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Polymorphism in the MHC2TA Gene Is Associated with Features of the Metabolic Syndrome and Cardiovascular Mortality

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Background. Recently, a -168A→G polymorphism in the MHC class II transactivator gene (MHC2TA) was shown to be associated with increased susceptibility to myocardial infarction (MI). Aim. To confirm the association between the MHC2TA -168A→G polymorphism and MI and to study its putative role for microalbuminuria, the metabolic syndrome (MetS) and cardiovascular mortality. Materials and Methods. Using an allelic discrimination method we genotyped 11,064 individuals from three study populations: 1) 4,432 individuals from the Botnia type 2 diabetes (T2D) study, 2) 1,222 patients with MI and 2,345 control subjects participating in the Malmö Diet and Cancer study and comprising an MI case-control sample, and 3) 3,065 T2D patients from the Local Swedish Diabetes registry. Results. No association between the -168A→G polymorphism in MHC2TA and MI was observed. However, in the Botnia cohort the AG/GG genotypes were associated with cardiovascular mortality after MI (1.78 [1.09–2.92], p = 0.02). In addition, the AG/GG genotypes were more common in subjects with MetS (40.1% vs. 36.9%, p = 0.03) and in non-diabetic subjects with microalbuminuria (45.4% vs. 36.5%, p = 0.003) compared to control subjects. Conclusions. A polymorphism in MHC2TA was associated with cardiovascular mortality and predictors of cardiovascular mortality, microalbuminuria and MetS.

INTRODUCTION
Cardiovascular disease is the leading cause of death in Sweden and in most Western countries. Almost 50% of deceased individuals died due to cardiovascular causes in Sweden 2005 (Swedish National Board of Health and Welfare http://www.socialstyrelsen.se). Both genetic and environmental factors modify the risk for cardiovascular diseases including myocardial infarction (MI) [1], smoking, dyslipidemia, diabetes, obesity and hypertension, are present in up to 90% of patients with MI [2,3]. Family history of MI has been shown to be a strong independent risk factor for coronary heart disease [4-7].

Microalbuminuria is an established risk marker for cardiovascular morbidity and mortality both in diabetic [8] and non-diabetic patients [9]. Inflammation is believed to play a major role in the pathogenesis of both microalbuminuria [10] and MI [11]. Insulin resistance has been proposed as a common denominator for these conditions, and has also been related to subclinical chronic inflammation [12].

A -168A→G polymorphism in the MHC class II transactivator gene (MHC2TA) was recently found to be associated with MI, rheumatoid arthritis and multiple sclerosis [13]. The -168A→G polymorphism was associated with lower expression of MHC2TA after stimulation of leukocytes with interferon-γ in humans and differences in expression of MHC class II molecules in different rat strains. Because of the role of MHC class II molecules in recognition of antigen molecules, genes like MHC2TA that can influence expression of MHC class II, are also candidate genes for autoimmune diseases [13].

To address this issue, we searched for any association between MHC2TA -168A→G polymorphism and cardiovascular morbidity and mortality as well as their predictors, microalbuminuria and the metabolic syndrome (MetS).

MATERIALS AND METHODS
Study Subjects
Patients were selected from three large populations in Finland and Sweden; the Botnia study, the Malmö Diet and Cancer Study (MDC) and the Diabetes Registry in Southern Sweden (DR). The protocols were approved by local Ethics committees, and informed consent was obtained from all subjects.

The Botnia Study
The Botnia Study was initiated in 1990 and represents a large population-based type 2 diabetes (T2D)
family study in Finland and Sweden, aiming at identification of genes increasing susceptibility to T2D, MetS and associated complications. Details of the study cohort, sampling strategy as well as anthropometric and metabolic measurements have been described earlier [14,15]. At the baseline examination, a structured questionnaire was completed by specially trained nurses, covering information on personal and family history of T2D (particularly hypertension, coronary heart disease, MI and stroke) and data on smoking habits. Both previous and current smokers were recorded as smokers.

Microalbuminuria was defined as urinary albumin excretion rate $>20$ μg/min in an overnight urine collection.

