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Distribution and clinical associations of integrating conjugative elements and *cag* pathogenicity islands of *Helicobacter pylori* in Indonesia

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The clinical associations and correlations with other virulence factors such as *cag* pathogenicity island (PAI) of the Integrating Conjugative Elements *Helicobacter pylori* TFSS (ICEHptfs), a new type IV secretion system (TFSS) in *H. pylori* has not been described. Among 103 studied strains from Indonesia, almost all strains (99.0%) contained *cag* PAI with more than half (55.8%) were intact *cag* PAI. Patients infected with intact *cag* PAI strains showed significantly higher antral activity, inflammation and atrophy as well as corporal inflammation than those with non-intact *cag* PAI strains, confirming the virulence of *cag* PAI. Over half of strains (53.8%) contained ICEHptfs, predominantly consisted of ICEHptfs3-*tfs4a* (42.8%) and ICEHptfs3 (16.3%). Although patients infected with ICEHptfs-positive strains had lower *H. pylori* density, those with the complete ICEHptfs4b strains tended to have higher antral activity than the negative one. In combination, patients infected with combination of intact *cag* PAI-ICEHptfs-positive strains had more severe inflammation than those with non-intact *cag* PAI-ICEHptfs-negative, suggesting a possibility of a mutual correlation between these TFSS(s).

Helicobacter pylori is a human-specific bacterium, colonizing the stomach of approximately 50% of the modern human population¹. Infection is associated with several gastro-duodenal pathologies, including chronic gastritis, peptic ulcers, and even gastric cancer in a subset of individuals, depending on the variation of bacterial virulence, host genetics and/or environmental factors^{2,3}. *H. pylori* is the most genetically diverse pathogenic bacteria^{4,5}, which might be associated with frequent horizontal gene transfer (HGT) and recombination within species as an adaptation process to the host over years of infection⁶. Therefore, its genome contains many putative genes, which are generally classified into three categories⁷. The first is phase-variable genes, defined as those with functional status that could change due to particular conditions. An example is the slipped-strand mispairing mechanism, which often shown in outer membrane proteins such as *oipA* and *sabA*, that can switch genes 'on' and 'off' very rapidly^{8,9}. The second is genes with different structures/genotypes, such as the repeat region of CagA. The 3' repeat region of CagA can differ between two genotypes, associated with a different risk of developing gastric cancer^{10,11}. The last is strain-specific genes, defined if the gene only exists in a particular strain. The most studied genes in this category are *cag* pathogenicity island (PAI), which encodes a type IV secretion system (TFSS)^{7,12}.

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TFSS is a flexible secretion system found in both Gram-positive and -negative bacteria. In Gram-negative bacteria, it mediates secretion of various protein substrates, from monomeric proteins, multi-subunit protein toxins and nucleoprotein complexes¹³. Importantly, more than one TFSS could be found in one species of bacteria, including in the *H. pylori*. *H. pylori* has four types of TFSS with varied functionalities^{4,12,14,15}. The first is *cag* PAI, which primarily injects CagA into host cells¹². The second is the *comB* system which has a principal function of DNA uptake and natural transformation within *H. pylori* genome¹⁵. The most recently revealed TFSS is within Integrating Conjugative Elements (ICEs). In case of *H. pylori*, this is known as ICE *H. pylori* TFSS (ICE*Hptfs*)¹⁶. ICE*Hptfs* was initially named as plasticity regions, the regions within the *H. pylori* genome which have considerably lower guanine and cytosine content (~35%) compared with the rest of the genome (39%)¹⁷. The lower G + C content indicates that plasticity regions may be the result of HGT^{8,17}. With the increasing number of *H. pylori* complete genomes deposited in the GenBank, plasticity regions are considered as conserved mobile elements, rather than a region with genomic plasticity, and are usually organized as a complete set of TFSS machinery. In addition, based on the acquisition of these elements through conjugative HGT, these elements are best described as ICEs. The TFSS within ICE*Hptfs*(s) is called TFSS3 and TFSS4a/4b/4c^{4,16}. Those differences between ICE*Hptfs*3 and ICE*Hptfs*4a/b/c were determined by the nucleotide diversity of the *virB*-*virD* orthologues genes, resulting very distinctive diversity between TFSS3 and TFSS4 in general¹⁶. In addition, the TFSS4 possesses sub-type based on nucleotide diversity in the *virB2*, *virB3*, *virB4*, *topA*, *virB7* and *virB8*, discriminating TFSS4a and TFSS4b, and diversity in *virB11*, *virD4* and *virD2*, distinguishing TFSS4a and TFSS4c¹⁶. The terminology of this region was inconsistent in several previous studies. A study conducted in 2009 reported a new TFSS termed as TFSS3, TFSS3a, and TFSS3b¹⁴ within a mobile element called transposon of plasticity zones (TnPZ) type 2 for TFSS3, TnPZ1 for TFSS3a and TnPZ1b for TFSS3b. However a year later the TFSS3b were termed as TFSS4 for the TFSS inside the mobile element plasticity zones 1 (PZ1) and TFSS3 for the TFSS inside the mobile element PZ3. Following with the newest terminology is ICE*Hptfs*3 which containing TFSS3 and ICE*Hptfs*4a/4b/4c which containing TFSS4a/4b/4c¹⁶. In order to make consistent terminology, in this study we used ICE*Hptfs*3 and ICE*Hptfs*4a/4b/4c for TFSS3 and TFSS4a/4b/4c, respectively¹⁶. Currently, the distribution and association of these new TFSSs to gastro-duodenal diseases are not fully described.

