Identification of Genetic Loci Associated With Helicobacter pylori Serologic Status

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Importance Helicobacter pylori is a major cause of gastritis and gastroduodenal ulcer disease and can cause cancer. H pylori prevalence is as high as 90% in some developing countries but 10% of a given population is never colonized, regardless of exposure. Genetic factors are hypothesized to confer H pylori susceptibility.

Objective To identify genetic loci associated with H pylori seroprevalence in 2 independent population-based cohorts and to determine their putative pathophysiological role by whole-blood RNA gene expression profiling.

Design, Setting, and Participants Two independent genome-wide association studies (GWASs) and a subsequent meta-analysis were conducted for anti-H pylori IgG serology in the Study of Health in Pomerania (SHIP) (recruitment, 1997-2001 [n = 3830]) as well as the Rotterdam Study (RS-I) (recruitment, 1990-1993) and RS-II (recruitment, 2000-2001 [n = 7108]) populations. Whole-blood RNA gene expression profiles were analyzed in RS-III (recruitment, 2006-2008 [n = 762]) and SHIP-TREND (recruitment, 2008-2012 [n = 991]), and fecal H pylori antigen in SHIP-TREND (n = 961).

Main Outcomes and Measures H pylori seroprevalence.

Results Of 10,938 participants, 6160 (56.3%) were seropositive for H pylori. GWASs identified the toll-like receptor (TLR) locus at 4p14; top-ranked single-nucleotide polymorphism (SNP), rs10004195; odds ratio, 0.70 [95% CI, 0.65 to 0.76]) and the FCGR2A locus (1q23.3; top-ranked SNP, rs368433; P = 2.1 × 10⁻⁸; odds ratio, 0.73 [95% CI, 0.65 to 0.81]) as associated with H pylori seroprevalence. Among the 3 TLR genes at 4p14, only TLR1 was differentially expressed per copy number of the minor rs10004195-A allele (β = −0.23 [95% CI, −0.34 to −0.11]; P = 2.1 × 10⁻⁴). Individuals with high fecal H pylori antigen titers (optical density > 1) also exhibited the highest 25% of TLR1 expression levels (P = 0.01 by χ² test). Furthermore, TLR1 exhibited an Asn248Ser substitution in the extracellular domain strongly linked to the rs10004195 SNP.

Conclusions and Relevance GWAS meta-analysis identified an association between TLR1 and H pylori seroprevalence, a finding that requires replication in nonwhite populations. If confirmed, genetic variations in TLR1 may help explain some of the observed variation in individual risk for H pylori infection.

JAMA. 2013;309(18):1912-1920 www.jama.com

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For editorial comment see p 1939.
of gastritis (80%) and gastroduodenal ulcer disease (15%–20%) and the only bacterial pathogen believed to cause cancer (IARC Working Group 1994).\textsuperscript{3,4} Prevalence of infection with \textit{H pylori} varies from less than 10% in asymptomatic children in Western countries to approximately 90% in some developing countries. Most infections occur during childhood, whereas the \textit{H pylori} status of adults remains stable.\textsuperscript{5} Furthermore, although there are wide interindividual variations in the level of gastritis as well as in the inflammatory response to \textit{H pylori}, the intrindividual gastritis pattern is constant over time.\textsuperscript{6}

Approximately 5% to 10% of a population is never infected with \textit{H pylori}, even in the presence of high exposure rates.\textsuperscript{7} A contribution of genetic factors to \textit{H pylori} susceptibility is supported by differences in \textit{H pylori} susceptibility between African Americans and US residents of European ancestry after adjusting for socioeconomic status, age, and living conditions.\textsuperscript{8} Significantly higher concordance for \textit{H pylori} infection in monozygotic compared with dizygotic twins, or for household members who are siblings rather than unrelated persons,\textsuperscript{9} also argues for a genetic influence, with a heritability estimate in twins of 57%.\textsuperscript{10}

The key pathophysiological event in \textit{H pylori} infection is the initiation of an inflammatory response. This response is triggered by bacterial membrane components, namely, lipopolysaccharides and lipid A, as well as cytoxins and \textit{H pylori} urease activity.\textsuperscript{11} So far, few candidate gene studies have analyzed human host genetic factors for susceptibility to \textit{H pylori} infection and persistence.\textsuperscript{12-14} Several studies have demonstrated that genetic variations, eg, in \textit{IL1B}, modulate the susceptibility for gastric cancer among \textit{H pylori}–infected individuals.\textsuperscript{15,16}

This genome-wide association study (GWAS) for determinants of \textit{H pylori} seroprevalence was conducted in 2 large population-based cohorts, the Study of Health in Pomerania (SHIP) and the Rotterdam Study (RS-I and RS-II). Subsequent whole-blood transcriptome analyses were conducted in the independent SHIP-TREND and RS-III populations.