Total and cardiovascular mortality were assessed with a median follow up time of 7.9 years and the mortality data was obtained from the central death-certificate registry in Finland. Cardiovascular mortality was classified using the 9th revision of the International Classification of Diseases (cardiovascular diagnosis codes 390–459) before 1997 and the 10th revision (codes 100–199) thereafter. Causes of death were classified as 1) cardiovascular death (coronary heart disease), cerebrovascular disease (including both thrombotic stroke and cerebral haemorrhage) or other cardiovascular (including pulmonary embolism, abdominal aortic aneurysm, hypertensive complications, general atherosclerosis and peripheral artery disease with gangrene); or 2) other causes of death (neoplasms, violent or other). MetS was defined according to the National Cholesterol Education Program [16].

In total, 4,432 individuals were genotyped for the MHC2TA -168A→G polymorphism including 2,864 individuals without diabetes mellitus and 1,557 with T2D. Data on MI was available in 97% and on microalbuminuria in 64% of the subjects. Data on cardiovascular mortality was available for all populations.

The MI case-control population from the Malmo diet and cancer study (MDC) The Malmö Diet and Cancer study population (MDC) [17] included 25,086 randomly selected men (born 1923–1945) and women (born 1923–1950) living in the city of Malmö (population 250,000) in Sweden. A baseline examination was carried out between 1991 and 1996 encompassing a comprehensive assessment of lifestyle factors, heredity, medic... as well as previous and current diseases. On December 31st, 2000 the study population was checked against the Swedish National Board of Health and Welfare’s National Patient Registry and Cause of Death Registry. MI cases (first MI) were identified in the Swedish Patient Registry or in the Swedish Cause of Death Registry, using ICD-10 codes 410 and E21 in the Swedish Patient Registry and 410–414 and E21–E25 in the Swedish Cause of Death Registry.

Total age (±1 year) and gender-matched controls without MI from MDC were assigned to each MI patient, resulting in a case-control material consisting of 1,244 MI patients and 2,488 controls. Of total 3,732 individuals, 3,657 were successfully genotyped for the A→G polymorphism in MHC2TA. Diabetes diagnosis was defined as self reported earlier diagnosis, fasting blood glucose ≥ 6.1 mmol/l and/or treatment for earlier diagnosed diabetes mellitus.

Diabetes registry in Southern Sweden (DR) 3,065 T2D patients from a local diabetes registry in Southern Sweden [18], most of them enrolled at the Department of Endocrinology, University Hospital MAS, Malmö, were selected and genotyped for the MHC2TA -168A→G polymorphism. Data on MI was obtained from the patient records and was available in 77% and on microalbuminuria in 70% of the subjects.

Analytical techniques HbA1c, total cholesterol, HDL-cholesterol, triglycerides and P-creatinine were measured with standard laboratory methods. A detailed description of the methods are found elsewhere [15,18,19]. The urinary albumin concentration was in DR determined first by immunonephelometric method (Beckman Instruments, CA, USA) until 1998, and thereafter by an immunoturbidometric method (Beckman Coulter, Beckman Instruments, CA, USA). In the Botnia study, urine albumin concentration was determined with a radioimmunoassay with a detection limit of 2 mg/l. Microalbuminuria was defined as AER of 20 μg/min.

Genotyping In total 11,064 individuals were successfully genotyped for the -168 A→G polymorphism (rs907456) using allelic discrimination method on the ABI 7900 instrument (Applied Biosystems, Foster City, CA). Risk genotypes were defined according to earlier published report [13]. The genotyping success rate was 97.9, 99.0 and 99.9% in Botnia, MDC and DR cohorts, respectively.

Statistical methods Data were presented as mean ± SD or as median [25th–75th] percentile. Chi-square tests were used to analyze differences between allele- and genotype frequencies. To test differences between group means, the Student’s two-tailed t-test was used for normally distributed values and Mann-Whitney U-test for non-normally distributed medians. In order to identify factors associated with MI and microalbuminuria, a multiple logistic regression analysis with forward selection was performed. Because of the nature of Botnia cohort as a family collection, the analyses were adjusted for the family relations. For the mortality analyses, clinical variables together with MHC2TA genotypes were entered into a forward stepwise Cox regression model adjusted for sex, age and family relations.

All data were analyzed with a NCSS 2004 (NCSS statistical software, Kaysville, UT, USA). A-p-value of <0.05 was considered statistically significant. Power analysis was made using Genetic Power Calculator [20].

RESULTS The clinical characteristics of the study groups are given in Table 1. The genotype and allele frequencies of the MHC2TA polymorphism were similar in patients with or without MI, regardless of the study population and T2D status (Table 2). No association with T2D was observed, neither in the Finnish (Botnia), nor in the Swedish (MDC or DR) cohort.