Indonesia is a country in South-East Asia, consisting of more than 13,600 islands and 400 ethnicities¹⁸. As described previously, *H. pylori* infected the ancestors of modern humans in Africa about 100,000 years ago (100 kya) and migrated with its host from Africa to Asian and American continents^{19,20}. Therefore, ethnic diversity is associated with *H. pylori* infection as well as genome diversity, especially in Indonesia. We have described that ethnicity is a risk factor for *H. pylori* infection²¹. In addition, ethnicity is also a factor for the diversity of virulence genes in *H. pylori*. We have described that different ethnicity had a different genetic polymorphism on the several virulence genes in the nucleotides and amino acids level. For example, strains possessing pre-EPIYA motif of CagA isolated from Batak ethnic showed 6 bp deletion-type pre-EPIYA motif with East Asian-type CagA. The 6 bp deletion-type is unique type among East Asian-type CagA since almost all pre-EPIYA motif types of strains isolated from Japan and Vietnam was reported to have 39 bp deletion-type and 18 bp deletion-type, respectively²². Patients infected with this 6 bp deletion-type/East Asian-type CagA strains showed to have lower gastric mucosal histologic scores compared to those with Western-type CagA²³, although it is well known that East Asian-type CagA had generally more virulent than Western-type CagA. In addition, the predominant type of CagA was also different in each ethnic group.

As the distribution and clinical association of ICE*Hptfs*(s) have not been reported, it is interesting to investigate the distribution and clinical association of these regions as well as the correlation with other virulence genes in relation to the clinical outcome. Here, we reported the distribution of ICE*Hptfs* in Indonesia using high throughput next-generation sequencing technology and revealed that strains from some geographic areas lack this genomic region, and the intactness of this region had an association with clinical outcome.

Results

Characteristic of patients and prevalence of ICE*Hptfs* and *cag* PAI. We performed endoscopic examination on 1072 dyspeptic patients in 17 cities in Indonesia from August 2012 to August 2016, and a total of 103 *H. pylori* were isolated from patients (66 male and 37 female; mean age 49.2 ± 13 years; range 24–80 years), comprising 92 patients with gastritis, 10 with peptic ulcer disease (PUD) and 1 with gastric cancer. Among 103 isolates, 75 isolates were from our previous study with information of *cagA* genotypes²⁴. Strains originated in Indonesia are shown in Supplementary Figure 1.