### METHODS

#### Study Cohorts

The SHIP study consists of 2 independent prospectively collected population-based cohorts in Northeastern Germany, SHIP and SHIP-TREND. The study design of SHIP has been previously described in detail.\textsuperscript{17} The first patient for the SHIP study was recruited in October 1997 and the last in May 2001. SHIP-TREND is an additional independent cohort from the same region, with individuals newly recruited between September 2008 and summer 2012; for details of SHIP-TREND, see the eAppendix available at http://www.jama.com.

The SHIP study has 2 main objectives: to assess prevalence and incidence of common risk factors, subclinical disorders, and clinical diseases; and to investigate the complex associations among risk factors, subclinical disorders, and clinical diseases. A particular characteristic of SHIP is that it does not specifically address a single selected disease; rather, it attempts to describe health-related conditions with the widest focus possible.

The Rotterdam Study is a large, population-based prospective study of elderly individuals of European ancestry consisting of 3 cohorts (RS-I, RS-II, RS-III) of individuals residing in a suburb of Rotterdam, the Netherlands, and has been described in detail.\textsuperscript{18-20} The study targets cardiovascular, endocrine, hepatic, neurologic, ophthalmic, psychiatric, and respiratory diseases. Baseline recruitment and measurements for the RS-I study were obtained between 1990 and 1993. A second cohort, RS-II, was established in 2000-2001. The third cohort, RS-III, started in 2006, with recruitment ending in December 2008.

Data from SHIP, RS-I, and RS-II were used for the GWAS; data from SHIP-TREND and RS-III were used for the transcriptome analysis.

Written informed consent was obtained from all participants, and the medical ethics committee of the Erasmus Medical Center Rotterdam and University Medicine Greifswald approved the study.

#### Phenotype Determination: Seroprevalence and Bacterial Load

Anti–\textit{H pylori} serum IgG antibody titers were measured using commercial enzyme immunoassays (Pyloriset EIA-G III ELISA; Orion). Seroprevalence, an indicator for current or previous infection, was defined as an anti–\textit{H pylori} IgG titer equal to or greater than 20 U/mL, according to the manufacturer’s recommendation.\textsuperscript{21} In comparison with culture or CLO (\textit{Campylobacter}-like organism) testing (rapid urease activity testing), using this cutoff value should detect \textit{H pylori} infection with a sensitivity of 97.8%, a specificity of 58.0%, and an accuracy of 78.7%. The positive predictive value for the Pyloriset EIA-G III ELISA immunoassay is reported as 71.5% and the negative predictive value as 96.2%.\textsuperscript{22} Individuals with the lowest 75% of the IgG titer distribution comprised the control group. Infection was defined in accordance with international convention when \textit{H pylori} was detected by fecal \textit{H pylori} antigen testing.\textsuperscript{23} A significant correlation between titer levels and actual infection has been reported.\textsuperscript{22} To investigate the association of gene expression levels and the fecal \textit{H pylori} antigen titer, individuals with high bacterial load (based on fecal \textit{H pylori} antigen titer, optical density [OD] >1; see below) were studied to determine if they also exhibited the highest 25% of gene expression levels of the respective \textit{4p14}-region genes.

The \textit{H pylori} antigen ELISA kit (Immunodiagnostics) was used to detect \textit{H pylori} antigen in stool. One hundred mg of feces was stored at \(-20\)°C before analysis. According to the manufacturer’s instructions, all participants with an OD greater than or equal to 0.025 at 450 nm are positive for \textit{H pylori} infection. Sensitivity for this test is reported as 97.7% and specificity as...
96.3%. For the quantitative correlation between fecal \( H \) pylori antigen and bacterial load, a Pearson correlation coefficient of 0.222 is reported in the literature.\(^{22} \)

**Genotyping and Imputation**

Genotyping of the SHIP probands using the Affymetrix SNP 6.0 array was performed as described previously.\(^{24} \) Genotyping of the SHIP-TREND participants was performed using the Illumina HumanOmniv2.5-Quad array, of RS-I participants using the Illumina 550K (V.3) single and duo arrays, and of RS-II participants using the Illumina 550K (V.3) duo and Illumina 610K Quad arrays, following manufacturer's protocols. All data sets were imputed to the HapMap v22 CEU reference panel (\( >2.5 \) million single-nucleotide polymorphisms [SNPs]) for the meta-analysis. The discovery stage of the GWAS was independently performed in SHIP and RS-I and RS-II. SHIP and RS-I and RS-II served as replication cohorts for each other. For the meta-analysis the 2 data sets were combined. For details, see Study Population and Genotyping in the eAppendix.

