A Common Variant of PNPLA3 (p.I148M) Is Not Associated with Alcoholic Chronic Pancreatitis

Jonas Rosendahl1*, Anke Tönjes2,3, Dorit Schleinitz4, Peter Kovacs4, Johannes Wiegand1, Claudia Ruffert1, Moritz Jesinghaus1, Robert Schober1, Max Herms1, Robert Grützmann5, Hans-Ulrich Schulz6, Felix Stöckel7, Jens Werner8, Peter Bugert9, Matthias Blüher2,3, Michael Stumvoll2,3, Stephan Böhml, Thomas Berg1, Henning Wittenburg1, Joachim Mössner1, Rene te Morsche10, Monique Derixk10, Volker Keim1, Heiko Witt11, Joost P. H. Drenth10

1 Division of Gastroenterology and Rheumatology, Department for Internal Medicine, Neurology and Dermatology, University of Leipzig, Leipzig, Germany, 2 Division of Endocrinology, Department for Internal Medicine, Neurology and Dermatology, University of Leipzig, Leipzig, Germany, 3 IFB Adiposity Diseases, University of Leipzig, Leipzig, Germany, 4 Interdisciplinary Center for Clinical Research Leipzig, University of Leipzig, Leipzig, Germany, 5 Department of General, Thoracic and Vascular Surgery, University Hospital Carl Gustav Carus, Technische Universität Dresden, Dresden, Germany, 6 Department of Surgery, Otto-von-Guericke University Magdeburg, Magdeburg, Germany, 7 Department of Visceral Surgery and Medicine, Inselspital, University of Bern, Bern, Switzerland, 8 Department of Surgery, University of Heidelberg, Heidelberg, Germany, 9 Medical Faculty Mannheim, Institute of Transfusion Medicine and Immunology, Heidelberg University, German Red Cross Blood Service of Baden-Württemberg-Hessen, Mannheim, Germany, 10 Department of Gastroenterology and Hepatology, Nijmegen Medical Center, Radboud University, Nijmegen, The Netherlands, 11 Department of Pediatrics and Else Kröner-Fresenius-Zentrum (EKFZ), Technical University Munich (TUM), Munich, Germany

Abstract

Background: Chronic pancreatitis (CP) is an inflammatory disease that in some patients leads to exocrine and endocrine dysfunction. In industrialized countries the most common aetiology is chronic alcohol abuse. Descriptions of associated genetic alterations in alcoholic CP are rare. However, a common PNPLA3 variant (p.I148M) is associated with the development of alcoholic liver cirrhosis (ALC). Since, alcoholic CP and ALC share the same aetiology PNPLA3 variant (p.I148M) possibly influences the development of alcoholic CP.

Methods: Using melting curve analysis we genotyped the variant in 1510 patients with pancreatitis or liver disease (961 German and Dutch alcoholic CP patients, 414 German patients with idiopathic or hereditary CP, and 135 patients with ALC). In addition, we included in total 2781 healthy controls in the study.

Results: The previously published overrepresentation of GG-genotype was replicated in our cohort of ALC (p-value <0.0001, OR 2.3, 95% CI 1.6–3.3). Distributions of genotype and allele frequencies of the p.I148M variant were comparable in patients with alcoholic CP, idiopathic and hereditary CP and in healthy controls.

Conclusions: The absence of an association of PNPLA3 p.I148M with alcoholic CP seems not to point to a common pathway in the development of alcoholic CP and alcoholic liver cirrhosis.

Introduction

Chronic pancreatitis (CP) is a recurring or continuous inflammatory disease that can lead to permanent impairment of endocrine and exocrine function. In industrialized countries chronic alcohol abuse is the most common underlying cause. Additionally, smoking increases the risk for CP [1]. Contrary to other alcohol-induced disorders, such as liver cirrhosis, only 5% of alcohol abusers develop CP [2]. In addition, familial clustering suggests a contribution of genetic alterations to the pathogenesis of alcoholic CP. In recent years several genetic associations have been discovered for hereditary and idiopathic CP [3–7]. Although, genetic case control studies in alcoholic CP have established robust associations with variants of serine protease inhibitor, kazal type 1 (SPINK1) and chymotrypsinogen C (CTRC) search for other risk variants have been less successful [8,9]. However, a Japanese study performed a genome wide genetic analysis using microsatellite markers in alcoholic CP and discovered several susceptibility regions [10]. This suggests that whole genome information could provide new insights to understanding the pathogenesis of alcoholic CP and indicates that common variants might be of importance.