We evaluated the *cag* PAI and determined the functional status of each gene present (Table 1). We categorized these into i) Intact *cag* PAI, if all the genes were detected and there was no deletion, stop codon or frameshift in each gene; ii.) Non-intact *cag* PAI, if at least one of the genes were lacking or had stop codon and/or frameshift in the gene; and iii.) *cag* PAI-negative, if none of the *cag* PAI genes were detected. In total, *cag* PAI was detected in most isolates (99.1%), either intact or non-intact. Among the detected *cag* PAI strains, 57 strains possessed intact *cag* PAI (55.8%). The gastric cancer patient had intact *cag* PAI *H. pylori*. The *cagA* was detected in 101 strains (98%). Sequence analysis of the 27 new *cagA*-positive strains showed that 5 (18.5%) strains possessed Western-type CagA and 12 (44.4%) strains possessed East-Asian type CagA. In addition, we also confirmed a unique genotype of CagA (AB and B type) which mostly were isolated from Merauke city, Papua Island. Those B segment of CagA genotypes had very similar amino acids sequences with ABB type CagA from our previous report²³ (Supplementary Figure 2). Therefore, we deemed it a subtype of the ABB type CagA. Taken together with our previous study²⁴, the result was 60 (58.2%) strains possessed the East-Asian type CagA (AABD, AAD and ABD type), whereas 30 strains (29.1%) were Western-type CagA (ABC, ABCC and BC type) and 15 strains (14.5%) were ABB type CagA (ABB, AB and B) (Fig. 1A).

ICE*Hptfs* were detected in 56 of 103 (54.3%) strains. Among gastritis patients, 51 strains (55.4%) and 5 strains (50.0%) from PUD patients possessed ICE*Hptfs*. Interestingly, the strain isolated from the gastric cancer

Characteristic	Total (n = 103)	Clinical Outcome (%)		
		Gastritis (n = 92)	PUD (n = 10)	Cancer (n = 1)
<i>cagA</i> positive	101 (98.0)	90 (97.8)	10 (100)	1 (100)
Intact <i>cag</i> PAI	57 (55.4)	50 (54.3)	6 (60.0)	1 (100)
non-intact <i>cag</i> PAI	45 (43.7)	41 (44.5)	4 (40.0)	0 (0.0)
<i>cag</i> PAI negative	1 (0.9)	1 (1.1)	0 (0.0)	0 (0.0)
ICEHptfs	56 (54.3)	51 (55.4)	5 (50.0)	0 (0.0)
Type of ICEHptfs				
TFSS3	9 (16.0)	9 (9.7)	0 (0.0)	0 (0.0)
TFSS4a	8 (14.4)	6 (6.5)	2 (20.0)	0 (0.0)
TFSS4b	6 (10.7)	6 (6.5)	0 (0.0)	0 (0.0)
TFSS3-TFSS4a	24 (42.8)	22 (23.9)	2 (20.0)	0 (0.0)
TFSS3-TFSS4b	5 (8.9)	4 (4.3)	1 (10.0)	0 (0.0)
TFSS3-TFSS4a/b	4 (7.2)	4 (4.3)	0 (0.0)	0 (0.0)

Table 1. Prevalence of ICEHptfs and *cag* PAI. Abbreviations: PAI, patogenicity island; TFSS, type IV secretion system; PUD, peptic ulcer disease.

patient did not contain ICEHptfs (Table 1). Sequence analysis showed there were no mutations leading to premature stop codons or frameshift mutation; thus, we concluded that all of the genes were functional. Among the ICEHptfs-positive strains the single ICEHptfs was observed as ICEHptfs3 (16.0%), ICEHptfs4a (14.4%) and ICEHptfs4b (10.7%). There was no strain with ICEHptfs4c. Aside from single ICEHptfs in the genome, strains possessing multiple ICEHptfs were also observed: ICEHptfs3-*tfs4a* (42.8%), ICEHptfs3-*tfs4b* (8.9%) and ICEHptfs3-*4a/4b* (7.2%) (Table 1).

The distribution of ICEHptfs and the ethnic groups. There was a significant association between ethnic group and prevalence of ICEHptfs ($P = 0.031$). Timor tribe strains had the highest prevalence of ICEHptfs (10/12, 83.3%) and the lowest prevalence was observed in Minahasanese strains (14.2%) (Table 2). There was also a significant association between ethnic groups and the type of ICEHptfs ($P = 0.002$). Batak tribes possessed predominantly ICEHptfs3-*tfs4a* (77.8%), whereas Chinese ethnicities possessed predominantly ICEHptfs3 (57.1%). As for the Timor ethnicity, the types of ICEHptfs were distributed evenly (Table 2).

