



■ 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 | | |

Clinical Science

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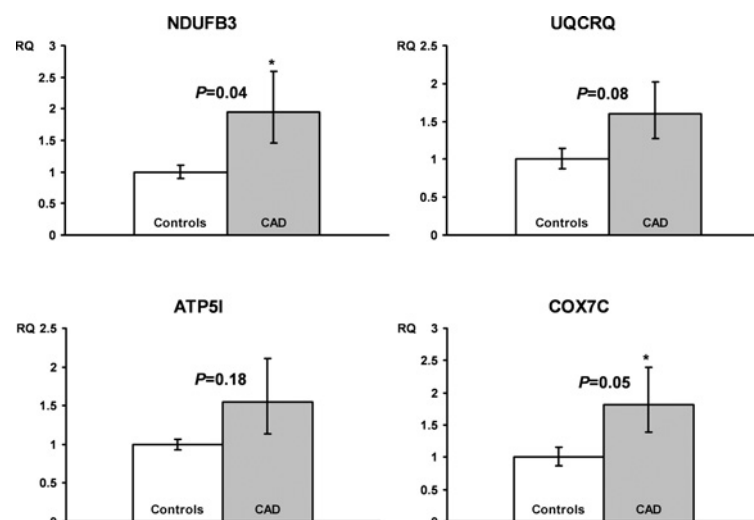


Figure S1 TaqMan[®] qRT-PCR analysis of expression of candidate genes in healthy controls and patients with CAD

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

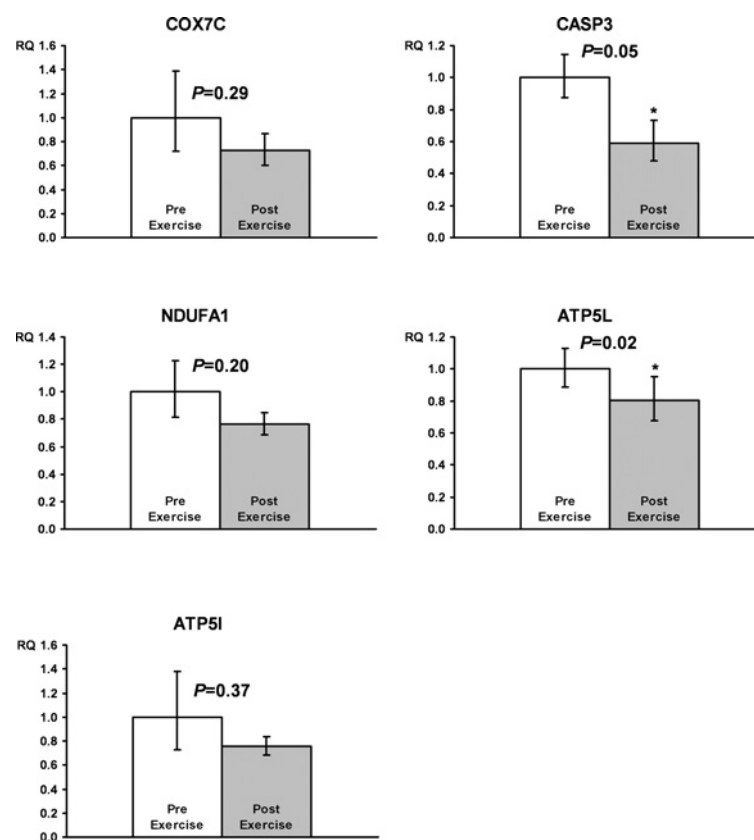


Figure S2 TaqMan[®] qRT-PCR analysis of expression of candidate genes in patients with CAD before and after an exercise rehabilitation programme

* $P < 0.05$ 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>NDUFSS</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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