Novel Antigens of Helicobacter pylori Correspond to Ulcer-Related Antibody Pattern of Sera from Infected Patients

Christo Atanassov,1* Leon Pezennec,1 Jacques d’Alayer,2 Ghislaine Grollier,1 Bertrand Picard,3 and Jean-Louis Fauchère1

Department of Microbiology A, IFR 59, University Hospital Center, 86021 Poitiers,1 Laboratory of Protein Microsequencing, Institut Pasteur, 75724 Paris,2 and Laboratory of Microbiology, Faculty of Medicine, 29200 Brest,3 France

Received 15 June 2001/Returned for modification 24 September 2001/Accepted 18 November 2001

Recently, we reported that the patterns of antibodies to Helicobacter pylori protein antigens in serum may be useful for screening patients at high risk for ulcers (P. Aucher et al., J. Clin. Microbiol. 36:931–936, 1998). Here we report the identification, by a combination of electrophoretic, immunochemical, and protein sequencing methods, of five antigens that correspond to this antibody pattern: groEL, catalase A, flagellin A, beta-ketoacyl-acyl carrier protein synthase I (β-ketoacyl-ACP S), and peptidyl prolyl cis-trans isomerase (PPIase). β-Ketoacyl-ACP S and PPIase are reported for the first time as antigens of diagnostic interest in infections by H. pylori. The antigenicity of the five antigens, together with those of CagA and VacA, was tested in an immunoblot assay with water-soluble protein extracts from two H. pylori pathogenic strains (HP 141 and ATCC 43579) and panels of sera from H. pylori-positive patients with gastroduodenal ulcers (GDU), nonulcer dyspepsia (NUD), as well as sera from H. pylori-negative healthy volunteers. For catalase A, groEL, and flagellin A antigens, no overall statistically important values were found making it possible to discriminate between patients with GDU and NUD. For both H. pylori strains, the mean performance indices (MPI) presenting percentages of correctly classified patients with GDU and NUD showed that the most significant antibody patterns were as follows: anti-VacA + anti-β-ketoacyl-ACP S (MPI = 76.1), anti-VacA + anti-PPIase (MPI = 71.8), and anti-CagA + anti-VacA + anti-β-ketoacyl-ACP S (MPI = 70.5). Antibody patterns detected with these antigen profiles may therefore be useful in developing a diagnostic test designed to predict the clinical severity of the H. pylori infection within the adult population of France.

Serological tests and assays for the diagnosis of Helicobacter pylori infection are included among the noninvasive methods recommended by the European Helicobacter pylori Study Group (7). Evaluation of the humoral immune response to H. pylori antigens by immunoblotting is a valuable alternative and complement to the more routinely used enzyme-linked immunosorbent assay (ELISA) tests (8, 13, 14, 19, 25). Immunoblotting appears to be sometimes more sensitive and useful for detecting low-abundance antibodies and antibodies directed toward nonconformational epitopes of immunodominant antigens. By this method, we recently reported that several antigens of H. pylori are preferentially recognized by the serum antibodies of adult French patients with gastroduodenal ulcers (GDU) that had been infected by this gastric pathogen. We therefore postulated that the five antigens corresponding to this antibody pattern could be useful for differentiating patients at high risk of GDU from patients with nonulcer dyspepsia (NUD) (2). Under the conditions of an immunoblot assay, two proteins of this antigenic profile were identified as CagA (125 kDa) and VacA (87 kDa), while the three other proteins were assigned only as immunoreactive bands with approximate molecular masses of 54, 42, and 35 kDa (denoted, respectively, p54, p42, and p35). Knowledge of the exact primary structure of p54, p42, and p35 is thus an essential prerequisite for preparing and further analyzing the antigenic preparation designed for the development of a test predicting the clinical outcome of the H. pylori infection.