**Whole-Blood Transcriptome Analysis**

For SHIP-TREND and RS-III, whole blood was collected in PAXgene tubes (BD). Total RNA in SHIP-TREND was prepared using a QIA cube device in combination with the Blood miRNA Kit (Qiagen), according to manufacturer's protocols. Subsequent RNA sample processing and hybridization with Illumina HumanHT-12 v3 Expression BeadChips was performed as described by the manufacturer (Illumina) at the Helmholtz Zentrum München. The SHIP-TREND expression data set is available at the GEO (Gene Expression Omnibus) public repository under accession number GSE36382. For details, see the eAppendix.

In RS-III, RNA was amplified and labeled (Ambion TotalPrep RNA) and hybridized with Illumina HumanHT-12 v4 Expression BeadChips as described by the manufacturer's protocol. The RS-III expression data set is available at the GEO public repository under accession number GSE33828. For details see the eAppendix.

**Statistical Analyses**

The case and control groups were defined according to their anti-\( H \) pylori IgG-titer as described above. Detailed information on the study cohort characteristics are provided in **Table 1**. Genome-wide association analysis for SHIP was performed with Quicktest (http://toby.freeshell.org/software/quicktest.shtml) using a logistic regression model with adjustment for sex and age. For RS-I and RS-II, sex- and age-adjusted GWASs were performed using MACH2DAT (http://www.sph.umich.edu/csg/abecasis/MaCH/) implemented in GRIMP.\(^{25} \) Only SNPs with a minor allele frequency (MAF) greater than 1% as well as those available in all 3 cohorts were considered for further analyses.

Meta-analyses were conducted by an inverse-variance weighted fixed-effects model using METAL (www.sph.umich.edu/csg/abecasis/metal).\(^{26} \) The random-effects model was

**Table 1. Characteristics of Study of Health in Pomerania (SHIP) and Rotterdam Study (RS) Population-Based Cohorts**

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>SHIP</th>
<th>SHIP-TREND</th>
<th>RS-I</th>
<th>RS-II</th>
<th>RS-III</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total sample size, No.</td>
<td>3830</td>
<td>1001</td>
<td>4542</td>
<td>2566</td>
<td>762</td>
</tr>
<tr>
<td>Age (range), y</td>
<td>50 (20-81)</td>
<td>50 (20-81)</td>
<td>69 (55-99)</td>
<td>65 (55-95)</td>
<td>60 (46-89)</td>
</tr>
<tr>
<td>Women</td>
<td>1957 (51.1)</td>
<td>561 (56.0)</td>
<td>2454 (54.0)</td>
<td>1401 (54.6)</td>
<td>410 (53.8)</td>
</tr>
<tr>
<td>Total No. of samples with measured anti-( H ) pylori IgG titer</td>
<td>3830</td>
<td>998</td>
<td>4542</td>
<td>2566</td>
<td>NA</td>
</tr>
<tr>
<td>No. of samples with anti-( H ) pylori IgG titer &gt;20 U/mL</td>
<td>2269 (59.2)</td>
<td>551 (55.8)</td>
<td>2696 (59.3)</td>
<td>1196 (46.6)</td>
<td>NA</td>
</tr>
<tr>
<td>No. of samples with the highest 25% IgG titer values (cutoff in U/mL)</td>
<td>968 (124.5)</td>
<td>247 (82.8)</td>
<td>1136 (136.8)</td>
<td>642 (88.9)</td>
<td>NA</td>
</tr>
<tr>
<td>IgG titer values, mean (SD), [median], U/mL</td>
<td>32.0 (29.3) [18.1]</td>
<td>19.0 (15.2) [12.4]</td>
<td>32.9 (31.6) [18.0]</td>
<td>20.6 (17.1) [12.9]</td>
<td>NA</td>
</tr>
<tr>
<td>Group with the lowest 75% values</td>
<td>268.6 (120.0) [230.9]</td>
<td>262.2 (140.1) [227.3]</td>
<td>459.7 (589.0) [320.7]</td>
<td>309.5 (255.0) [233.4]</td>
<td>NA</td>
</tr>
<tr>
<td>No. of samples with measured ( H ) pylori antigen</td>
<td>NA</td>
<td>961</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>No. of samples with ( H ) pylori antigen OD&gt;0.025</td>
<td>NA</td>
<td>325 (33.8)</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>No. of samples with ( H ) pylori antigen OD&gt;1</td>
<td>NA</td>
<td>139 (14.5)</td>
<td>NA</td>
<td>NA</td>
<td>NA</td>
</tr>
</tbody>
</table>