Complete ICEHptfs were assessed as a cluster with complete TFSS machineries, composed of VirB2, VirB3, VirB4, VirB6, VirB7, VirB8, VirB9, VirB9, VirB10, VirB11, VirD2, VirD4, XerT and TopA. Among the positive ICEHptfs strains, 32 strains (57.1%) possessed incomplete ICEHptfs. The complete ICEHptfs were found in 24 strains: 19 (33.9%) with complete ICEHptfs3 and 5 (9.0%) with complete ICEHptfs4b. There was a significant association between the completeness of ICEHptfs and the ethnic groups ($P = 0.03$). Timor tribe strains showed the highest prevalence of complete ICEHptfs (80.0%), in which 5 strains (50.0%) possessed complete ICEHptfs3 and 3 strains (30.0%) possessed complete ICEHptfs4b (Table 2).

The ICEHptfs, CagA and CagL. Among totally 30 strains with Western-type CagA, we could find 18 strains (60.0%) containing ICEHptfs (Supplementary Table 2). However, we could not obtain any ICEHptfs elements from strains which possessed ABCC- and B-type CagA (Fig. 1B). Interestingly, the B-type CagA strains were isolated from Merauke city, Papua island, suggesting there is an association with the human population. Among the East Asian-type CagA, 32 strains (53.3%) possessed ICEHptfs. The ABBD type *cagA* strain did not contain any ICEHptfs elements. The ABB type *cagA* containing ICEHptfs were 4 of 11 strains (36.3%) and seemed to be equally distributed.

CagL Hypervariable Motif (CagLHM) had a close relationship with the geographical origin of *H. pylori*, as recently reported²⁵. We evaluated the CagLHM and found 8 unique motifs. The predominant motifs were YEIGK, DEIGK and DKMGE (38.6%, 14.8% and 13.8%) (Fig. 1C). Interestingly we also found a novel motif DKMGK and this motif mostly was observed from *H. pylori* isolated from Samosir Island (Supplementary Table 1). This novel motif strains almost exclusively (91%) possessed ICEHptfs elements as exclusive as the DKMGE motif strains (92.8%) (Fig. 1D).

The *cag* PAI and histological findings. Comparison between histological findings and *cag* PAI intactness showed that patients infected with intact *cag* PAI had higher both corporal and antral inflammation than those with non-intact *cag* PAI ($P = 0.011$ and $P < 0.001$, respectively). Patients infected with intact *cag* PAI strains also showed higher activity and atrophy in the antrum than those with non-intact *cag* PAI strains ($P < 0.001$) (Fig. 2). Patients infected with intact *cag* PAI strains had significantly higher risk of antral activity, inflammation and atrophy and corporal inflammation and atrophy after adjusted with age and sex (Supplementary Table 3).

The ICEHptfs and histological findings. Histological examination showed the patients infected with strains possessing ICEHptfs elements (either complete or incomplete) had significantly lower antral *H. pylori* density than those without ($P = 0.039$) (Table 3). As for the comparison between complete and incomplete ICEHptfs(s), histological findings did not show any significant association; however, the patients infected with

Genetic Profiles	Total (n = 103)	Ethnic Groups (%)								
		Javanese (n = 3)	Chinese (n = 9)	Balinese (n = 6)	Bugis (n = 13)	Batak (n = 31)	Papuan (n = 20)	Minahasanese (n = 7)	Dayak (n = 2)	Timor (n = 12)
ICEHptfs*	56 (54.3)	1 (33.3)	7 (77.8)	4 (66.7)	7 (53.8)	19 (58.0)	6 (30.0)	1 (14.2)	1 (50.0)	10 (83.3)
Type of ICEHptfs*										
TFSS3	9 (16.3)	0 (0.0)	4 (57.1)	1 (25.0)	2 (28.5)	2 (11.1)	0 (0.0)	0 (0.0)	1 (100)	0 (0.0)
TFSS4a	8 (14.5)	0 (0.0)	1 (14.2)	2 (50.0)	2 (28.5)	2 (11.1)	0 (0.0)	1 (100)	0 (0.0)	0 (0.0)
TFSS4b	6 (10.9)	1 (100)	0 (0.0)	0 (0.0)	1 (14.2)	1 (5.5)	1 (16.7)	0 (0.0)	0 (0.0)	2 (20.0)
TFSS3-TFSS4a	24 (43.6)	0 (0.0)	1 (14.2)	1 (50.0)	2 (28.5)	14 (77.8)	3 (50.0)	0 (0.0)	0 (0.0)	3 (30.0)
TFSS3-TFSS4b	4 (7.2)	0 (0.0)	1 (14.2)	0 (0.0)	0 (0.0)	0 (0.0)	1 (16.7)	0 (0.0)	0 (0.0)	2 (20.0)
TFSS3-TFSS4a/b	4 (7.2)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (16.7)	0 (0.0)	0 (0.0)	3 (30.0)
Complete tfss*										
Incomplete TFSS	32 (57.1)	1 (33.3)	5 (71.4)	3 (75.0)	6 (85.7)	9 (47.3)	4 (66.7)	1 (100)	1 (100)	2 (20.0)
Complete TFSS3	19 (33.9)	0 (0.0)	2 (28.6)	1 (25.0)	0 (0.0)	9 (47.3)	2 (33.3)	0 (0.0)	0 (0.0)	5 (50.0)
Complete TFSS4b	5 (9.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (14.3)	1 (5.4)	0 (0.0)	0 (0.0)	0 (0.0)	3 (30.0)
cag PAI										
cag PAI positive	101 (98.0)	3 (100)	9 (100)	6 (100)	12 (92.3)	31 (100)	20 (100)	7 (100)	2 (100)	12 (100)
Intact cag PAI	57 (55.3)	0 (0.0)	3 (33.3)	5 (83.3)	8 (72.7)	16 (51.6)	11 (55.0)	2 (28.5)	2 (100)	10 (83.3)

