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Immunochip SNP array identifies novel genetic variants conferring susceptibility to candidaemia

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Candidaemia is the fourth most common cause of bloodstream infection, with a high mortality rate of up to 40%. Identification of host genetic factors that confer susceptibility to candidaemia may aid in designing adjunctive immunotherapeutic strategies. Here we hypothesize that variation in immune genes may predispose to candidaemia. We analyse 118,989 single-nucleotide polymorphisms (SNPs) across 186 loci known to be associated with immune-mediated diseases in the largest candidaemia cohort to date of 217 patients of European ancestry and a group of 11,920 controls. We validate the significant associations by comparison with a disease-matched control group. We observe significant association between candidaemia and SNPs in the CD58 (P = 1.97 x 10^-11; odds ratio (OR) = 4.68), LCE4A-C1orf68 (P = 1.98 x 10^-10; OR = 4.25) and TAGAP (P = 1.84 x 10^-8; OR = 2.96) loci. Individuals carrying two or more risk alleles have an increased risk for candidaemia of 19.4-fold compared with individuals carrying no risk allele. We identify three novel genetic risk factors for candidaemia, which we subsequently validate for their role in antifungal host defence.

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Candidaemia is the fourth most common bloodstream infection, with known risk factors such as neutropenia, mucosal barrier injury, transplantation, immunosuppressive drugs, intravascular catheters and extended intensive care unit stay. Despite the availability of potent antifungal drugs, the mortality of patients with candidaemia remains high (up to 37–44%). It has therefore been proposed that only intensified patient care, using risk assessment and adjuvant immunotherapy, may improve the outcome.

The host immune status is crucial for the outcome of Candida infection, and identifying genetic variation in immune genes that confer susceptibility to Candida infection may aid in designing effective preventive strategies. Several small-scale candidate gene association studies suggest a role in candidaemia risk for single-nucleotide polymorphisms (SNPs) in toll-like receptors (TLR-1, TLR-2, TLR-3 and TLR-4), interleukins (ILs) (IL-12B and IL-10) and lymphoid protein tyrosine phosphatase PTPN22 (ref. 3). Interestingly, ~10 monogenic disorders have been reported to be associated with chronic mucocutaneous candidiasis, and almost all are caused by defects in genes of the immune system.

Intriguingly, common SNPs in 8 out of these 10 monogenic disorder genes (AIRE, CARD9, STAT1, STAT3, TYK2, CD25, IL17RA and IL17F) are also associated with susceptibility to different immune-mediated diseases (NHGRI GWAS catalog), implying that genes necessary for immune regulation are strong candidates in determining susceptibility to fungal infections.

Here we report the first genome-wide screen of candidaemia SNPs, and identify three novel genetic risk factors for candidaemia that were validated using transcriptomics, pathway analysis and immunological studies.

**Results**

**Association analysis identifies three candidaemia risk loci.** After filtering the Immunochip data using standard quality parameters, we obtained 118,889 SNPs from the 217 candidaemia cases and 11,920 healthy controls, which we analysed using logistic regression analysis. The results of this analysis revealed significant association \((P < 5 \times 10^{-8})\) to three independent loci with candidaemia (Fig. 1a). The top SNPs from these three loci were rare in healthy controls, with risk allele frequencies <2%, whereas the risk allele frequencies were >5% in candidaemia cases (Table 1). The top-associated SNP, rs17035850 \((P = 1.97 \times 10^{-11};\) odds ratio = 4.68), is located in a block of linkage disequilibrium (LD) of ~30 kb at 1p13.1, which contains the CD58 gene (Fig. 1b), two long non-coding RNAs (lncRNA), RP5-1086K13.1 and RP4-655J12.4, and the pseudogene NAPI1P1 (Supplementary Fig. 1). The second hit was with rs4845320 \((P = 1.98 \times 10^{-10};\) odds ratio = 4.25), which lies in an LD block of 150 kb at 1q21.3 (Fig. 1c) that contains a cluster of genes encoding late cornified envelope (LCE) proteins. The third significantly associated SNP, rs3127214 \((P = 1.84 \times 10^{-8};\) odds ratio = 2.96), is located at the 5' end of TAGAP (Fig. 1d), encoding T-cell activation RheoGFPTase-activating protein 14, in an LD block of 120 kb at 6q25.3.

