) mg/dL	1.17E-21	Teslovich TM et al. (2010)[f]

Genome-wide significant associations for TG

GWAS SNP[a]	Chromosome	Position[b]	Gene(s)[c]	Alleles (maj/min)	Risk allele[d]	Risk allele freq.	Sample *n*[e]	Beta (SE) risk-allele[f,g,h]	*P*-value*	Reference
rs7205804	16q.13	57004889	*CETP*	G,A	G	0.55	95070	2.88 (0.38) mg/dL	1.15E-12	Teslovich TM et al. (2010)[f]
rs4846914	1q42.13	230295691	*GALNT2*	A,G	G	0.40	21312	0.08 (0.01) SD	7.00E-15	Kathiresan et al. (2008)[h]
rs1321257	1q42.13	230305312	*GALNT2*	A,G	G	0.39	92418	2.76 (0.38) mg/dL	2.09E-14	Teslovich TM et al. (2010)[f]
rs1553318	5q33.3	156479323	*TIMD4,HAVCR1*	C,G	C	0.64	96598	2.63 (0.39) mg/dL	3.68E-12	Teslovich TM et al. (2010)[f]
rs1260326	2p23.3	27730940	*GCKR*	C,T	T	0.41	96590	8.76 (0.40) mg/dL	5.7E-133	Teslovich TM et al. (2010)[f]
rs1260326	2p23.3	27730940	*GCKR*	C,T	T	0.45	19840	0.12 (0.02) SD	2.00E-31	Kathiresan et al. (2009)[h]
rs1260326	2p23.3	27730940	*GCKR*	C,T	T	0.37	12435	0.112 (0.013) SD	5.17E-17	Aulchenko et al. (2009)
rs1260326	2p23.3	27730940	*GCKR*	C,T	T	0.35	4501	0.093 (0.015) SD	3.56E-10	Sabatti et al. (2009)[h]
rs780094	2p23.3	27741237	*GCKR*	T,C	C	0.39	18407	8.59 (NR) mg/dL	6.1E-32	Willer et al. (2008)[g]
rs2954029	8q24.13	126490972	*TRIB1*	A,T	A	0.53	96598	5.64 (0.39) mg/dL	3.29E-55	Teslovich TM et al. (2010)[f]
rs2131925	1p31.3	63025942	*ANGPTL3,DOCK7*	T,G	T	0.68	96598	4.94 (0.40) mg/dL	8.84E-43	Teslovich TM et al. (2010)[f]
rs1167998	1p31.3	62931632	*ANGPTL3,DOCK7*	A,C	A	0.68	14268	0.091 (0.013) SD	1.95E-12	Aulchenko et al. (2009)

rs439401	19q13.32	63025942	*APOE,APOC1,APOC2*	C,T	C	0.64	65871	5.50 (0.44) mg/dL	1.14E-30	Teslovich TM et al. (2010)[f]
rs439401	19q13.32	63025942	*APOE,APOC1,APOC2*	C,T	C	0.68	11885	0.086 (0.014) SD	1.78E-09	Aulchenko et al. (2009)
rs174546	11q12.2	61569830	*FADS1,FADS2,FADS3*	C,T	T	0.34	96598	3.82 (0.38) mg/dL	5.41E-24	Teslovich TM et al. (2010)[f]
rs174547	11q12.2	61570783	*FADS1,FADS2,FADS3*	T,C	C	0.34	38846	0.06 (0.02) SD	2.00E-14	Kathiresan et al. (2009)[h]

[a]SNP shown in previous GWAS to exhibit the strongest association in that gene with the trait.
[b]Positions in base pairs are from Human Genome NCBI Build 37.5.
[c]Biological candidate gene(s) or nearest gene(s) is indicated.
[d]Allele associated with adverse lipid profile: increase in TC, LDL-C and TG or decrease in HDL-C.
[e]*n* is the number of individuals included in the association analysis of the SNP and the trait.
[f]The effect sizes for HDL, LDL, and TC expressed in mg/dL were estimated directly. Effect sizes for TG were estimated as percent changes due to a single copy of the minor allele; effect in mg/dL was determined at mean triglyceride level 137.9 mg/dL.
[g]The effect sizes shown were estimated from stage 2 samples only.
[h]The effect on the untransformed trait for each copy of the minor allele expressed as proportion of 1 SD change.

GWAS genome-wide association study; *HDL-C* high density lipoprotein cholesterol; *LDL-C* low density lipoprotein-cholesterol; *MAF* minor allele frequency; *SE* standard error; *SNP* single nucleotide polymorphism; *TC* total cholesterol; *TG* triglyceride.

*Significance of the test of association derived from linear regression models. GWAS significance taken as $P < 5.00E-08$.

References

Aulchenko YS et al. (2009). Nat Genet 41:47-55.
Kathiresan S et al. (2008). Nat Genet 40:189-97.
Kathiresan S et al. (2009). Nat Genet 41:56-65.
Sabatti C et al. (2009). Nat Genet 41:35-46.
Teslovich TM et al. (2010). Nature 466:707-13.
Willer CJ et al. (2008). Nat Genet 40:161-9.