A genome wide association study in patients with non-alcoholic fatty liver disease revealed a link between PNPLA3 (OMIM *609567) variants and liver fat content [11]. Subsequent investigations analysed PNPLA3 variant p.I148M (rs738409) in
alcoholic Mestizo individuals and demonstrated an overrepresentation of the GG-genotype in those with alcoholic liver disease [12]. This genetic association was confirmed in different cohorts from different ethnicities and the verdict is that rs738409 represents an independent risk factor for ALC with odds-ratios (OR) in the range of 2 that withstands multivariate analysis. In Caucasian alcoholics, rs738409 was also associated with elevated aminotransferase levels and in patients with chronic hepatitis C it appears to influence progression to fibrosis and development of cirrhosis [13–17]. Alcohol abuse is the predominant aetiology of CP and liver cirrhosis in industrialized countries. Given the fact that steatosis [13–17].

In our cohort of 755 German patients with alcoholic CP we screened 1950 blood donors from south-western and eastern Germany (853 male, age range 18–81 years, median 49 years) and 831 healthy controls without CP from the Netherlands (377 male, age range 18–96 years, median 50 years).**Genotyping**

We extracted genomic DNA from peripheral blood leucocytes according to a standard protocol (Qiagen, Hilden, Germany) and performed polymerase chain reaction (PCR) using 0.75 U AmpliTag Gold polymerase (Applied Biosystems, Foster City, CA, USA), 400 μM dNTPs, 1.5 mM MgCl₂ and 0.4 μM F-Primer as well as 0.1 μM R-primer in a total volume of 25 μl. Cycle conditions were an initial denaturation for 12 minutes at 95°C followed by 35 cycles of 20 seconds denaturation at 95°C, 40 seconds annealing at 60°C, 90 seconds primer extension at 72°C and a final extension for 2 minutes at 72°C in an automated thermal cycler (Applied Biosystems, Carlsbad, USA). Primers were synthesized according to the published nucleotide sequences (PNPLA3: GenBank: NM_025225.2; F-Primer 5’-CTTCTCTG-TTCCTTTgCTTTCAC-3’, R-Primer 5’-gAAggAgTgTgAg-CAC-3’).

We performed melting curve analysis in the LightCycler 480 instrument (Roche Diagnostics, Mannheim, Germany) using a pair of fluorescent resonance energy transfer (FRET) probes. FRET probes were designed complementary to the mutated sequence. Probes were devised and synthesized by TIB Molbiol (Berlin, Germany): Anchor probe 5’-ACCCACgCCTCTgAAg-gAAggATgA-Ag-FL-3’, Sensor probe 5’-610-CCACCTgTA-gACggCATgAAgC-3’. Analytical melting included the following steps: 95°C for 60 seconds, 35°C for 60 seconds and an increase to 70°C at a 0.14°C/s ramp rate. If melting curves distinguished differently than expected from WT or mutated samples, we performed DNA sequencing of the accordant sample to identify the responsible variant.

**Results**

We tested the significance of the differences between variant frequencies in affected individuals and controls by two-tailed Fisher’s exact test and calculated p-values using GraphPad Prism (v 4.03). For PNPLA3 variant p.I148M we utilised a dominant model, defined as CC vs. GC+GG, for calculations and considered p-values <0.05 to be of statistical significance. In addition, calculations were performed following a recessive model (CC+GC vs. GG) and for allele frequencies.

**Statistics**

Power analysis was performed using QUANTO 1.1 in a case control model [22]. We used the detected allele frequency of the G-allele in German controls (23%) and performed analysis in an additive model. The corresponding samples to controls ratio was 2.6, respectively (German patients, n = 755; German controls, n = 1950).

We tested the significance of the differences between variant frequencies in affected individuals and controls by two-tailed Fisher’s exact test and calculated p-values using GraphPad Prism (v 4.03). For PNPLA3 variant p.I148M we utilised a dominant model, defined as CC vs. GC+GG, for calculations and considered p-values <0.05 to be of statistical significance. In addition, calculations were performed following a recessive model (CC+GC vs. GG) and for allele frequencies.

**Results**

**Power calculations**

Considering a minor allele frequency of 23% that was obtained in German controls we had a statistical power of at least 0.9 (α = 0.05) to detect genetic effects with an OR ≥1.25. Of course effects below a threshold of 1.25 (OR) might be missed, but we reasoned that effects below this threshold should be of negligible relevance for the pathogenesis of ACP.