No correlation between the MHC2TA -168 A/G genotypes and cardiovascular mortality was found in the Botnia Study population [HR 0.96 [0.75–1.22], p = 0.74] (Table 3). As the MHC2TA polymorphism was earlier shown to be associated with MI, we performed a subgroup analysis of individuals with previous history of MI. In fact, among these patients the MHC2TA AG/GG genotypes were associated with increased risk of cardiovascular death compared with AA genotype carriers [HR 1.76 [1.09–2.82], p = 0.02] (Table 3, Figure 1). We also tested the MHC2TA GG genotype against the AA or AG genotypes and found that the GG genotype was protective against cardiovascular death in the whole group [HR 0.31 [0.16–0.62], p = 0.05], but not in patients with previous MI [HR 0.45 [0.29–0.69], p = 0.00].

The MHC2TA AG/GG genotypes were more frequently found among patients with MetS (30.1 vs. 36.9%, p = 0.030) as well as among non-diabetic individuals with microalbuminuria in the Botnia cohort (30.0% vs. 36.0%, p = 0.003, Table 2). In contrast, the AG/GG genotypes were not associated with microalbuminuria among T2D patients, neither in the Botnia, nor the DR cohort (Table 2). Correspondingly, logistic regression analysis with age, waist-hip ratio, fasting insulin, systolic and diastolic blood
pressure, smoking, gender and MHC2TA AG/GG genotypes as independent factors, revealed the AG/GG genotypes as risk factors for microalbuminuria in non-diabetic subjects (OR 2.07).

### Table 1. Clinical characteristics of the study subjects.

|                   | Non-diabetic | MDC | T2D | p   | Non-diabetic | T2D | p   |
|-------------------|--------------|-----|-----|-----|--------------|-----|-----|
| Male/Female       | 1307/1566    | 731 | 828 | 0.37| 2492/891     | 202/72 | 0.98 |
| Age (Yrs.)        | 54.1±13      | 67.12| <1x10⁻⁶| 63.7| 63.6±0.14    | 63.1±12 | 0.14 |
| BMI (Kg/m²)       | 26.2±4.1     | 28.1±4.7| <1x10⁻⁶| 26.2±3.7 | 28.1±4.3 | <1x10⁻⁶ | 29.5±5.6 |
| SBP (mmHg)        | 135±20       | 150±22| <1x10⁻⁶| 147±21 | 153±19 | 7±10⁻³ | 144±20 |
| DBP (mmHg)        | 81±10        | 83±11| <1x10⁻⁶| 88±10 | 88±10 | 0.41 | 80±11 |
| HbA1c (%)         | 5.5±0.5      | 7.5±1.7| <1x10⁻⁶| 4.8±0.4 (N=575) | 6.8±1.8 (N=82) | <1x10⁻⁶ | 6.9±1.7 |
| Age at onset of diabetes (Yrs.) | - | - | - | - | - | 54.1±15 | 0.02 | 50.1 |
| Male/Female       | 1307/1566    | 731 | 828 | 0.37| 2492/891     | 202/72 | 0.98 |
| Age (Yrs.)        | 54.1±13      | 67.12| <1x10⁻⁶| 63.7| 63.6±0.14    | 63.1±12 | 0.14 |
| BMI (Kg/m²)       | 26.2±4.1     | 28.1±4.7| <1x10⁻⁶| 26.2±3.7 | 28.1±4.3 | <1x10⁻⁶ | 29.5±5.6 |
| SBP (mmHg)        | 135±20       | 150±22| <1x10⁻⁶| 147±21 | 153±19 | 7±10⁻³ | 144±20 |
| DBP (mmHg)        | 81±10        | 83±11| <1x10⁻⁶| 88±10 | 88±10 | 0.41 | 80±11 |
| HbA1c (%)         | 5.5±0.5      | 7.5±1.7| <1x10⁻⁶| 4.8±0.4 (N=575) | 6.8±1.8 (N=82) | <1x10⁻⁶ | 6.9±1.7 |
| Age at onset of diabetes (Yrs.) | - | - | - | - | - | 54.1±15 | 0.02 | 50.1 |
| Male/Female       | 1307/1566    | 731 | 828 | 0.37| 2492/891     | 202/72 | 0.98 |
| Age (Yrs.)        | 54.1±13      | 67.12| <1x10⁻⁶| 63.7| 63.6±0.14    | 63.1±12 | 0.14 |
| BMI (Kg/m²)       | 26.2±4.1     | 28.1±4.7| <1x10⁻⁶| 26.2±3.7 | 28.1±4.3 | <1x10⁻⁶ | 29.5±5.6 |
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| DBP (mmHg)        | 81±10        | 83±11| <1x10⁻⁶| 88±10 | 88±10 | 0.41 | 80±11 |
| HbA1c (%)         | 5.5±0.5      | 7.5±1.7| <1x10⁻⁶| 4.8±0.4 (N=575) | 6.8±1.8 (N=82) | <1x10⁻⁶ | 6.9±1.7 |
| Age at onset of diabetes (Yrs.) | - | - | - | - | - | 54.1±15 | 0.02 | 50.1 |