**Validation and replication of three associated SNPs.** Since we used a large population-based control cohort for discovering candidaemia susceptibility loci, we tested whether these associations could be confirmed using 146 disease-matched controls (Table 2). We observed a significant difference between cases and controls at two loci (LCE4A-C1orf68 and TAGAP), whereas the CD58 locus we observed a trend of association (Table 1). This latter effect could be explained by the small number of controls and/or low frequency of the risk allele at rs17035850 (Table 1).

The top CD58 SNP (rs17035850) is a rare variant with a minor allele frequency (MAF) of 0.012, and the second CD58 SNP (rs12025416) is a frequent one with MAF of 0.13. We assessed the pairwise LD between these two CD58 SNPs in our population-based controls. We observed both a low correlation \((r^2 = 0.09)\) and a high \(D' > 0.96\) between these two SNPs, indicating the existence of rare risk haplotype that carry the risk alleles of these two SNPs. Therefore, we also tested for association at the second CD58 top SNP, rs12025416, which is more frequent, and we observed a significant association with susceptibility to candidaemia \((P = 0.022)\). Therefore, these results suggest that the observed associations are true genetic associations.

To further evaluate these associations genetically, we carried out replication analysis by genotyping the four SNPs in two independent candidaemia cohorts (one of 75 African-American patients and one of 27 European patients from Switzerland). Because of the small size of these additional cohorts, we found no successful replication in two independent cohorts, although we observed only a trend of association for rs4845320 SNP in the TAGAP locus in the African-American cohort (Supplementary Table 1). Intriguingly, common SNPs in 8 out of these 10 monogenic disorder genes (AIRE, CARD9, STAT1, STAT3, TYK2, CD25, IL17RA and IL17F) are also associated with susceptibility to different immune-mediated diseases (NHGRI GWAS catalog), implying that genes necessary for immune regulation are strong candidates in determining susceptibility to fungal infections.
polymorphisms identified above may also influence the severity of the disease. Indeed, assessment of the effect of these SNPs revealed that CD58 SNP rs17035850 associated with persistent fungemia, defined as positive blood cultures for >5 days despite adequate therapy (P = 0.005), while TAGAP SNP rs3127214 associated with disseminated disease in the organs (P = 0.017) (see also Supplementary Table 5).

The transcriptomes of CD58- and TAGAP-deficient macrophages. Practically nothing is known regarding the roles of CD58 and TAGAP in antifungal host defence. To identify the antifungal host defence mechanisms influenced by these two genes, we assessed genome-wide transcriptional changes in wild-type macrophages, as well as macrophages in which the expression of CD58 and TAGAP was strongly reduced by small interfering RNA (siRNA) transfection at 6 and 24 h upon Candida infection. Efficient downregulation of CD58 messenger RNA (mRNA) was obtained by siRNA transfection, whereas only a mild effect was seen on TAGAP mRNA levels (Supplementary Fig. 2). Genome-wide transcriptional changes in wild-type and CD58-deficient macrophages showed a total of 169 (at 6 h) and 93 (at 24 h) transcripts with at least a 1.25-fold differential expression (Supplementary Fig. 3). Enrichment analysis showed that the differentially expressed genes are enriched for innate immune function, regulation of cytokine production and general cellular responses to bacterial infections (Supplementary Fig. 4). Furthermore, we investigated whether mutations in these differentially expressed genes show any common phenotypes in the mouse using the Mouse Genome Informatics phenotype data integrated in the GeneNetwork database. Indeed, we observed a significant enrichment for genes in which mutations may cause altered levels of IL-6 and tumor necrosis factor (TNF)-α secretion, and impaired macrophage phagocytosis (Fig. 2a). These data suggest that altered expression levels of CD58 may regulate Candida phagocytosis on one hand, and indirectly regulate IL-6 and TNF-α secretion on the other hand.

Functional validation of CD58 for anti-Candida host defence. We next tested the CD58 mRNA levels in macrophages at 6 and 24 h upon Candida infection using microarray data. We observed...
Table 1 | Significantly associated loci with candidaemia that were validated using disease-matched controls.