Abbreviations: NA, not available; OD, optical density; RS, Rotterdam Study; SHIP, Study of Health in Pomerania.
calculated in R using the package metafor. Genomic control was applied to the individual studies’ GWAS results ($\lambda_{RS}=1.008$, $\lambda_{RS-II}=1.012$, $\lambda_{SHIP}=1.000$). Because the genomic inflation factor of the combined meta-analysis was below 1 ($\lambda=0.999$), no genomic control was applied for those results.

To assess whether there were multiple independently associated SNPs within the loci found in the combined meta-analysis, a clumping analysis was performed using PLINK (1-megabase distance, $r^2>0.01$, HapMap R28 CEU genotype data set), but no additional hits were found. $P=5 \times 10^{-8}$ was used as the threshold for genome-wide significance, and 2-sided significance testing was performed.

Expression analyses in SHIP-TREND were performed using quantile-normalized and log2-transformed gene expression data. Expression quantitative trait loci (eQTL) analyses in SHIP-TREND and RS-II used quantile-normalized, log2-transformed, probe-centered, and standardized gene expression data. To reduce the number of false-positive and false-negative eQTL association results, in a first step a principal component analysis of the matrix of gene expression data was performed. In a second step, the gene expression profiles of the individuals were adjusted for the first 50 principal components, which represent the largest factors related to variation of gene expression levels. For details see eAppendix, eTable 1A and B, and eFigure 1A-F.

RESULTS
Prevalence and Frequency of H pylori Seroprevalence

Some level of seroprevalence throughout the study was detected in 6160 of 10 938 participants (56.3%) (SHIP, RS-I, and RS-II) (Table 1). Based on the predefined phenotypic seroprevalence in the top 25% of the study population, a total of 2623 cases (25%) and 7862 controls (75%) were used for GWAS meta-analysis (SHIP, RS-I, and RS-II) (Table 1). To increase specificity and reduce the number of false-positive H pylori infections in the case group of the GWAS, the cutoff was set to the upper 25% of the IgG titer distribution of the corresponding cohort (124.5 U/mL for SHIP, 136.8 U/mL for RS-I, and 88.9 U/mL for RS-II).

GWAS Meta-analysis

Two genome-wide significant loci were identified (Figure 1) by combining the data from RS-I, RS-II, and SHIP (n=10 485, for which H pylori serology and genotyping data were available) using a fixed-effects meta-analysis model. The TLR locus on 4p14 exhibited the lowest $P$ value (Figure 2A), with rs10004195 as the lead SNP (OR for the minor allele, 0.70 [95% CI, 0.65-0.76]; $P=1.42 \times 10^{-18}$; MAF=24.7%), closely followed by rs4833095 (OR for the minor allele, 0.70 [95% CI, 0.65-0.76]; $P=5.43 \times 10^{-18}$; MAF=24.9%) (Table 2). The second genome-wide significant locus was located on chromosome 1q23.3, with $P=2.1 \times 10^{-8}$ for the lead SNP, rs368433 (OR for the minor allele, 0.73 [95% CI, 0.65-0.81]; MAF=16%) (Figure 2B). This SNP is located in an intron of FCGR2A encoding the Fcγ receptor 2a. The $F$ heterogeneity measures for the top-ranked SNPs (57.3% for rs10004195; 22.6% for rs368433) indicated high and low between-study heterogeneity, respectively. To take into account that the effect of the SNP might differ between the studies as implicated by the high heterogeneity, a random-effects meta-analysis was applied to the genome-wide significant findings to ensure that the combined effect of the SNP was not the result of a large effect in a single cohort. For rs10004195 the association $P$ value increased to $6.5 \times 10^{-9}$ using this model, and the combined effect estimate was nearly the same (OR, 0.69 [95% CI, 0.61-0.79]), indicating that the observed association was not completely driven by a single study. For SNP rs368433, the association $P$ value and...
combined effect size were essentially unchanged compared with the fixed-effects meta-analysis (OR, 0.73 [95% CI, 0.65-0.82]; \(P = 9.2 \times 10^{-8}\)), but the \(P\) value no longer met the genome-wide significance threshold (eTable 2). In the complete meta-analysis comprising SHIP, RS-I, and RS-II (n = 10,938), the numbers of cases (samples with the highest 25% IgG titer values) were 985 for SHIP, 1136 for RS-I, and 642 for RS-II (n = 2763), whereas the numbers of con-