Our initial aim was to purify the three unidentified antigens in order to determine their amino acid sequences. After optimizing the electrophoretic separation of these antigens, we differentiated three antigens within the zone of p54. This prompted us to reinvestigate all members of antigenic profile by an immunoblot assay by using panels of sera from H. pylori-positive patients with GDU and NUD, as well as with the control sera of H. pylori-negative healthy volunteers.

MATERIALS AND METHODS

Patients and patient sera. A total of 115 individual sera were collected in the university hospitals of Poitiers (southwest), Nancy (east), and Brest (northwest). These cities represent three geographical locations in France situated at a distance of more than 700 km from one another. Eighty-five sera were obtained from patients attending the departments of hepatogastroenterology from 1995 to 2000. All patients underwent upper gastrointestinal endoscopy with multiple antral and fundic biopsies that were processed for histology. These subjects had received neither antimicrobial nor anticid therapies during the previous 3 months. As determined by in-house ELISA (29), all patients were seropositive for H. pylori. Of the 85 patients, 55 (43 males and 12 females) had GDU, and 30 (17 males and 13 females) showed signs of gastritis or a dyspeptic symptoms but were ulcer-free (NUD). For the GDU patient group, the median ages were 60.8 years (range, 26 to 89 years) and 69.5 years (range, 51 to 93 years) for males and females, respectively; the mean ELISA index was 0.89. (The threshold ELISA index for a positive result was 0.3.) For NUD patient group, the median ages were 45.4 years (range, 24 to 77 years) and 64 years (range, 27 to 86 years) for males and females, respectively; the mean ELISA index was 0.63. Thirty control sera were collected from healthy blood donors (16 males and 14 females). The median ages were 40.8 years (range, 28 to 51 years) and 35.8 years (range, 21 to 46 years) for males and females, respectively. All persons within this control...
group were seronegative for \textit{H. pylori}; the mean ELISA index was 0.023. Handling, storage, and processing of these sera were as described previously (2).

### Table 1. Characteristics of identified protein antigens of \textit{H. pylori} HP 141

<table>
<thead>
<tr>
<th>Antigen</th>
<th>Classification (J99/26695)</th>
<th>Pairwise protein identity (%)</th>
<th>Mol mass (kDa) (J99/26695)</th>
<th>Protein length (aa)$^a$</th>
<th>Predicted pI (J99/26695)</th>
<th>Sequeined fragment (strain HP 141)$^b$</th>
<th>Identity of HP 141 sequences with J99/26695 (%)</th>
<th>N-terminal position on J99/26695</th>
</tr>
</thead>
<tbody>
<tr>
<td>Catalase A subunit</td>
<td>JHP 809/HP 875</td>
<td>97.4</td>
<td>58.63/58.63</td>
<td>350/505</td>
<td>9.04/8.89</td>
<td>MVNKKDV</td>
<td>100/100</td>
<td>1–6</td>
</tr>
<tr>
<td>Flagellin A subunit</td>
<td>JHP 008/HP 010</td>
<td>99.6</td>
<td>58.26/58.24</td>
<td>546/546</td>
<td>5.48/5.46</td>
<td>AKEIKFS</td>
<td>100/100</td>
<td>2–8</td>
</tr>
<tr>
<td>β-Ketoacyl-ACP S</td>
<td>JHP 505/HP 558</td>
<td>97.3</td>
<td>43.60/43.56</td>
<td>412/412</td>
<td>6.63/6.52</td>
<td>VEYGYYVN</td>
<td>100/87$^c$</td>
<td>296–302</td>
</tr>
<tr>
<td>PPIase</td>
<td>JHP 161/HP 175</td>
<td>97</td>
<td>34.03/34.04</td>
<td>299/299</td>
<td>9.96/10.04</td>
<td>KPANNNATHNTK$^d$</td>
<td>100/87$^e$</td>
<td>22–36$^f$</td>
</tr>
</tbody>
</table>

*a aa, amino acids.

*b Sequenced fragments of catalase A subunit, flagellin A subunit, and PPIase were obtained by Northern Edman degradation; the fragment of (β-ketoacyl-ACP S was obtained by internal microsequencing of major HPLC peak 25 (see Materials and Methods).