**PNPLA3 and pancreatitis**

In our cohort of 755 German patients with alcoholic CP we detected the rs738409 GG-genotype in 37/755 patients (4.9%) and...
found similar results in the Dutch group of patients with alcoholic CP (8/206, 3.9%) (Table 1). Upon comparison with German and Dutch controls our genotype data yielded similar distributions (dominant model, p-value 0.07, 0.7). This was similar for the overall cohort of alcoholic CP patients compared to the pooled controls (dominant model, p-value 0.2). Allele frequencies of the G-Alele were comparable in all groups (German ACP 323/1510, 21.4%; Dutch ACP 92/412, 22.3%; German controls 912/3900, 23.4%; Dutch controls 382/1662, 23%). However, when we summarized all patients with alcoholic CP and compared genotype and allele data with ALC patients we obtained a significant attributed risk. We found a GG-Genotype in 45/961 (4.7%) of all patients with alcoholic CP, compared to 25/135 (18.5%) of ALC patients (dominant model, p-value <0.0001, OR 2.2, 95% CI 1.9–3.9) (Table 2). If we focus on allele frequencies we found that the G-allele was detectable in 415/1922 (21.6%) alleles in all alcoholic CP patients, while in ALC the G-allele was present in 40.4% of all alleles (p-value <0.0001, OR 2.5, 95% CI 1.9–3.2).

In patients with idiopathic and hereditary CP allele frequencies of rs738409 G-allele (193/828, 23.3%; p-value 0.4) were comparable to those in controls, but the GG-genotype was more frequent in patients (31/414, 7.5%) than in controls (97/1950, 5.0%). There was also no statistical significant difference between groups with respect to genotype data (dominant model, p-value 1.0; recessive model, p-value 0.05).

**PNPLA3 and alcoholic liver disease**

In patients with ALC GG-genotype of rs738409 was more frequent (3.7-fold) and present in 25/135 (18.5%) patients compared to 97/1950 (5.0%) in German controls (dominant model, p-value <0.0001, OR 2.7, 95% CI 1.9–3.9) (Table 2). When we pooled all controls GG-Genotype was 3.4-fold more frequent, respectively (dominant model, 153/2781, 5.5%; p-value <0.0001, OR 2.4, 95% CI 1.7–3.4). In patients with ALC G-Alele accounted for 40.4% (109/270) of all alleles in comparison to 23.3% in controls (1294/5562; p-value <0.0001, OR 2.2, 95% CI 1.7–2.9).

**Discussion**

The current study examines the influence of PNPLA3 variant p.I148M in a large cohort of patients with alcoholic liver and pancreas disease and controls.

We confirmed the association of PNPLA3 GG-genotype with ALC in our cohort (p-value <0.0001) and the overrepresentation of GG-genotype compared to controls was 3.7-fold (OR 2.3, 95% CI 1.6–3.3), respectively 3.4-fold (OR 2.4, 95% CI 1.7–3.4) for the pooled control group, which is higher than found in recent studies [13,14]. The difference might be due to a type 2 error as our ALC patient group is relatively small precluding an accurate estimation of the risk. Our analysis further supports the current knowledge that PNPLA3 rs738409 represents a risk factor for ALC in different ethnic groups with odds ratios around two.

Apart from putative genetic associations, little is known about the functional consequences of PNPLA3 variant p.I148M. Recent data demonstrated a reduced capacity of mutated PNPLA3 to hydrolyse triglycerides with subsequent accumulation in the liver [23]. One might speculate that also in patients with ACP triglyceride haemostasis is disturbed with the result of CP due to inflammatory processes in the pancreas. Due to the limited knowledge of PNPLA3 function available so far one has to be aware of the speculative character of the aforementioned theory.

Contrary to ALC, little is known about potential genetic associations of alcoholic CP, despite knowledge of the role of SPINK1 and CTRC variants in CP. Some patients with alcoholic CP also suffer from ALC. Epidemiological data on simultaneous presence of ALC and ACP are scarce and according to recent findings more than one third of patients with alcoholic CP may have concomitant ALC while around 20% of patients with ALC suffer from CP [21]. It is worthy to point out that prevalence data on the coexisting of alcoholic CP and ALC are inconsistent among different studies [18–21]. The fact that precursor lesions of both disease forms, steatosis and pancreatic fibrosis, are often found concurrently, portends to potential concerted risk factors.

Our analysis of PNPLA3 variant p.I148M in German and Dutch patients with alcoholic CP demonstrated similar data for genotype and allele frequencies, when compared to pooled controls (p-value 0.2 and

**Table 1.** Genotype data of PNPLA3 variant rs738409 in German and Dutch patients with alcoholic CP and in German and Dutch controls.

<table>
<thead>
<tr>
<th>Variant</th>
<th>Genotype</th>
<th>Patients ACP</th>
<th>Controls</th>
<th>p-Value</th>
<th>OR</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>German ACP</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>CC 469/755 (62.1%)</td>
<td>1135/1950 (58.2%)</td>
<td>n.s.</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td></td>
<td>GC 249/755 (33%)</td>
<td>718/1950 (36.8%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>GG 37/755 (4.9%)</td>
<td>97/1950 (5.0%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Dutch</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>CC 122/206 (59.2%)</td>
<td>505/831 (60.8%)</td>
<td>n.s.</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td></td>
<td>GC 76/206 (36.9%)</td>
<td>270/831 (32.5%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>GG 8/206 (3.9%)</td>
<td>56/831 (6.7%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Pooled (German/Dutch)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>CC 591/961 (61.5%)</td>
<td>1640/2781 (59%)</td>
<td>n.s.</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td></td>
<td>GC 325/961 (33.8%)</td>
<td>988/2781 (35.5%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>GG 45/961 (4.7%)</td>
<td>153/2781 (5.5%)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Percentages are given in brackets. P-values were calculated for these groups in a dominant (CC vs. GC+GG) and recessive model (CC+GC vs. GG). Abbreviations: ACP = alcoholic CP, n.s. = not significant.