Table 2. Distribution of *cag* PAI and ICEHptfs among Ethnic Group. Abbreviations: TFSS, type IV secretion system; PAI, pathogenicity island. (*) $P < 0.05$, Fischer's exact test.

Histology score	ICEHptfs positive (mean [median]) n = 47	ICEHptfs negative (mean [median]) n = 56
Antrum		
Activity	1.44 [1.5]	1.20 [1]
Inflammation	1.82 [2]	1.79 [2]
Atrophy	1.24 [1]	1.18 [1]
Density*	1.19 [1]	1.53 [2]
Corpus		
Activity	0.72 [1]	0.73 [1]
Inflammation	1.04 [1]	1.04 [1]
Atrophy	0.32 [0]	0.28 [0]
Density	1.13 [1]	1.27 [1]

Table 3. Association of ICEHptfs status and histology score. (*) $P = 0.039$, Mann-Whitney U test.

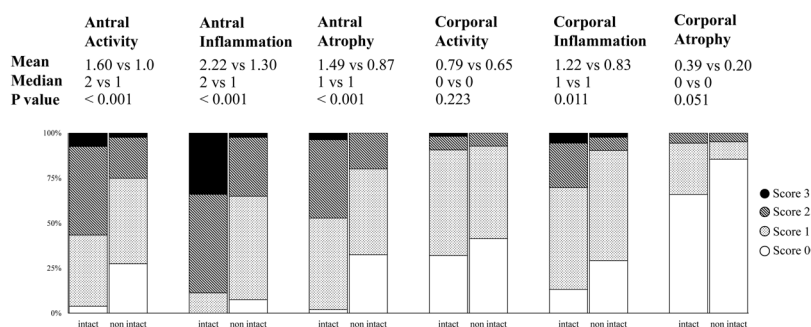


Figure 2. Association of *cag* PAI intactness and the histological findings. Patients infected with the intact *cag* PAI (n = 53) showed significantly higher antral activity, inflammation and atrophy as well as corporal inflammation than the non-intact counterpart (n = 40).

possessing intact *cag* PAI-complete ICEHptfs4b (n = 3), we found that patients infected with these strains had higher antral activity and inflammation compared to those with non-intact *cag* PAI-incomplete ICEHptfs strains ($P = 0.024$ and $P = 0.009$, respectively) (Table 4).

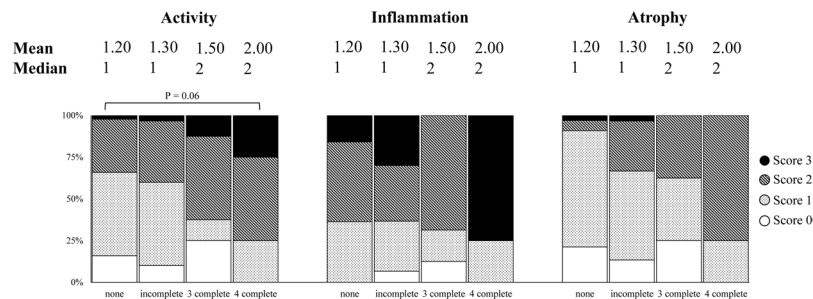


Figure 3. Association of *ICEHptfs* and histological findings in antrum. Patients infected with the complete *ICEHptfs4b* ($n = 4$) tended to have higher antral activity than antral activity than the *ICEHptfs* negative ($n = 44$).

