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
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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 3 Association between individual risk SNPs and plasma TC, LDL-C, HDL-C and TG concentration at baseline[a]

Association of TC SNPs with TC at baseline

SNP	Gene	Effect	SE	*P**	r^2	*n*	Risk allele	Risk allele freq.	Original SNP (LD r^2)[b]
rs3764261	*CETP*	0.007	0.123	0.91	0.039	270	T	0.36	
rs1532085	*LIPC*	-0.059	0.127	0.34	0.028	279	A	0.43	
rs1367117	*APOB*	0.002	0.123	0.97	0.028	270	A	0.30	
rs4299376	*ABCG5,ABCG8*	0.009	0.117	0.89	0.026	278	G	0.32	
rs6882076	*TIMD4,HAVCR1*	-0.11	0.117	0.060	0.038	288	C	0.64	
rs1260326	*GCKR*	-0.132	0.124	0.030	0.045	282	T	0.39	
rs2954029	*TRIB1*	-0.075	0.134	0.21	0.051	273	A	0.53	
rs2131925	*ANGPTL3,DOCK7*	-0.11	0.119	0.85	0.031	284	T	0.63	rs3850634 (1.0), rs1167998 (1.0)
rs174546	*FADS1,FADS2,FADS3*	0.034	0.123	0.59	0.038	268	T	0.71	rs174550 (1.0)

Association of LDL-C SNPs with LDL-C at baseline

SNP	Gene	Effect	SE	*P**	r^2	*n*	Risk allele	Risk allele freq.	Original SNP (LD r^2)[b]
rs3764261	*CETP*	0.004	0.099	0.95	0.032	270	G	0.63	rs247616 (1.0)
rs1367117	*APOB*	-0.037	0.099	0.71	0.030	271	A	0.30	
rs4299376	*ABCG5,ABCG8*	-0.021	0.094	0.72	0.025	287	G	0.32	
rs6882076	*TIMD4,HAVCR1*	-0.146	0.094	0.12	0.036	288	C	0.64	
rs2954029	*TRIB1*	-0.046	0.108	0.45	0.030	273	A	0.53	rs2954022 (0.94)
rs2131925	*ANGPTL3,DOCK7*	-0.009	0.094	0.87	0.036	284	T	0.63	rs3850634 (1.0)
rs174546	*FADS1,FADS2,FADS3*	0.052	0.098	0.40	0.030	268	T	0.71	

Association of HDL-C SNPs with HDL-C at baseline

SNP	Gene	Effect	SE	*P**	r^2	*n*	Risk allele	Risk allele freq.	Original SNP (LD r^2)[b]
rs3764261	*CETP*	0.076	0.052	0.15	0.206	270	G	0.63	
rs1532085	*LIPC*	-0.022	0.043	0.66	0.304	303	G	0.57	
rs4846914	*GALNT2*	0.023	0.043	0.47	0.299	297	G	0.47	
rs4149268	*ABCA1*	-0.033	0.052	0.52	0.226	281	C	0.58	
rs2954029	*TRIB1*	-0.099	0.046	0.05	0.301	300	A	0.53	rs10808546 (1.0)
rs174546	*FADS1,FADS2,FADS3*	-0.082	0.042	0.11	0.287	295	T	0.29	rs174547 (1.0)

Association of TG SNPs with lnTG at baseline[c]

SNP	Gene	Effect	SE	*P**	r^2	*n*	Risk allele	Risk allele freq.	Original SNP (LD r^2)[b]
rs3764261	*CETP*	-0.081	0.054	0.16	0.157	270	G	0.63	rs7205804 (1.0)
rs4846914	*GALNT2*	-0.012	0.057	0.83	0.127	270	G	0.47	
rs6882076	*TIMD4,HAVCR1*	-0.021	0.051	0.71	0.132	288	C	0.64	rs1553318 (1.0)
rs1260326	*GCKR*	0.035	0.054	0.52	0.136	282	T	0.39	
rs2954029	*TRIB1*	-0.002	0.059	0.97	0.15	270	A	0.53	
rs2131925	*ANGPTL3,DOCK7*	0.067	0.052	0.24	0.237	284	T	0.63	
rs439401	*APOE,APOC1,APOC2*	-0.003	0.053	0.96	0.123	287	C	0.63	
rs174546	*FADS1,FADS2,FADS3*	-0.003	0.053	0.95	0.152	268	T	0.29	

[a] Data are the coefficients of associations of SNP with the trait at baseline presented as effect size and standard error derived from linear regression models of SNP against trait at baseline. The proportion of explained variance is indicated by r^2 and *n* is the number of participants in each subgroup.

[b] The original SNP identified in GWAS and the LD r^2 value to the proxy SNP used in this analysis.

[c] TG data was logged for analysis and is presented in that form.

BMI Body mass index; *GWAS* genome-wide association study; *HDL-C* high density lipoprotein cholesterol; *LD* linkage disequilibrium; *LDL-C* low density lipoprotein-cholesterol; *SE* standard error; *SNP* single nucleotide polymorphism; *TC* total cholesterol; *TG* triglyceride.

*Significance derived from linear regression models. *P*-values for adjusted for BMI, age, gender and ethnicity.