**Figure 2.** Genome-wide Association Studies Meta-analysis: Loci Associated With Anti–Helicobacter pylori IgG Titers on a Genome-Wide Level of Significance

(A) TLR region on chromosome 4

(B) FCGR2A region on chromosome 1

Regional plots of the 2 loci associated with anti-\(H\) \(p\)ylori IgG titers on a genome-wide level of significance. The y-axis on the left indicates the \(-\log_{10}\) \(P\) value for the association with the anti-\(H\) pylori IgG phenotype. Single-nucleotide polymorphisms (SNPs) available in all 3 cohorts are plotted on the x-axis according to their chromosomal position against the association with the phenotype on the y-axis. Shown are the TLR (left) and FCGR2A (right) regions: purple diamonds indicate the top-ranked SNPs of the respective regions exhibiting the lowest \(P\) value for association with the phenotype. The blue y-axes on the right of each plot indicate the estimated recombination rates (based on HapMap phase II); the bottom of each panel shows the respective annotated genes at the locus and their transcriptional direction. cM indicates centimorgans; Mb, megabases.

**Table 2.** Top-Ranked SNPs From the Genome-Wide Association Studies Meta-analysis of the Defined Anti–Helicobacter pylori IgG Titer Phenotype in RS-I, RS-II, and SHIP

<table>
<thead>
<tr>
<th>Chromosome</th>
<th>Analysis</th>
<th>MAF</th>
<th>OR (95% CI)</th>
<th>(P) Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>4p14 (top-ranked SNP: rs10004195)(^a)</td>
<td>Meta-analysis</td>
<td>0.25</td>
<td>0.70 (0.65-0.76)</td>
<td>(1.4 \times 10^{-16})</td>
</tr>
<tr>
<td>SHIP</td>
<td>0.22</td>
<td>0.62 (0.54-0.72)</td>
<td>(5.0 \times 10^{-11})</td>
<td></td>
</tr>
<tr>
<td>RS-I and RS-II</td>
<td>0.26</td>
<td>0.74 (0.67-0.81)</td>
<td>(7.4 \times 10^{-10})</td>
<td></td>
</tr>
<tr>
<td>1q23.3 (top-ranked SNP: rs368433)(^b)</td>
<td>Meta-analysis</td>
<td>0.16</td>
<td>0.73 (0.66-0.81)</td>
<td>(2.1 \times 10^{-8})</td>
</tr>
<tr>
<td>SHIP</td>
<td>0.15</td>
<td>0.67 (0.55-0.81)</td>
<td>(2.4 \times 10^{-7})</td>
<td></td>
</tr>
<tr>
<td>RS-I and RS-II</td>
<td>0.16</td>
<td>0.76 (0.68-0.87)</td>
<td>(1.3 \times 10^{-4})</td>
<td></td>
</tr>
</tbody>
</table>

**Abbreviations:** MAF, minor allele frequency; OR, odds ratio; RS, Rotterdam Study; SHIP, Study of Health in Pomerania; SNP, single-nucleotide polymorphism.

\(^a\)Top-ranked SNP refers to the locus’ SNP with the smallest \(P\) value.

\(^b\)Genes: TLR10, TLR9, TLR6, FAM114A1. Major/minor allele: A/T.

\(^c\)Genes: FCGR5A, HSPA6. Major/minor allele: C/T.

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controls (samples with the lowest 75% IgG titer values) in each population were 2845 for SHIP, 3406 for RS-I, and 1924 for RS-II (n=8175). The MAF of the protective TLR locus lead SNP rs10004195 was 0.22 in SHIP, 0.26 in RS-I/II, and 0.25 in the meta-analysis. The MAF of the protective FCGR2A locus lead SNP rs368433 was 0.15 in SHIP, 0.16 in RS-I/II, and 0.16 in the meta-analysis.