<i>cag</i> PAI and <i>ICEHptfs</i>	n	Antrum (Mean [Median])				Body (Mean [Median])			
		Activity	Inflammation	Atrophy	Density	Activity	Inflammation	Atrophy	Density
<i>cag</i> PAI and <i>ICEHptfs</i> status									
Intact <i>cag</i> PAI- <i>ICEHptfs</i> +	34	1.75 [2]	2.25 [2]	1.47 [1]	1.45 [1]	0.75 [1]	1.13 [1]	0.38 [0]	1.25 [1]
Intact <i>cag</i> PAI- <i>ICEHptfs</i> -	23	1.38 [1]	2.19 [2]	1.52 [1]	1.62 [2]	0.86 [1]	1.38 [1]	0.43 [0]	1.38 [1]
Non Intact <i>cag</i> PAI- <i>ICEHptfs</i> +	21	0.94 [1]	1.13 [1]	0.94 [1]	0.76 [1]	0.69 [1]	0.94 [1]	0.25 [0]	1.00 [1]
Non Intact <i>cag</i> PAI- <i>ICEHptfs</i> -	24	1.04 [1]	1.43 [1]	0.87 [1]	1.46 [1.5]	0.63 [1]	0.75 [1]	0.17 [0]	1.17 [1]
<i>cag</i> PAI and type of TFSS									
Intact <i>cag</i> PAI-incomplete TFSS	21	1.58 [2]	2.37 [2]	1.47 [1]	1.60 [1.5]	0.53 [1]	1.11 [1]	0.32 [0]	1.21 [1]
Intact <i>cag</i> PAI-complete TFSS3	10	1.90 [2]	1.80 [2]	1.30 [1]	1.20 [1]	1.10 [1]	1.30 [1]	0.60 [0]	1.40 [1]
Intact <i>cag</i> PAI-complete TFSS4b	3	2.33 [2]	3.00 [3]	2.00 [2]	1.00 [1]	1.00 [1]	0.67 [0]	0.00 [0]	1.00 [1]
Non intact <i>cag</i> PAI-incomplete TFSS	10	1.00 [1]	1.11 [1]	1.00 [1]	1.25 [1]	0.88 [1]	1.13 [1]	0.50 [0]	1.25 [1]
Non intact <i>cag</i> PAI-complete TFSS3	9	0.83 [0.5]	1.17 [1.5]	0.83 [0.5]	0.75 [0]	0.43 [0]	0.71 [1]	0.00 [0]	0.83 [0.5]
Non intact <i>cag</i> PAI-complete TFSS4b [‡]	1	1	1	1	0	1	1	1	1

Table 4. Association of *ICEHptfs* and *cag* PAI status and histology score. Abbreviations: PAI, Pathogenicity Island, TFSS, type IV secretion system [‡]Number samples of this group only one sample. So we cannot calculate the mean and median.

Discussion

This is the first study to evaluate the pathogenic role of *ICEHptfs* in combination with *cag* PAI at a population level. We examined the prevalence of *ICEHptfs* and *cag* PAI using high throughput sequencing. The previous genomic comparison showed that the *ICEHptfs* has high prevalence (86.7%) in 45 strains worldwide¹⁶. We applied the same methods to determine the prevalence of *ICEHptfs* among Indonesian strains, which showed a lower prevalence of *ICEHptfs* (53.4%). In general, ICEs were transferred between genomes using conjugative HGT. This different prevalence might be due to observation only performed in one country compared to the worldwide observation. In addition, the distribution of *ICEHptfs* had a significant association with ethnic groups in Indonesia, suggesting the prevalence and type of *ICEHptfs* had an association with geographical origin. Some particular CagA genotypes strains did not possess any *ICEHptfs*, especially the strains isolated from Merauke city. All our strains isolated from Merauke city were assigned as hpSahul (data not shown) and other strains deposited in the GenBank belonging to hpSahul, PNG84A and ausaBRJ05²⁶, also did not contain *ICEHptfs*, strongly supporting this association.