<table>
<thead>
<tr>
<th>rs ID</th>
<th>Chr</th>
<th>Cohorts</th>
<th>Case (AA AB BB MAF)</th>
<th>Controls (AA AB BB MAF)</th>
<th>P-value</th>
<th>OR (95% CI)</th>
<th>Gene</th>
</tr>
</thead>
<tbody>
<tr>
<td>rs17035850</td>
<td>1</td>
<td>Cases vs population-based controls</td>
<td>3 16 198 0.051</td>
<td>0 277 11,642 0.012</td>
<td>1.97 x 10^{-11}</td>
<td>4.68 (2.98-7.35)</td>
<td>CDS8</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Cases vs disease-matched controls</td>
<td>3 16 198 0.051</td>
<td>0 8 138 0.027</td>
<td>0.15</td>
<td>1.58 (0.66-3.78)</td>
<td></td>
</tr>
<tr>
<td>rs12025416</td>
<td>1</td>
<td>Cases vs population-based controls</td>
<td>11 57 147 0.184</td>
<td>179 2,643 9,097 0.126</td>
<td>0.00035</td>
<td>1.57 (1.22-2.01)</td>
<td>CDS8</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Cases vs disease-matched controls</td>
<td>11 57 147 0.184</td>
<td>1 32 111 0.118</td>
<td>0.022</td>
<td>1.69 (1.08-2.56)</td>
<td></td>
</tr>
<tr>
<td>rs4845320</td>
<td>1</td>
<td>Cases vs population-based controls</td>
<td>3 16 198 0.051</td>
<td>2 290 11,627 0.012</td>
<td>1.98 x 10^{-10}</td>
<td>4.25 (2.72-6.65)</td>
<td>LCE4A-Corf68</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Cases vs disease-matched controls</td>
<td>3 16 198 0.051</td>
<td>0 3 143 0.010</td>
<td>0.008</td>
<td>4.09 (1.21-13.85)</td>
<td></td>
</tr>
<tr>
<td>rs3127214</td>
<td>6</td>
<td>Cases vs population-based controls</td>
<td>3 23 191 0.067</td>
<td>11 522 11,386 0.023</td>
<td>1.84 x 10^{-8}</td>
<td>2.96 (2.03-4.43)</td>
<td>TAGAP</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Cases vs disease-matched controls</td>
<td>3 23 191 0.067</td>
<td>0 8 137 0.027</td>
<td>0.026</td>
<td>2.51 (1.13-5.55)</td>
<td></td>
</tr>
</tbody>
</table>

Chr, chromosome; CI, confidence interval; MAF, minor allele frequency; MDS, multidimensional scaling; OR, odds ratio.
*P-values are derived from logistic regression analysis by including MDS components as covariates.

Table 2 | Clinical characteristics of the candidaemia cohort.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Controls</th>
<th>Patients</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean age (s.d.) (years)</td>
<td>60.2 (17.5)</td>
<td>54.7 (20.2)</td>
<td>0.01</td>
</tr>
<tr>
<td>Male gender (%)</td>
<td>49.3</td>
<td>64.0</td>
<td>0.008</td>
</tr>
<tr>
<td>Immuno compromised state (%)</td>
<td>36.3</td>
<td>61.7</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Hematopoietic stem cell transplantation (%)</td>
<td>0</td>
<td>2.8</td>
<td>0.06</td>
</tr>
<tr>
<td>Solid organ transplant (%)</td>
<td>0.7</td>
<td>15.4</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Active malignancy (%)</td>
<td>21.9</td>
<td>35.0</td>
<td>0.008</td>
</tr>
<tr>
<td>- Solid tumour</td>
<td>12.3</td>
<td>26.0</td>
<td>0.008</td>
</tr>
<tr>
<td>- Leukaemia</td>
<td>6.2</td>
<td>5.7</td>
<td></td>
</tr>
<tr>
<td>- Lymphoma</td>
<td>4.1</td>
<td>4.0</td>
<td></td>
</tr>
<tr>
<td>Chemotherapy within the past 3 months (%)</td>
<td>12.3</td>
<td>18.9</td>
<td>0.11</td>
</tr>
<tr>
<td>Neutropenia (ANC &lt;500 cells per μL) (%)</td>
<td>2.7</td>
<td>10.3</td>
<td>0.008</td>
</tr>
<tr>
<td>HIV-infected (%)</td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>Surgery within the past 30 days (%)</td>
<td>56.2</td>
<td>49.1</td>
<td>0.21</td>
</tr>
<tr>
<td>- Receipt of total parental nutrition (%)</td>
<td>3.4</td>
<td>21.5</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>- Dialysis dependent (%)</td>
<td>4.1</td>
<td>11.6</td>
<td>0.02</td>
</tr>
<tr>
<td>- Acute renal failure (%)</td>
<td>15.8</td>
<td>31.6</td>
<td>0.001</td>
</tr>
<tr>
<td>- Liver disease (%)</td>
<td>2.8</td>
<td>19.4</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Intensive care unit admission within the past 14 days (%)</td>
<td>34.2</td>
<td>54.4</td>
<td>0.0003</td>
</tr>
</tbody>
</table>