From a pathophysiological point of view, associations of other TLR genes with H pylori seroprevalence might be of relevance. Therefore, the meta-analysis data were used to search for associated SNPs (genotyped or imputed analysis data were used to search for associations of other SNPs in linkage disequilibrium with the top-ranked SNP) in all 3 cohorts, MAF >0.01) within or in ±100-kilobase windows upstream and downstream of TLR9, TLR2, or TLR4. The smallest P value observed was for TLR2 (rs11736691; OR, 0.79 [95% CI, 0.65-0.96]; P = .02); this did not meet genome-wide significance. A complete list of these results is provided in eTable 3; a list of all genome-wide significant SNPs is provided in eTable 4.

Putative Functional Context of the Genome-wide Significant SNPs

The protein-coding sequences of the genes closest to the top-ranked SNPs were analyzed for nonsynonymous SNPs in linkage disequilibrium with r-sq=0.6. Using the 1000 Genomes database in the SNAP SNP Proxy search tool,31 2 nonsynonymous SNPs were identified in TLR1 and 1 SNP in TLR10 in linkage disequilibrium with the top-ranked SNP (rs10004195). In TLR1, the previously mentioned rs4833095 (r-sq=1.0) and rs5743618 (r-sq=0.95) are nonsynonymous SNPs. Whereas rs4833095 causes the amino acid substitution Asn248Ser, rs5743618 results in the Ser602Le substitution. In TLR10, rs4129009 (r-sq=0.77) is located close to the 3’ end of the single protein-coding exon of the gene and corresponds to the Ile775Val substitution. This TLR10 amino acid position is localized within the intracellular TIR (toll/interleukin-1 receptor) domain that participates in the transduction of extracellular signaling.32 For the top-ranked SNP at the 1q23.3 locus (rs368433; Figure 2B), no nonsynonymous SNPs in linkage disequilibrium were found.

Association of Anti–H pylori IgG Titers and H pylori Stool Antigen in SHIP-TREND

To explore the relationship between the TLR locus and H pylori infection in more detail, additional analyses in SHIP-TREND were carried out. H pylori stool antigen levels and measured anti–H pylori IgG titers were found to have a significant positive correlation (Spearman ρ=0.59, P = 2×10-30).

Cis-eQTL Analysis of the Significant GWAS Hits in Whole Blood

Integrative analysis of blood expression profiles with genome-wide SNP data in 1763 participants from SHIP-TREND and RS-III were used to investigate the potential causal relationship between gene(s) located at the loci shown to be associated with H pylori susceptibility. Variation at rs10004195, the top-ranked SNP at the TLR locus (4p14), was significantly correlated with the mRNA levels of TLR1 (ID: 6520451; P = 2.1×10-4 for SHIP-TREND and P = 3.2×10-17 for RS-III) (Figure 3A, eFigure 3A and B). Variation at the linked nonsynonymous SNP rs4833095 was also significantly associated with TLR1 (ID:6520451) mRNA expression levels. Among the three TLR genes only TLR1 was differentially expressed. TLR1 was differentially expressed per copy number of the minor rs10004195-A allele (β = -0.23 [95% CI, -0.34 to -0.11]; P = 2.1×10-4). The eQTL-results for rs10004195 and all available TLR probes are shown in eTable 6.

Variation at rs368433, the top-ranked SNP of the second genome-wide significant locus (1q23.3), was significantly associated with expression levels of FCGR2A, FCGR2B, and HSPA6 represented by 7 probes (Figure 3B, eTable 6, eFigure 3A and B). Significant associations were found for...
FCGR2B (ID:6650341; \(P=9.5 \times 10^{-10}\) for SHIP-TREND and \(P=2.5 \times 10^{-20}\) for RS-III). FCGR2B expression levels increased in participants carrying 1 or more minor alleles in both populations, whereas expression levels of HSPA6 and FCGR2A decreased with each minor allele.

