

■ SUPPLEMENTARY ONLINE DATA

Gene expression profiling in whole blood of patients with coronary artery disease

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Table S1 Clinical characteristics of patients with CAD and healthy controls

ACEI, angiotensin-converting enzyme inhibitor; ARB, angiotensin receptor blocker; BMI, body mass index; DBP, diastolic blood pressure; LDL, low-density lipoprotein; HDL, high-density lipoprotein; SBP, systolic blood pressure.

Characteristic	Patients with CAD (n = 12)	Healthy controls (n = 12)	P value
Age (years)	66 ± 11	59 ± 7	NS
Male gender (n)	12	12	
SBP (mmHg)	130 ± 23	135 ± 22	NS
DBP (mmHg)	78 ± 13	85 ± 12	NS
Heart rate (beats/min)	58 ± 5	71 ± 15	< 0.05
BMI (kg/m ²)	26 ± 3	27 ± 3	NS
Waist/hip ratio	0.90 ± 0.04	0.90 ± 0.10	NS
Active smoker (n)	0	0	
Type 2 diabetes mellitus (n)	0	0	
Hypertension (n)	9 (75%)	0	
Total cholesterol (mmol/l)	3.8 ± 0.6	5.1 ± 0.5	< 0.05
LDL-cholesterol (mmol/l)	1.9 ± 0.7	3.4 ± 0.5	< 0.05
HDL-cholesterol (mmol/l)	1.1 ± 0.3	1.2 ± 0.2	NS
CRP (mg/l)	7.6 ± 11.0	1.5 ± 0.9	NS
Medication (n)			
Antiplatelet	11	2	< 0.001
β-Blocker	12	0	< 0.001
Statin	11	0	< 0.001
ACEI or ARB	4	0	0.093
Calcium channel blocker	3	0	NS

Table S2 Clinical characteristics of patients with CAD before and after taking part in the cardiac rehabilitation programme

Medication was not changed after compared with before participation in the rehabilitation programme. ACEI, angiotensin-converting enzyme inhibitor; ARB, angiotensin receptor blocker; BMI, body mass index; DBP, diastolic blood pressure; LDL, low-density lipoprotein; HDL, high-density lipoprotein; SBP, systolic blood pressure.

Characteristic	Before (n = 10)	After (n = 10)	P value
Age (years)	69 ± 9		
Male gender	10		
SBP (mmHg)	135 ± 20	135 ± 23	NS
DBP (mmHg)	77 ± 8	76 ± 9	NS
Heart rate (beats/min)	71 ± 11	67 ± 12	NS
BMI (kg/m ²)	27.4 ± 2.4	28.0 ± 2.6	NS
Waist/hip ratio	0.96 ± 0.03	0.96 ± 0.04	NS
Active smoker	0	0	
Type 2 diabetes mellitus	0	0	
Hypertension (n)	8 (80%)	8 (80%)	
Total cholesterol (mmol/l)	4.0 ± 0.7	4.0 ± 0.7	NS
LDL-cholesterol (mmol/l)	2.2 ± 0.7	2.1 ± 0.8	NS
HDL-cholesterol (mmol/l)	1.2 ± 0.2	1.4 ± 0.3	0.052
CRP (mg/l)	9.2 ± 13.4	4.6 ± 7.4	0.058
Medication (n)			
Antiplatelet	12		
β-Blocker	7		
Statin	8		
ACEI or ARB	4		
Calcium channel blocker	0		

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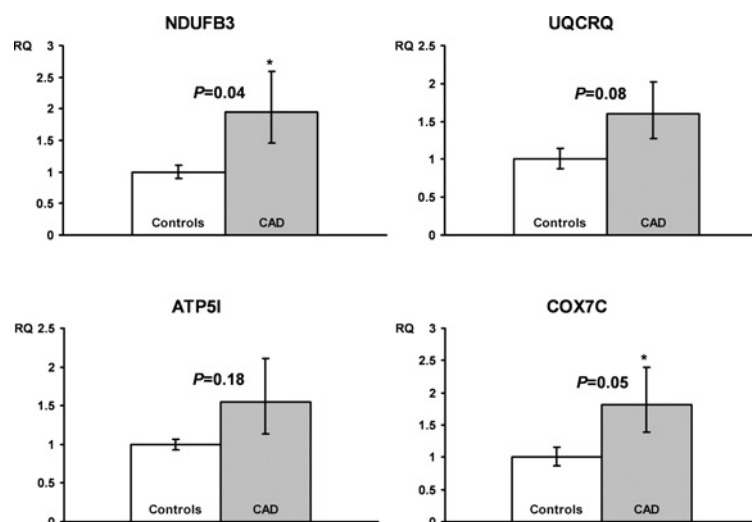


Figure S1 TaqMan® qRT-PCR analysis of expression of candidate genes in healthy controls and patients with CAD

* $P < 0.05$ compared with control ($n = 12$ per group).