Candida spp. (%)
- albicans: 43
- glabrata: 27
- parapsilosis: 16
- tropicalis: 13
- kruzei: 3
- Other Candida spp.: 4

Functional validation of TAGAP for anti-Candida host defence. Because TAGAP siRNA inhibition in primary macrophages implicated altered levels of IL-6 and TNF-α secretion, we tested the role of CD58 SNPs with these cytokine levels. The cytokines IL-6 and TNF-α were quantified from macrophages stimulated with either lipopolysaccharide (LPS) or Candida. The top CD58 SNP, rs17035850, is a rare SNP with very low risk allele frequency. Therefore, we tested the second CD58 top SNP, rs12025416, which occurs more frequently, for association with cytokine levels. Functional genetic validation showed that CD58 SNP rs12025416 genotypes modulated altered levels of IL-6 and TNF-α secretion, confirming the specific role of CD58 polymorphisms in response to Candida infection.
macrophages was not efficient, we interrogated the GeneNetwork database to predict TAGAP function based on co-expression data extracted from approximately 80,000 Affymetrix microarray experiments (see www.genenetwork.nl/genenetwork). Several gene ontology molecular functions, such as chemoattractant receptor activity and cytokine production, were strongly influenced by TAGAP (Fig. 3a). To validate these pathways, the role of TAGAP was tested in an in vivo disseminated candidiasis model in Tagap−/− mice. While the fungal loads did not differ between control and knockout mice early during infection, the Tagap−/− mice were incapable of clearing the fungus from organs at the later stages of infection (Fig. 3b). In addition, splenocytes isolated from Tagap−/− mice produced significantly less TNF-α compared with control animals (Fig. 3c).

Discussion

This first genome-wide association study assessing genetic susceptibility to a fungal infection identified three novel risk factors for susceptibility to candidaemia, namely CD58, the LCE4A-C1orf68 locus and TAGAP. Carrying two or more risk alleles from these loci increases the risk for candidaemia by >19-fold (Supplementary Fig. 6). Using transcriptomic analysis and immunological validation, we identified unknown roles of CD58 and TAGAP in host defense against Candida species.

Genetic association studies are extremely challenging in systemic fungal infections owing to the inherent difficulty of the relatively low number of patients available. The difficulty of enrolling a large number of candidaemia patients is exemplified by the fact that earlier cohorts had no more than 60 patients16,17. To surpass these difficulties, we took several steps. First, we increased the number of underlying disease-matched control cohort. Additional validation studies were performed in independent cohorts. Third, we focused...
on genes and gene regions known to be involved in immune-mediated diseases by using the Immunochip array. Finally, we confirmed the biological significance of our findings by immunological and functional genomics experiments.

Our findings have important implications. On one hand, the 19-fold increased risk of developing candidaemia in individuals carrying two or more risk alleles opens the possibility of using these SNPs to classify at-risk patients, and identify individuals who could benefit from prophylactic antifungal treatment. On the other hand, we have identified novel pathways of host defence mechanisms against fungi that contribute to a better understanding of host defence, and which may also be used for designing future immunotherapeutic strategies. In this respect, the unexpected identification of CD58 as an important factor mediating *Candida* phagocytosis and the inhibition of germination on one hand, and modulation of *Candida*-specific cytokine production on the other hand, is an important step towards understanding the pathogenesis of the infection. CD58 is known as a member of the immunoglobulin superfamily and mediates adhesion and activation of T lymphocytes. It has been shown to be involved in the host defence against viral infections, such as hepatitis B. The role identified here in inhibiting fungal germination at the level of the phagosome is unexpected and sheds light on a novel function of this molecule.