*c 100% homology with respective sequences VEYGYYVN of TIGR HP 558 (β-ketoacyl-ACP synthase II), and KPANNNATHNTK of TIGR HP 175 (cell binding factor 2). Nontiodentical amino acids are underlined.

*d Corresponds to the second (by importance) most likely cleavage site between positions 21 and 22 (LMA-KP) producing N-terminal signal peptide. Determined by using SignalP predictions based on neural networks and hidden Markov models of gram-negative bacteria (Nielsen et al. [18]; SignalIP server [http://www.cbs.dtu.dk/services/SignalP-2.0/]).

**Results**

Identification of protein antigens. In an initial experiment, the electrophoretically separated proteins of both strains HP 141 and ATCC 43579 displayed very similar band profiles within the zones of interest encompassing silver-stained p54, p42, and p35. However, the protein bands of HP 141 extract within the zone of p54 were better differentiated than those of ATCC 43579 (data not shown). Strain HP 141 was therefore used as the sole source for further protein purification and sequence analysis. We next optimized the electrophoretic separations of proteins in terms of migration time and protein concentrations to be loaded, conditions of Western transfer, and immunolocalization of protein bands to be sequenced. Four proteins were successfully sequenced by N-terminal Edman degradation: three proteins within the zone of p54 and one protein within the zone of p35. The antigenic protein within the zone of p42 turned out to be blocked at its N terminus, and its sequence was determined by internal microsequencing.

As presented in Table 1, comparisons of determined sequences of HP 141 strain with those of both \textit{H. pylori} strains with known complete genomes (26695 and J99) made it possible to identify five antigenic proteins, namely, catalase A subunit (catalase A), groEL (other common or recent denominations of this protein are HspB and HSP60), flagellin A subunit (flagellin A), beta-ketoacyl-acyl carrier protein syn-

---

\[ \text{ATANASSOV ET AL. J. CLIN. MICROBIOL.} \]

---

\[ \text{Downloaded from http://jcm.asm.org/ on October 14, 2017 by guest} \]
TABLE 2. Absolute and relative (%) numbers of immunoreactive bands\(^a\) and the performance index\(^b\) as detected by immunoblot assay in the sera of patients with GDU and NUD and of clinically healthy controls

<table>
<thead>
<tr>
<th>Antigen</th>
<th>Patients with GDU (n = 55)</th>
<th>Patients with NUD (n = 30)</th>
<th>Healthy volunteers (n = 30)</th>
<th>Performance index (%) (n = 115)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>HP 141 ATCC 43579</td>
<td>HP 141 ATCC 43579</td>
<td>HP 141 ATCC 43579</td>
<td>HP 141 ATCC 43579 Mean(^c)</td>
</tr>
<tr>
<td>CagA</td>
<td>41 (75)</td>
<td>19 (63)</td>
<td>12 (40)</td>
<td>60.9</td>
</tr>
<tr>
<td>VacA</td>
<td>49 (89)</td>
<td>16 (53)</td>
<td>1 (3)</td>
<td>80.0</td>
</tr>
<tr>
<td>Catalase A subunit</td>
<td>51 (93)</td>
<td>20 (67)</td>
<td>22 (73)</td>
<td>60.0</td>
</tr>
<tr>
<td>groEL</td>
<td>51 (93)</td>
<td>23 (77)</td>
<td>20 (67)</td>
<td>59.1</td>
</tr>
<tr>
<td>Flagellin A subunit</td>
<td>54 (98)</td>
<td>30 (100)</td>
<td>29 (97)</td>
<td>47.8</td>
</tr>
<tr>
<td>β-Ketoacyl-ACP S</td>
<td>50 (91)</td>
<td>18 (60)</td>
<td>1 (3)</td>
<td>79.1</td>
</tr>
<tr>
<td>PPIase</td>
<td>33 (60)</td>
<td>8 (27)</td>
<td>0 (0)</td>
<td>82.6</td>
</tr>
</tbody>
</table>

\(^a\) Antibody specificities more frequent in patients with GDU than in patients with NUD concern antigens VacA and catalase A of strain HP 141 and β-ketoacyl-ACP S and PPIase of both H. pylori strains (as determined by chi-square test; \( P < 0.05 \)).