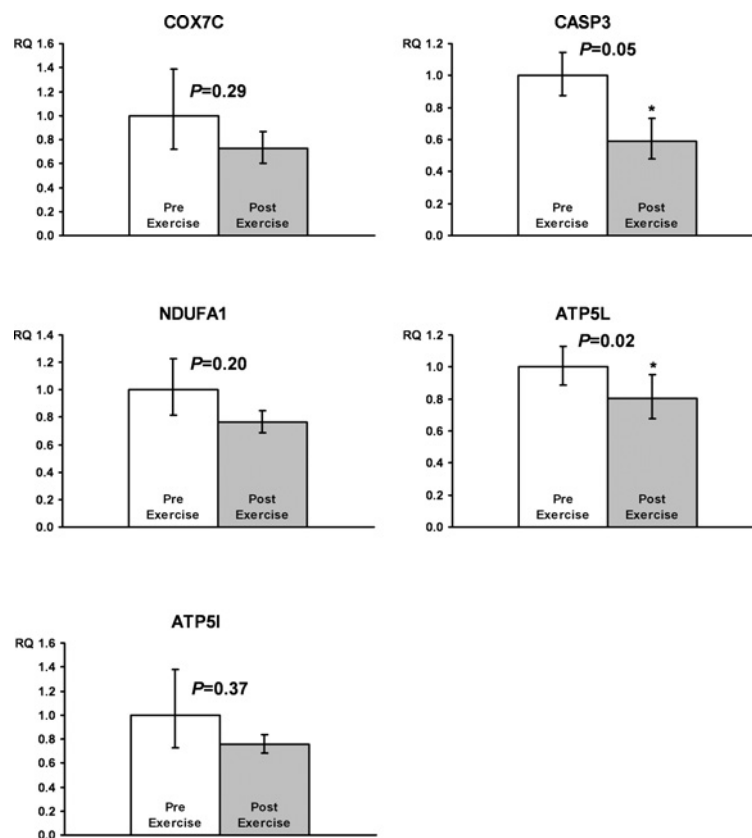


Figure S2 TaqMan® qRT-PCR analysis of expression of candidate genes in patients with CAD before and after an exercise rehabilitation programme

* $P < 0.05$ compared with pre-exercise ($n = 10$ per group).

Table S3 TaqMan[®] probes for qRT-PCR confirmation of gene expression profiling data

Gene	TaqMan [®] probe
<i>COX7C</i>	Hs01595220_g1
<i>UQCRCQ</i>	Hs00429571_g1
<i>NDUFB3</i>	Hs00427185_m1
<i>NDUFA1</i>	Hs00244980_m1
<i>ATPSL</i>	Hs00758883_s1
<i>CASP3</i>	Hs00234387_m1
<i>ATPS1</i>	Hs00273015_m1
<i>GAPDH</i>	Hs99999905_m1

Table S4 Differentially expressed genes (microarray data) between patients with CAD and healthy control subjects (a and c), and in patients with CAD pre- and post-cardiac rehabilitation (b and d), assigned to oxidative phosphorylation (a and b) and mitochondrial dysfunction (c and d) pathways

(a) Oxidative phosphorylation: patients with CAD compared with healthy controls

Gene symbol	Entrez Gene name	Illumina	FDR (<i>q</i> value)	Fold change	Entrez Gene ID
<i>ATP5C1</i>	ATP synthase, H ⁺ transporting, mitochondrial F1 complex γ polypeptide 1	ILMN_1701269	0.049	1.232	509
<i>ATP5I</i>	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit E	ILMN_1726603	0.011	1.356	521
<i>COX7B</i>	Cytochrome <i>c</i> oxidase subunit VIIb	ILMN_2184049	0.005	1.346	1349
<i>COX7C</i> (includes EG:1350)	Cytochrome <i>c</i> oxidase subunit VIIc	ILMN_1798189	0.02	1.266	1350
<i>NDUFA4</i>	NADH dehydrogenase (ubiquinone) I α subcomplex 4, 9 kDa	ILMN_1751258	0.007	1.362	4697
<i>NDUFB3</i>	NADH dehydrogenase (ubiquinone) I β subcomplex 3, 12 kDa	ILMN_2119945	0.002	1.441	4709
<i>UQCRCQ</i>	Ubiquinol-cytochrome <i>c</i> reductase, complex III subunit VII, 9.5 kDa	ILMN_1666471	0	1.484	27089