The role of the *LCE4A-C1orf68* locus for anti-*Candida* host defence could have been anticipated from its involvement in the barrier function of the epithelium, as *Candida* colonization of the mucosa is one of the main risk factors for candidaemia in at-risk patients. In contrast, nothing was known regarding a potential role for TAGAP in antifungal host defence. Using a GeneNetwork microarray database and co-expression analysis, and immunological validation in mice with a genetic defect in Tagap, we demonstrate its role in *Candida*-induced inflammation and antifungal host defence.

Interestingly, the genes we have identified as being involved in the susceptibility to candidaemia are also involved in the genetic susceptibility to immune-mediated diseases. Polymorphisms in *CD58* have been reported to increase susceptibility to multiple sclerosis and rheumatoid arthritis. *LCE4A-C1orf68* locus variants are associated with rheumatoid arthritis and psoriasis and TAGAP polymorphisms influence several autoimmune inflammatory diseases. These data point to strong similarities between the immune-mediated mechanisms involved in the host defence against fungal pathogens and those for immune-mediated pathology. This hypothesis is strengthened by the associations described between anti-*Candida*-specific antibodies and Crohn’s disease. Similar shared relationships have been proposed for other pathologies such as leprosy and...
Crohn’s disease\textsuperscript{28}, and it has even been hypothesized that the genetic susceptibility to autoimmune diseases in modern human populations was shaped by evolutionary pressure exerted by infections\textsuperscript{31,32}.

In conclusion, this first, unbiased, genetic association study in a fungal infection demonstrates the potential of functional genomics approaches to identify novel risk factors in infections even in clinical conditions, in which a limited number of patients are available. Our study highlights genetic variants in three novel antifungal host defence mechanisms that increase susceptibility to candidaemia.

Methods

Discovery cohort. Adult candidaemia patients were enrolled after informed consent at the Duke University Hospital (DUMC, Durham, North Carolina, USA) and Radboud University Nijmegen Medical Centre (Nijmegen, The Netherlands). Disease-matched controls were enrolled after informed consent at the Duke University Hospital (DUMC). The study was approved by the institutional review boards (Supplementary Table 6) at each study centre, and enrollment occurred between January 2003 and January 2009 (refs 33,34). Patients must have had at least one positive blood culture for a Candida species. A total of 217 patients of European ancestry (36 of the Netherlands origin and 181 of USA origin) were included in the study (for clinical characteristics, see Table 2).

Two different control groups were employed. One, consisting of 11,920 population-based individuals of European ancestry\textsuperscript{26,35} was used for the discovery phase of the study. The second control group consisted of 146 candidaemia-free but otherwise matched patients. Non-infected patients were recruited from the same hospital wards as infected patients so that co-morbidities and clinical risk factors for infection were similar. This second control group was used to confirm the candidate SNPs identified in the discovery phase. The infected subjects at DUMC were followed prospectively for up to 12 weeks following diagnosis of candidaemia to determine their clinical outcome. Disseminated infection was defined as the presence of Candida species at normally sterile body sites other than the bloodstream or urine. Persistent fungemia was defined as ≥5 days of persistently positive blood cultures.

Validation cohorts. Two independent cohorts of patients with candidaemia were used for validation\textsuperscript{26}. First, a cohort of African-American descent with candidaemia was recruited at DUMC, and 54 patients of African-American descent without candidaemia from the same wards served as a disease-matched control group. Second, a cohort of 69 European surgical intensive care unit patients, including 29 cases of invasive candidiasis (without candidaemia) and 40 non-infected controls, were recruited for the Funginos study, as described elsewhere\textsuperscript{36}.

Genotyping and quality control. The case and the control samples of the discovery cohort were genotyped using the Illumina chip according to Illumina’s protocols\textsuperscript{36}. We applied SNP quality-control filters to exclude SNPs with (a) a low call rate (<99%), (b) a Hardy–Weinberg equilibrium of P<0.01 in control samples only and (c) a MAF of <0.01. In the end, 118,989 SNPs were used for case-control analysis. We also excluded 54 samples with a low genotyping rate (<98%) and 40 ethnic outlier samples based on multidimensional scaling analysis (Supplementary Fig. 7)\textsuperscript{37}. We included 217 candidaemia cases and 11,920 controls of Caucasian descent in the discovery phase of the case-control association analysis. The replication cohorts were genotyped at four SNPs using the Competitive Allele-Specific PCR (KASP) system according to the manufacturer’s protocol (LGC Genomics; http://www.lgcgenomics.com, formerly KBioscience). The KASP allele-specific forward primers and common reverse primer were designed by the manufacturer to map to non-immune regions but are present on the Illumina chip to calculate the inflation factor. Comparison of the genetic inflation factor of all SNPs (λ=1.22) with the genetic inflation factor of non-immune SNPs (λ=1.102) indicated that there was little population stratification effect (Supplementary Fig. 8). We considered P<5×10\textsuperscript{-8} as the threshold for significant association. The association to the top-associated SNPs within the validation and replication cohorts was tested using the Cochran–Armitage trend test, and meta-analysis was conducted using the Mantel–Haenszel method. Heterogeneity across the two cohorts was examined using the Breslow–Day test.