\(^b\) That is, the percentage of patients with ulcers that are correctly classified (i.e., The number of true positive plus the number of negative immunoblot controls/total number), where the total number is 115.

\(^c\) MPI for both H. pylori strains.

...antibody patterns. After electrophoretically differentiating catalase A, groEL, and flagellin A subunit within the zone of p54 from strain HP 141 and then performing corresponding immunoblots with 15 positive sera (mean ELISA of index 1.1) from patients with GDU, we found that all three bands remained immunoreactive. This result was in contrast to our previous study with ATCC 43579 extract (mean ELISA of index 1.1) from patients with GDU, where we observed only one immunoreactive p54 band that was supposed to be HspB (2). For this reason, we reinvestigated the antigenicity of the proteins to be sequenced by immunoblotting with extracts of both H. pylori strains. In this case, the plane \( F1/F2 \), which accounted for 89.1% of the variance, clearly discriminated the sera from healthy volunteers from the GDU sera. These two categories of sera are graphically concentrated on both sides of a virtual diagonal line drawn on Fig. 1. The sera from the patients with NUD appeared interspersed in the factorial analysis plane. This was also valid for five other antibody patterns selected (data not shown).

**Antibody frequencies to single antigens.** After electrophoretically differentiating catalase A, groEL, and flagellin A, we found that all three bands remained immunoreactive. This result was in contrast to our previous study with ATCC 43579 extract separated on a gradient PAA gel, where we observed only one immunoreactive p54 band that was supposed to be HspB (2).

**Antibody patterns.** Another interpretation of our results takes into consideration antibody patterns that provide statistical differences between the groups of patients with GDU or NUD and the control subjects. The antibody pattern of a given serum has been defined as the combination of antibodies present in this serum and immunoreacting with two or more of the seven antigens targeted. We looked for antibody patterns characterizing particular clinical categories of patients. Because the number of expected antibody patterns is relatively high, we used FAC, a one-step computerized analysis, allowing us to gather sera according to their antibody patterns and clinical categories. Figure 1 shows the results of the FAC analysis for the antibody pattern defined by the presence of antibodies to CagA, VacA, and β-ketoacyl-ACP S with the HP 141 strain. In this case, the plane \( F1/F2 \), which accounted for 89.1% of the total variance, clearly discriminated the sera from healthy volunteers from the GDU sera. These two categories of sera are graphically concentrated on both sides of a virtual diagonal line drawn on Fig. 1. The sera from the patients with NUD appeared interspersed in the factorial analysis plane. This was also valid for five other antibody patterns selected (data not shown). The application of another analysis (i.e., chi-square test and calculation of the performance indices) on the six selected antibody patterns made it possible to quantitatively evaluate their discriminating potential with respect to the patients with GDU and NUD (Table 3).

**DISCUSSION**

The antigenic material used in our study was obtained by a method that is considered to be optimized for the extraction of water-soluble proteins from the outer membrane of viable bacteria. However, only one identified antigen (i.e., flagellin A) meets the criteria for such proteins. At least three proteins (catalase A, groEL, and β-ketoacyl-ACP S) are cytoplasmic and theoretically should not be present in the extract. This apparent methodological discrepancy may be explained in view of the existing data on membrane expression of groEL and urease by a specific secretory system (28) or by genetically
programmed bacterial autolysis that occurs in vitro (22), as well in vivo (6). The latter means of membrane expression has also been suggested for catalase (22), and there is evidence that *H. pylori* catalase may be located both throughout the cytosol and in the periplasmic space (9). In this regard, it is not excluded that, due to unique characteristics of the outer membrane of *H. pylori*, other cytoplasmic proteins may become absorbed. It is also possible that *H. pylori* possesses an as-yet-unknown mechanism for exporting to the cell surface enzymes and other molecules that are important for colonizing the stomach.