**Relationship Between Bacterial Load, TLR Gene Expression, and Genotype**

TLR6, TLR1, or TLR10 mRNA amounts were analyzed to determine if expression levels increased in parallel with bacterial load as determined by \(H\) pylori stool antigen testing. To minimize false-positive results, only samples with an OD greater than 1 (high bacterial load as defined in previously published studies\(^{25}\)) were used to study correlations between \(H\) pylori fecal load and gene expression levels. Individuals with high fecal \(H\) pylori antigen titers (OD>1) also exhibited the highest 25% of TLR1 expression levels \((P=.01\) by \(\chi^2\) test; TLR1 gene probe ID: 6520451). This result was independent of the rs10004195 SNP genotype. This significantly increased expression implied a specific and genotype-independent transcriptional up-regulation of TLR1, but not of TLR6 or TLR10, in the presence of \(H\) pylori (TLR6: \(P=26\) [TLR6 gene probe ID: 5340427] and \(P=80\) [TLR6 gene probe ID:2600735]; TLR10: \(P=.05\) [TLR10 gene probe ID:4480543], \(P=.72\) [TLR10 gene probe ID:620441], and \(P=.95\) [TLR10 gene probe ID:380639] [all results by \(\chi^2\) test]). For TLR6 and TLR10, more than 1 gene-specific probe was present on the HumanHT-12 Expression BeadChips. These findings identify TLR1 to be the receptor most likely involved in recognition of \(H\) pylori.

No significant association between fecal \(H\) pylori antigen and the expression of FCGR2A and 2B was detected in whole blood.

**DISCUSSION**

This GWAS on \(H\) pylori seroprevalence, conducted in 2 population-based cohorts including a total of 10,938 participants, identified 2 genome-wide significant loci located at 4p14 and 1q23.3 associated with \(H\) pylori seroprevalence. These findings were further explored in 1763 additional study participants in whom gene expression levels were studied in whole blood and 961 participants in whom bacterial load was measured in stool samples.

The 4p14 region encodes the TLR1, TLR6, and TLR10 genes; TLR1 was identified as the receptor most likely causatively associated with \(H\) pylori seroprevalence. This conclusion is biologically plausible because TLRs are known to be essential for protective immunity against infection. Murine models have previously suggested that the TLRs 2, 9, and 8 could be involved in the recognition of \(H\) pylori by dendritic cells, which traverse epithelial tight junctions in the intestine to sample luminal bacteria.\(^{33,34}\) Among these, TLR2 represents the only cell surface receptor/ligand system that can cause a pronounced anti-inflammatory signature.\(^{33}\)

TLR1, on the other hand, is known to represent one of the coreceptors of TLR2. Both proteins can form a heterodimer that recognizes triacylated lipopeptides from the cell envelope of gram-negative bacteria.\(^{35,36}\) The fine structure of \(H\) pylori lipid A can consist of triacylated lipopeptides, which would make it an ideal ligand for TLR2-TLR1 binding.\(^{37}\) However, this conclusion remains speculative, because information was not available regarding the identities of the different \(H\) pylori strains in the study cohorts. Recent studies showed the association of rs5743618, a nonsynonymous SNP in 4p14, as the receptor most likely involved in recognition of \(H\) pylori.\(\) Additional studies have shown that the specific \(H\) pylori-induced dendritic cell cytokine profile polarizes the balance between mucosal T helper 1 (Th1) and T helper 17 (Th17) cells on one side and regulatory T helper (Treg) cells on the other side, toward a Treg-biased response. This would cause suppression of the \(H\) pylori–specific Th1/Th17–dependent responses and correlated with a higher degree of \(H\) pylori infection.\(^{40,41}\) These results demonstrated that \(H\) pylori, by inducing a Treg-skewed response via active tolerogenic programming of dendritic cells, limits the host’s ability to eradicate the pathogen and can result in persistence of \(H\) pylori infection.\(^{41}\)

In light of animal data\(^{35,34}\) and new data generated by this study, one hypothesis is that the protective minor allele–associated haplotype might confer less effective anti-inflammatory TLR1-TLR2 signaling. The single nonsynonymous SNP rs4833095 in TLR1 identified as associated with \(H\) pylori seroprevalence represents a putative candidate for such a predicted modification of TLR1-TLR2 function, because the position of the Asn248Ser amino acid substitution is located within the immediate vicinity of the TLR1 ligand binding and dimerization site.\(^{32}\) This hypothesis could be tested in a recently generated knockout animal.\(^{42}\) In the present study, the allele associated with higher anti–\(H\) pylori IgG titers was also associated with higher TLR1 expression. Whether the nonsynonymous SNP rs4833095 is associated with \(H\) pylori treatment failure or recurrence requires further investigation, because the cross-sectional design of this population-based study does not allow an evaluation of these parameters.

