Very recently the first whole-genome association study (WGAS) reported a strong association between sarcoidosis and ANXA11 (annexin A11) on chromosome 10q22.3, a member of the annexin family of calcium-dependent phospholipid-binding proteins involved in structural organisation of the cell, growth control, calcium signalling, cell division, vesicle trafficking and apoptosis.6 7 Different single nucleotide polymorphisms (SNPs) within and downstream of the ANXA11 gene were strongly associated with sarcoidosis, including one non-synonymous SNP rs1049550 (c.688T>C, p.C230R) and several intronic or intergenic SNPs (rs1953600, rs2573346, rs2784775, rs2796979). The associated SNPs were in strong linkage disequilibrium.

To replicate the association in an independent cohort, we performed a case-control association study in 325 patients (mean age 52.1 years) and 364 healthy matched controls (healthy white German subjects, mean age 49.7 years). The diagnosis of sarcoidosis was based on evidence of non-caseating epitheloid granulomas that involved in structural organisation of the cell, growth control, calcium signalling, cell division, vesicle trafficking and apoptosis.6 7 The criteria for sarcoidosis was determined in different studies and populations.3–5

Table 1 Statistical analysis of the case-control study

<table>
<thead>
<tr>
<th>SNPs</th>
<th>Controls</th>
<th>Cases</th>
<th>OR(95% CI)</th>
<th>p Value</th>
<th>Acute*</th>
<th>p Value</th>
<th>Chronic*</th>
<th>p Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>rs1049550</td>
<td>Allele</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>T</td>
<td>283 (45%)</td>
<td>244 (35%)</td>
<td>1</td>
<td>0.00014</td>
<td>82 (35%)</td>
<td>119 (34%)</td>
<td>104 (34%)</td>
<td>0.0005</td>
</tr>
<tr>
<td>C</td>
<td>343 (55%)</td>
<td>454 (65%)</td>
<td>1.54 (1.23 to 1.92)</td>
<td>0.0073</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Genotype</td>
<td></td>
<td></td>
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<td></td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TT</td>
<td>65 (21%)</td>
<td>48 (14%)</td>
<td>1</td>
<td>0.0254</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CT</td>
<td>153 (48%)</td>
<td>148 (42%)</td>
<td>1.31 (0.85 to 2.03)</td>
<td>0.2245</td>
<td></td>
<td></td>
<td></td>
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</tr>
<tr>
<td>CC</td>
<td>95 (30%)</td>
<td>153 (44%)</td>
<td>2.18 (1.39 to 3.43)</td>
<td>0.00065</td>
<td></td>
<td></td>
<td></td>
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</tr>
<tr>
<td>rs2573346</td>
<td>Allele</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>T</td>
<td>303 (47%)</td>
<td>260 (37%)</td>
<td>1</td>
<td>0.0131</td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C</td>
<td>341 (53%)</td>
<td>452 (63%)</td>
<td>1.55 (1.24 to 1.92)</td>
<td>0.0008</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Genotype</td>
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<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TT</td>
<td>71 (22%)</td>
<td>50 (14%)</td>
<td>1</td>
<td>0.017</td>
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<td></td>
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<tr>
<td>CT</td>
<td>161 (50%)</td>
<td>160 (45%)</td>
<td>1.41 (0.93 to 2.15)</td>
<td>0.1097</td>
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<tr>
<td>CC</td>
<td>90 (26%)</td>
<td>146 (41%)</td>
<td>2.30 (1.47 to 3.60)</td>
<td>0.00022</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Significant associations are shown in bold.
*Only patients with unequivocal classification were included.
Competing interests None.

Ethics approval This study was conducted with the approval of the University of Bonn 060/05.

Contributors SP and YL contributed equally to this work.

Provenance and peer review Not commissioned; not externally peer reviewed.

Accepted 3 April 2010
Published Online First 30 August 2010
doi:10.1136/thx.2010.138743

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First independent replication study confirms the strong genetic association of ANXA11 with sarcoidosis
Yun Li, Stefan Pabst, Christian Kubisch, Christian Grohé and Bernd Wollnik

Thorax 2010 65: 939-940 originally published online August 30, 2010
doi: 10.1136/thx.2010.138743

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