As far as we know, */H9252*-ketoacyl-ACP S and PPiase are reported here for the first time as *H. pylori* antigens of clinical relevance. Because of the lack of information about */H9252*-ketoacyl-ACP S and PPiase in *H. pylori*, we briefly mention here some aspects of the homologs to these two molecules in other bacterial species. In our opinion, these findings give an idea about the biological importance of these molecules and as

---

**TABLE 3.** Frequencies (absolute number and percentage) of seven antibody patterns* to *H. pylori* in 115 human sera and their abilities to predict GDU and differentiate it from NUD, as measured by the performance index**

<table>
<thead>
<tr>
<th>Antibody pattern to antigen combination (i.e., “profile”)</th>
<th>Patients with GDU (n = 55)</th>
<th>Patients with NUD (n = 30)</th>
<th>Healthy volunteers (n = 30)</th>
<th>Performance index (%) (n = 115)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>HP 141 ATCC 43579</td>
<td>HP 141 ATCC 43579</td>
<td>HP 141 ATCC 43579</td>
<td>HP 141 ATCC 43579 Mean</td>
</tr>
<tr>
<td>CagA + VacA + PPiase</td>
<td>27 (49.0) 21 (38.2)</td>
<td>4 (13.3) 4 (13.3)</td>
<td>0 (0) 0 (0)</td>
<td>72.2 67.0 69.6</td>
</tr>
<tr>
<td>CagA + VacA + β-ketoacyl-ACP S</td>
<td>37 (67.3) 21 (38.2)</td>
<td>10 (33.3) 6 (20.0)</td>
<td>0 (0) 0 (0)</td>
<td>75.7 65.2 70.5</td>
</tr>
<tr>
<td>VacA + PPiase</td>
<td>30 (54.5) 24 (43.6)</td>
<td>4 (13.3) 5 (16.7)</td>
<td>0 (0) 0 (0)</td>
<td>74.8 68.7 71.8</td>
</tr>
<tr>
<td>VacA + β-ketoacyl-ACP S + PPiase</td>
<td>27 (49.0) 14 (25.4)</td>
<td>2 (6.7) 4 (13.3)</td>
<td>0 (0) 0 (0)</td>
<td>73.9 60.9 67.4</td>
</tr>
<tr>
<td>VacA + β-ketoacyl-ACP S</td>
<td>45 (81.8) 28 (50.9)</td>
<td>11 (36.6) 7 (23.3)</td>
<td>0 (0) 0 (0)</td>
<td>81.7 70.4 76.1</td>
</tr>
<tr>
<td>β-Ketoacyl-ACP S + PPiase</td>
<td>28 (51.0) 18 (32.7)</td>
<td>4 (13.3) 2 (6.6)</td>
<td>0 (0) 0 (0)</td>
<td>73.0 66.9 70.0</td>
</tr>
</tbody>
</table>

*a* The antibody patterns for all antigen profiles were significantly more frequent in patients with GDU than in patients with NUD, except for the antigen combinations CagA + VacA + β-ketoacyl-ACP S and VacA + β-ketoacyl-ACPS + PPiase of strain ATCC 43579 (as determined by chi-square test; *P* ≤ 0.05).

*b* That is, the percentage of patients with ulcers that are correctly classified (i.e., the number of true positive + the number of negative immunoblot controls/the total number), where the total number is 115.