In the GWAS meta-analysis, the 1q23.3 region was also significantly associated with the \(H\) pylori phenotype. The minor allele of the top-ranked SNP, rs368433, was associated with low anti–\(H\) pylori IgG titers, decreased blood levels of HSPA6 and FCGR2A, and increased expression levels of FCGR2B. The FCGR2B-encoded Fcy receptor IIB also seems plausibly related to seroprevalence, because genetic variations affecting the receptor’s affinity for IgG subclass 2 (IgG2) have been reported.\(^{43}\) Furthermore, it has been observed that neutrophils from individu-
alys who are homozygous for one of these SNPs can phagocytose IgG2-opsonized bacteria more effectively. On the other hand, the increased expression of FCGR2B on the surface of immune cells might simply result in more pronounced cellular titration of IgGs and, consequently, decreased titers of soluble IgG. Additional studies are required to validate the association and, if validated, to explore the underlying biological mechanisms related to the observed effects.

At this time, the clinical implications of the current findings are unknown. Based on these data, genetic testing to evaluate H pylori susceptibility outside of research projects would be premature. This study has several limitations. First, the study was conducted among participants phenotyped only for seroprevalence and not symptomatic H pylori infection. In agreement with previous studies, this study shows a quantitative correlation for H pylori serology and H pylori fecal antigen; however, the correlation is weak (Spearman ρ = 0.59). Therefore, additional studies are needed to determine if the observed associations are present in populations phenotyped for clinically significant infection. Second, the validity of the current results are restricted to individuals of European ancestry. Additional GWASs of cohorts with non-European ancestry will be required to determine the extent to which the results can be generalized to other ethnic groups.

Third, it is also not clear if the results would be reproducible in a cohort exposed to a significantly higher pathogen pressure. A significant proportion of the study population had no definitive serological evidence of H pylori exposure, nor were study population-specific data available for H pylori exposure rates. It is technically possible that the observed associations are related to effective exposure to H pylori, rather than serologic conversion. Fourth, the FCGR2A/B locus shown genome-wide significant association in the meta-analysis under a fixed-effects model only and requires replication in independent, ethnically diverse, cohorts.

GWAS meta-analysis identified an association between TLR1 and H pylori se-roprevalence, a finding that requires replication in other independent populations. If confirmed, genetic variations in TLR1 may help explain some of the observed variation in individual risk for H pylori infection.

**Author Contributions:** Drs Lerch and Kuipers had full access to all of the data in the study and take responsibility for the integrity of the data and the accuracy of the data analysis. Drs Mayerle, the Hoed, and Stolk and Ms Schurmann contributed equally to the study. Drs Lerch and Kuipers share senior authorship.

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**Administrative, technical, or material support:** Mayerle, the Hoed, Homuth, Capelle, Zimmermann, Völkze, de Vries, Völk, Teumer, de Vries, Steinemetz, Nauck, Ernst, Weiss, Hofman, Zener, Kroemer, Prokisch, Utterlinden, Lerch, Kuipers

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**Conflicts of Interest Disclosures:** All authors have completed and submitted the ICMJE Form for Disclosure of Potential Conflicts of Interest. Dr Völkze reported receiving a grant from the Federal Ministry of Education and Research (BMBF). Dr Völk reported receiving a grant from BMBF. Dr Nauck reported receiving grants from BMBF (01ZZ0103). Dr Weiss reported receiving a grant pending from BMBF. Dr Nauck reported receiving grants from the Federal Ministry of Education and Research (01ZZ0403). Dr Weiss reported receiving a grant from BMBF. Dr Nauck reported receiving grants from the Federal Ministry of Education and Research (01ZZ0103), and the Social Ministry of Diemenza and, the Falk Foundation. Dr Mayerle reported providing expert testimony on behalf of AstraZeneca and Novartis; and receiving payment for lectures from the Falk Foundation.

**Funding/Support:** This study was funded by BMBF, the Center of Knowledge Interchange program of the Siemens AG, and the Leibniz-Campus program of the InterSystems GmbH. The Rotterdam Study is supported by the Netherlands Organisation of Scientific Research (NWO) Investments, the Research Institute for Diseases in the Elderly, and the Netherlands Genomics Initiative/NWO. Further funding and support is described in the eAppendix.

**Role of the Sponsors:** The funders had no role in the design and conduct of the study; the collection, analysis, and interpretation of the data; or the preparation, review, or approval of the manuscript.

**Online-Only Material:** The eAppendix, eTables 1-6, and eFigures 1-3 are available at http://www.jama.com.

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