The *cag* PAI was transferred into *H. pylori* far prior human migrate from Africa 60 kya²⁷ and interestingly, the *cag* PAI still can be observed in all the *H. pylori* populations after long period of human migration and shows the same evolution pattern as the house-keeping genes²⁷. This suggests the importance of *cag* PAI towards the host colonization process. Our study showed almost all the Indonesian strains (98%) contained *cag* PAI, supporting its importance. In addition to the *cag* PAI, CagLHM may also help to discriminate geographical origin²⁵. Our study showed that the predominant CagLHM in Indonesia were specifically observed in the East/Southeast Asia/Australasia groups, as previously reported²⁵. We also found a new motif of CagLHM which showed as high prevalence of *ICEHptfs* as the DKMGE motif. DKMGE is believed to be the progenitor of the CagLHM motif²⁵, and since the observed motifs only differed on the residue 62 (E62K), this observation suggests the new motifs were directly derived from the progenitor.

The *cag* PAI was originally designated as a TFSS, which mainly has a function to translocate CagA protein into host cell cytoplasm^{28,29}. However, the virulence of this island dependent to the intactness of this island, therefore it may successfully inject the CagA protein¹². Our previous study in Vietnam³⁰ classified the intactness of *cag* PAI based on the existence of the gene using the PCR method. Our current results showed similarly that the intact *cag* PAI has more severe histological score than the non-intact *cag* PAI. However, the previous criterion evaluated the intactness of *cag* PAI only based on the presence or absence of the member genes and the resulting

high prevalence of intact *cag* PAI, which may blur the association with histological scores. On the other hand, the evaluation of *cag* PAI sequences may give us a significant association with the histological scores. In addition, it may also discriminate the cluster of *cag* PAI genotype (East-Asian type and Western type cluster), of which the East-Asian type may bind stronger to the SHP-2 receptor¹¹. Therefore, we recommend the criteria to evaluate intactness of *cag* PAI also considering the functional status of the genes, as a more reliable method to predict clinical outcome.

Although strains with ICEHptfs showed significantly lower *H. pylori* density, there was an association between a complete TFSS and the histological scores. It was reported that strains with a complete cluster of *dupA*, the VirB4 homologue of ICEHptfs4b, lead to a higher risk of developing duodenal ulcers than those with incomplete *dupA* clusters or *dupA* negative strains³¹. Our data also showed the same tendency, even with a lower density in the antrum, suggesting this region has a more significant association to the *H. pylori* virulence, resulting in a higher active inflammation rather than attachment to the gastric mucosa.

In addition, we combined the status and type of ICEHptfs with the *cag* PAI intactness. Our data showed patients infected with intact *cag* PAI-ICEHptfs-positive strains had higher antral activity than those with non-intact *cag* PAI-ICEHptfs-negative strains. However, patients infected with the intact *cag* PAI-ICEHptfs-negative strains did not show difference of antral activity compared to those with non-intact *cag* PAI-ICEHptfs-negative strains. These data suggest that the *cag* PAI and ICEHptfs were dependent each other to induce higher antral activity. The TFSS can be divided into three groups according to their function³². The first group is the conjugation system, translocating single-stranded DNA substrates to recipient cells in a contact-dependent manner, resulting in the adaptation of bacteria to environmental changes. The second group is the effector translocation system, delivering protein directly into eukaryotic cells. The third group is the DNA uptake mediators, which uptake or release DNA or protein substrates extracellularly, independently of contact with another cell³³. Since there was an evidence that the ICEHptfs was a genetic mobile element which was transferred in the conjugation manner^{16,34}, we assumed the function of ICEHptfs in the pathogenesis of *H. pylori* infection was belongs to the conjugation group³³, suggesting the ICEHptfs might supporting the *cag* PAI to induce more severe clinical outcome.

Although we could not make strong conclusions due to a small sample size, particularly in the certain ICEHptfs groups, this study gives us new information about the distribution and clinical association of this relatively new TFSS in *H. pylori*. In addition, since there have not been many biological and structure evidences of this particular system, further study is needed to better understand the role of the TFSS in colonization by *H. pylori*.