*c* MPI for both *H. pylori* strains.
potential candidates in developing drug, vaccine, and diagnostic assays. β-Ketoacyl-ACP S of *H. pylori* (gene fabB) belongs to the family of β-ketoacyl synthases, key enzymes involved in the biosynthesis of fatty acids and polyketides. At present, β-ketoacyl-ACP S from *E. coli* is being studied structurally as a promising drug target for novel antibiotics to treat tuberculosis, as well as for inhibiting certain cancers (16, 23). Antigenic PPiase from *H. pylori* HP 141 is evolutionarily related to the cyclophilins, FKBBPs (proteins binding to the immunosuppressive drug FK506) and, more particularly, to parvulin (gene ppiC). Recent studies have shown that *E. coli* PPiase functions independently as an isomerase and as a chaperonin (3, 24).

Data dealing with antibodies to five identified antigens of *H. pylori* are interpreted in terms of the potential value these antigens may have as key compounds of an immunoblot assay that would allow differentiation of GDU disease from NUD. Differentiation of GDU from NUD seems to depend on factors such as age and population. Some reports provide evidence for the usefulness of the immunoblotting diagnosis of GDU in Brazilian children (25). Other authors claim that there is no association of specific *H. pylori* antigens with antibodies in adult patients suffering from various gastroduodenal pathologies in Germany (14) and Chile (20). Apparently, these contradictory findings reflect both the phenotypic heterogeneity of *H. pylori* and the specificity of the host immune response within various populations. However, a large-scale comparative immunoblotting study with sera from patients living in countries as geographically distant as the United States, China, and Peru has shown that, despite their diverse origins, all *H. pylori* strains show several major conserved bands in the range of 25 to 84 kDa (11). Other studies carried out in India and France also give evidence for relatively restricted, although differing, ranges of immunoreactive bands (2, 4). Therefore, it is possible that a pattern of immunoreactive bands may characterize, at least to some extent, the immune response to *H. pylori* within a given population, and this may be true irrespective of the *H. pylori* strain. In this latter regard, some 350 genes appear to be specific for *H. pylori*, but only 6 to 7% of them are considered to be strain specific (1, 27). This implies that some of the remaining 93 to 94% of these genes encode specific *H. pylori* antigens and/or epitopes that are common to all strains of this microorganism. The fact that we found similar antigen profiles in two *H. pylori* strains that were recognized by serum antibodies in patients from different regions of France supports this concept, although a prospective study with a greater number of *H. pylori* strains is needed to confirm our assumption.

The results presented in Tables 2 and 3 provide additional support that proteins such as catalase, groEL, and flagellin are strongly immunogenic but give nonspecific cross-reactions with antibodies to antigens from other gram-negative bacteria and, more particularly, *Campylobacter jejuni* (10, 12, 17, 21, 26). Catalase, groEL, and flagellin will therefore be of poor utility for the envisaged predictive test. Metabolic enzymes, such as identified β-ketoacyl-ACP S and PPiase, are considered to be promising candidates for a serological test kit because they have few cross-reactions with NUD sera and are more conserved than virulence factors such as CagA and VacA (14). Reported antibody frequencies to VacA, β-ketoacyl-ACP S, and PPiase make it possible to discriminate between the groups of NUD patients and ulcer patients, but it is rather unlikely that a single antigen could be sufficient as a highly reliable predictive tool. Neither the frequencies of positive sera for CagA and/or VacA nor the respective performance indices are sufficient as unique predictive markers for ulcer disease. This is due to the well-known fact that there exist *H. pylori* strains which are phenotypically negative for one or both antigens (5). In this regard, patterns including antibodies to β-ketoacyl-ACP S and PPiase could be promising for the prediction of GDU because their performance indices are close to 80%.

In conclusion, we identified the primary structure of five *H. pylori* protein antigens, and two of them—β-ketoacyl-ACP S and PPiase—are proposed for the first time as antigens of diagnostic interest. Antibody patterns detected by using these antigens may be useful in developing a diagnostic test designed to predict the clinical evolution of the *H. pylori* infection toward an ulcer disease within the adult population of France.

**ACKNOWLEDGMENTS**

This work was supported by the University and Hospital of Poitiers, Poitiers, France.

**REFERENCES**