Validation of candidate SNPs was performed on 217 candidaemia patients and 11,920 controls of Caucasian descent in the discovery phase of the case-control association analysis. Disease-matched controls were enrolled after informed consent at the Duke University Hospital (DUMC). The study was approved by the institutional review boards (Supplementary Table 6) at each study centre, and enrollment occurred between January 2003 and January 2009 (refs 33,34). Patients must have had at least one positive blood culture for a Candida species. A total of 217 patients of European ancestry (36 of the Netherlands origin and 181 of USA origin) were included in the study (for clinical characteristics, see Table 2).

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Two different control groups were employed. One, consisting of 11,920 population-based individuals of European ancestry\textsuperscript{26,35} was used for the discovery phase of the study. The second control group consisted of 146 candidaemia-free but otherwise matched patients. Non-infected patients were recruited from the same hospital wards as infected patients so that co-morbidities and clinical risk factors for infection were similar. This second control group was used to confirm the candidate SNPs identified in the discovery phase. The infected subjects at DUMC were followed prospectively for up to 12 weeks following diagnosis of candidaemia to determine their clinical outcome. Disseminated infection was defined as the presence of Candida species at normally sterile body sites other than the bloodstream or urine. Persistent fungemia was defined as ≥5 days of persistently positive blood cultures.

Second, a cohort of 69 European surgical intensive care unit patients, including 29 cases of invasive candidiasis (without candidaemia) and 40 non-infected controls, were recruited for the Funginos study, as described elsewhere\textsuperscript{36}.

Genotyping and quality control. The case and the control samples of the discovery cohort were genotyped using the Illumina chip according to Illumina’s protocols\textsuperscript{36}. We applied SNP quality-control filters to exclude SNPs with (a) a low call rate (<99%), (b) a Hardy–Weinberg equilibrium of P<0.01 in control samples only and (c) a MAF of <0.01. In the end, 118,989 SNPs were used for case-control analysis. We also excluded 54 samples with a low genotyping rate (<98%) and 40 ethnic outlier samples based on multidimensional scaling analysis (Supplementary Fig. 7)\textsuperscript{37}. We included 217 candidaemia cases and 11,920 controls of Caucasian descent in the discovery phase of the case-control association analysis. The replication cohorts were genotyped at four SNPs using the Competitive Allele-Specific PCR (KASP) system according to the manufacturer’s protocol (LGC Genomics; http://www.lgcgenomics.com, formerly KBioscience). The KASP allele-specific forward primers and common reverse primer were designed by the manufacturer to map to non-immune regions but are present on the Illumina chip to calculate the inflation factor. Comparison of the genetic inflation factor of all SNPs (λ=1.22) with the genetic inflation factor of non-immune SNPs (λ=1.102) indicated that there was little population stratification effect (Supplementary Fig. 8). We considered P<5×10\textsuperscript{-8} as the threshold for significant association. The association to the top-associated SNPs within the validation and replication cohorts was tested using the Cochran–Armitage trend test, and meta-analysis was conducted using the Mantel–Haenszel method. Heterogeneity across the two cohorts was examined using the Breslow–Day test.
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Author contributions

M.G.N., C.W. and V.K. conceived the study. V.K. analysed the genetic data and provided Tagap knock-out mice. H.S., H.B. and B.G.H. contributed to mouse experiments (Immunochip and gene expression). We also thank Thierry Calandra, Jacques Bille, Frederic Tissot, Frederic Lamothe, Christina Orasch, Philippe Eggmann (Lausanne), Chloe Kaeche, Martin Siegemund, Ursula kidnäcker (Basel), Stefan Zimmerlin (Bern) and all other members of the Funginos group involved in the validation study. We thank Jackie Senior for editing the final version of the manuscript. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

Additional information

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