Numbers are mean±SD or percent. *Both previous and current smoking. P-values refer to comparison between non-diabetic and T2D patients. doi:10.1371/journal.pone.0000064.t001

### Table 2. The genotype frequencies of the MHC2TA -168 A→G polymorphism in different study populations according to history of previous MI and microalbuminuria status.

|                   | MI+ | MI- | p     | Microalbuminuria (MALB) | MALB+ | MALB- | p     |
|-------------------|-----|-----|-------|--------------------------|-------|-------|-------|
| Botnia            | AA/AG/GG (N=112) | (62.8±33.3% (N=2066) 0.90 | (49.5±45.5% (N=1940) 0.003|
| MDC               | (59.2±38.0% (N=184) 0.90 | (59.7±36.0% (N=1326) 0.90 | (58.9±38.8% (N=129) 0.003|
| Diabetes registry | T2D (59.2±38.0% (N=123) 0.90 | (59.7±36.0% (N=123) 0.003 | (58.9±38.8% (N=129) 0.003|

The numbers are allele frequencies (%) and number of patients. P-values refer to comparison between genotype frequencies of the –168A→G risk genotypes (AG or GG) among individuals with or without MI and with or without microalbuminuria, respectively. doi:10.1371/journal.pone.0000064.t002

### Table 3. Predictors of cardiovascular mortality among all individuals and patients with previous MI from the Botnia study.

|                   | All patients | Previous MI |
|-------------------|--------------|-------------|
| Male Sex          | 1.34 [1.00–1.80] | 1.20 [0.84–2.23] |
| Smoking           | 1.42 [1.04–1.96] | 1.33 [0.78–2.31] |
| Cholesterol (mmol/l) | 1.11 [0.91–1.22] | 1.10 [0.87–1.38] |
| HDL cholesterol (mmol/l) | 0.57 [0.38–0.85] | 0.76 [0.27–2.02] |
| SBP (mmHg)*       | 1.00 [0.99–1.01] | 1.00 [0.98–1.01] |
| DBP (mmHg)*       | 1.00 [0.99–1.01] | 0.99 [0.97–1.02] |
| MHC2TA (AG or GG) | 0.96 [0.75–1.22] | 1.76 [0.99–2.82] |

Numbers are hazard ratio (HR) and 95% Confidence limits. HRs were mutually adjusted. *HR per mmHg doi:10.1371/journal.pone.0000064.t003

Figure 1. Cardiovascular mortality in the Botnia cohort in patients with previous MI according to MHC2TA -168 A→G genotypes. Kaplan Meier survival curves illustrating a higher risk for CV mortality (HR 1.76 [1.09–2.82], p = 0.02) in AG/GG genotype carriers with previous history of MI. doi:10.1371/journal.pone.0000064.g001

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Statistical power to detect differences in risk of MI according to genotype assuming dominant model and genotype relative risk of 1.5 were 95.0, 95.1% in the MDC cohort and 36.5% for Swedish T2D patients from DR. The corresponding power when assuming genotype relative risk of 1.5 were 95.0, 100.0, and 92.7%. In the pooled Swedish sample the power was 97.0% assuming a relative risk of 1.2 and 100% at the level of 1.5.

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Author Contributions

Conceptualized and designed the experiments: OM MO. Performed the experiments: EL. Analyzed the data: PA EL. Contributed reagents/materials/analysis tools: LG GB OM CA MO. Wrote the paper: LG GB EL OM CA MO.
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