(b) Oxidative phosphorylation: pre- compared with post-rehabilitation in patients with CAD

Symbol	Entrez Gene name	Illumina	FDR (<i>q</i> value)	Fold change	Entrez Gene ID
<i>ATP5I</i>	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit E	ILMN_1772506	0.007	-1.298	521
<i>ATP5J</i>	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F6	ILMN_1772929	0.009	-1.31	522
<i>ATP5L</i>	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit G	ILMN_1812638	0	-1.483	10632
<i>ATP5O</i>	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, O subunit	ILMN_1791332	0.028	-1.205	539
<i>ATP6VID</i>	ATPase, H ⁺ transporting, lysosomal 34 kDa, VI subunit D	ILMN_1797310	0.006	-1.28	51382
<i>COX7C</i> (includes EG:1350)	cytochrome <i>c</i> oxidase subunit VIIc	ILMN_1798189	0	-1.585	1350
<i>IHPK2</i>	Inositol hexakisphosphate kinase 2	ILMN_1683328	0.033	-1.186	51447
<i>NDUFA1</i>	NADH dehydrogenase (ubiquinone) I α subcomplex 1, 7.5 kDa	ILMN_1784286	0.005	-1.315	4694
<i>NDUFB2</i>	NADH dehydrogenase (ubiquinone) I β subcomplex 2, 8 kDa	ILMN_2117330	0.046	-1.198	4708
<i>NDUFB3</i>	NADH dehydrogenase (ubiquinone) I β subcomplex 3, 12 kDa	ILMN_2119945	0.002	-1.315	4709
<i>NDUFB6</i>	NADH dehydrogenase (ubiquinone) I β subcomplex 6, 17 kDa	ILMN_1763147	0.03	-1.207	4712
<i>NDUFS5</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15 kDa (NADH-coenzyme Q reductase)	ILMN_1776104	0.005	-1.332	4725

Table S4 Continued

(c) Mitochondrial dysfunction: patients with CAD compared with healthy controls

Symbol	Entrez Gene name	Illumina	FDR (q value)	Fold change	Entrez Gene ID
<i>ATP5C1</i>	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, gamma polypeptide 1	ILMN_1701269	0.049	1.232	509
<i>COX7B</i>	Cytochrome c oxidase subunit VIIb	ILMN_2184049	0.005	1.346	1349
<i>COX7C</i> (includes EG:1350)	Cytochrome c oxidase subunit VIIc	ILMN_1798189	0.02	1.266	1350
<i>NDUFA4</i>	NADH dehydrogenase (ubiquinone) 1 α subcomplex, 4, 9 kDa	ILMN_1751258	0.007	1.362	4697
<i>NDUFB3</i>	NADH dehydrogenase (ubiquinone) 1 β subcomplex, 3, 12 kDa	ILMN_2119945	0.002	1.441	4709

(d) Mitochondrial dysfunction: pre- compared with post-rehabilitation in patients with CAD

Symbol	Entrez Gene name	Illumina	FDR (q-value)	Fold change	Entrez Gene ID
<i>APH1A</i> (includes EG:51107)	Anterior pharynx defective 1 homologue A (<i>Caenorhabditis elegans</i>)	ILMN_2398388	0.026	1.22	51107
<i>ATP5J</i>	ATP synthase, H ⁺ transporting, mitochondrial FO complex, subunit F6	ILMN_1772929	0.009	-1.31	522
<i>CASP3</i>	Caspase 3, apoptosis-related cysteine peptidase	ILMN_2388155	0.006	-1.265	836
<i>CASP8</i>	Caspase 8, apoptosis-related cysteine peptidase	ILMN_1673757	0.001	-1.449	841
<i>CAT</i>	Catalase	ILMN_1651705	0.041	-1.302	847
<i>COX7C</i> (includes EG:1350)	Cytochrome c oxidase subunit VIIc	ILMN_1798189	0	-1.585	1350
<i>NDUFB2</i>	NADH dehydrogenase (ubiquinone) 1 β subcomplex 2, 8 kDa	ILMN_2117330	0.046	-1.198	4708
<i>NDUFB3</i>	NADH dehydrogenase (ubiquinone) 1 β subcomplex 3, 12 kDa	ILMN_2119945	0.002	-1.315	4709
<i>NDUFB6</i>	NADH dehydrogenase (ubiquinone) 1 β subcomplex 6, 17 kDa	ILMN_1763147	0.03	-1.207	4712
<i>NDUFS5</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15 kDa (NADH-coenzyme Q reductase)	ILMN_1776104	0.005	-1.332	4725

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