doi:10.1371/journal.pone.0029433.t001
We also confirmed the association of PNPLA3 GG-genotype with ALC when we analysed patients with alcoholic CP and compared them to ALC (p-value <0.0001). As a consequence, the obtained data of PNPLA3 variant rs738409 implicate that different pathways might be implicated in the development of alcoholic CP and ALC.

We screened patients with idiopathic and hereditary CP to describe the frequency of this variant in other forms of CP and found an overrepresentation of GG-genotype compared to our control group. However, calculation of genotype distribution in a dominant and recessive model (p-value 1.0 and 0.05) and comparison of allele frequencies (p-value 0.4) yielded no statistical significant different results. This genetic result accords with the commonly accepted pathophysiological model of idiopathic and hereditary CP.

Study limitations

Our study comes with limitations. Part of the control group used for comparison are blood donors and as such this introduces potential bias since ALC or APC may be prevalent among blood donors. We surmise that the contribution of such an effect is rather small. Blood donors are routinely screened for elevated liver enzymes and patients with chronic alcohol abuse should not be suitable to donate blood. Of note, in blood donors there might be a selection of a distinct group (healthy persons that are willing to donate blood), which may affect the obtained results. However, according to the low incidence of both disease entities in the general population we do not believe that will alter the results substantially. We think that the risk for bias is limited because genotype frequencies of rs738409 in our controls are similar to that in other Caucasian controls reported so far [24,25].

Most of all, it has to be noted that we only investigated one particular variant that was previously proven to be of importance for alcohol related liver disease. Our results seem to indicate, that the absence of an association of PNPLA3 variant p.I148M with alcoholic CP does not point to a common pathway in the development of alcoholic CP and ALC. However, we are aware that our conclusions are limited by the fact that only one variant with a modest risk for ALC whose pathogenic role is largely unknown, was investigated in patients with ACP.

Acknowledgments

We thank the individuals who have participated in this study. We also thank Susanne Kistner (Leipzig), Knut Krohn, Kathleen Schon and Birgit Oelzner (IZKF core unit DNA technologies, Leipzig) for excellent technical assistance.

Author Contributions

Conceived and designed the experiments: JR AT H. Witt JPHD. Performed the experiments: JR AT DS PK CR Rm. Analyzed the data: JR AT DS PK CR Rm. Contributed reagents/materials/analysis tools: J. Wiegand MJ RS MH PB MB MS SB TB H. Wittenburg JM RG HUS FS J. Werner Rm MD VK JPHD. Wrote the paper: JR JPHD.

References


Table 2. Genotype data of PNPLA3 variant rs738409 in German (n = 128) and Dutch (n = 7) patients with alcoholic liver cirrhosis, German patients with idiopathic and hereditary CP and in German controls.

<table>
<thead>
<tr>
<th>Variant</th>
<th>Genotype</th>
<th>Patients ALC</th>
<th>Patients Controls</th>
<th>p-value</th>
<th>OR</th>
</tr>
</thead>
<tbody>
<tr>
<td>p.148M c.444C&gt;G rs738409</td>
<td>CC</td>
<td>51/135 (37.8%)</td>
<td>1135/1950 (58.2%)</td>
<td>&lt;0.0001</td>
<td>2.3 (1.6–3.3)</td>
</tr>
<tr>
<td></td>
<td>GC</td>
<td>59/135 (43.7%)</td>
<td>718/1950 (36.8%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>GG</td>
<td>25/135 (18.5%)</td>
<td>97/1950 (5.0%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>ICP/HP</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>CC</td>
<td>240/414 (58%)</td>
<td>1135/1950 (58.2%)</td>
<td>n.s.</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>GC</td>
<td>143/414 (34.5%)</td>
<td>718/1950 (36.8%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>GG</td>
<td>31/414 (7.5%)</td>
<td>97/1950 (5.0%)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Percentages are given in brackets. P-values were calculated for these groups in a dominant and recessive model. The p-value represents the result of the dominant model (CC vs. GC+CC). Abbreviations: ALC = alcoholic liver cirrhosis, ICP = idiopathic CP, HCP = hereditary CP, n.s. = not significant.

doi:10.1371/journal.pone.0029433.t002