Conclusion

In conclusion, our data showed a high prevalence of *cag* PAI in Indonesia, half of which were complete. Criteria determining intactness of *cag* PAI based on the gene functionality is more reliable to evaluate the influence of *H. pylori* on gastric mucosal status. The ICEHptfs strains tended to induce more active inflammation in the antrum even with a lower density of bacteria. In combination, it was shown that patients infected with intact *cag* PAI-ICEHptfs-positive strains had more severe inflammation than those with non-intact *cag* PAI-ICEHptfs-negative strains, suggesting possibility a mutual correlation between these TFSS(s).

Materials and Methods

Samples and DNA sequencing. We performed endoscopic examination on 1072 dyspeptic patients in 17 cities in Indonesia from August 2012 to August 2016. We excluded patients with partial/total gastrectomy, non-fasted patients and those with contraindication for upper endoscopy. Written informed consent was obtained from all patients and the study protocol was approved by the ethics committees of Dr. Soetomo Teaching Hospital (Surabaya, Indonesia), Dr. Cipto Mangunkusumo Teaching Hospital (Jakarta, Indonesia), Dr. Wahidin Sudirohusodo Teaching Hospital (Makassar, Indonesia) and Oita University Faculty of Medicine (Yufu, Japan). We declare that all procedures contributing to this work comply with the ethical standards of the relevant national and institutional committees on human experimentation and with the Helsinki Declaration of 1975, as revised in 2008 and 2013. We used antral gastric biopsy to isolate *H. pylori* as previously described²⁴, resulting in 103 cultured isolates, including 75 isolates from our previous study²⁴.

DNA extraction was performed using QIAamp DNA Mini Kit (QIAGEN, Valencia, CA, USA) following the manufacturer's instructions. Whole genome sequencing was performed using a high throughput next generation sequencer; Illumina Hiseq. 2000 and Miseq as per the list in Supplementary Table 2. Briefly, high-quality genomic DNA was used, then was prepared using dual-indexed Nextera XT Illumina libraries and subjected to cluster generation and paired-end sequencing (2 × 300 bp) for Miseq and (2 × 150 bp) for Hiseq. We performed the quality control and de novo assembly prior the reference mapping to obtain the coverage and to select the result which may be used for further analysis using CLC Genomic Workbench v. 7.04, a commercial software (Qiagen Inc., Redwood, California, USA). The coverage we obtained was between 81–400 folds in each genome (Supplementary Table 1). The threshold for further analysis in this study, we use Q30 > 80% as recommended by Illumina and the average coverage more than 80 folds as had been described previously³⁵.

Analysis of ICE and other virulence genes. Identification of the ICEHptfs-type was performed by using a reference mapping method. Short-read outputs were mapped to the corresponding reference sequences consisting of ICEHptfs3 (strain Gambia94/24), ICEHptfs4a (strain P12) ICEHptfs4b (strain G27) ICEHptfs4c (strain SouthAfrica7) using CLC Genomic Workbench v. 7.04, a commercial software (Qiagen Inc., Redwood, California, USA) as described previously¹⁶. The unmapped reads then also assembled by using *de novo* assembly by the CLC Genomic Workbench. The ICE genes were identified by BLAST search (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>) from the mapped reads. The *cag* PAI were identified using BLAST method and the query from strain 26995^{8,27}. The functional status of the each gene was evaluated by visual inspection using MEGA7³⁶.

Histological evaluation. All biopsy material for histological evaluation was fixed in 10% buffered formalin and embedded in paraffin. Serial sections were stained with hematoxylin and eosin as well as May-Giemsa stains. Gastric mucosa were evaluated based on the updated Sydney system³⁷. Bacterial load was classified into four grades: 0, 'normal'; 1, 'mild'; 2, 'moderate'; and 3, 'marked' according to the updated Sydney system³⁷.

The degree of inflammation, neutrophil activity, atrophy and intestinal metaplasia were classified into four grades according to the updated Sydney system: 0, 'normal'; 1, 'mild'; 2, 'moderate'; and 3, 'marked'³⁷. Immunohistochemistry for anti-*H. pylori* antibody was performed as previously described³⁸.

Statistical analysis. Data were analyzed using IBM SPSS Statistics, version 22 (IBM Corp., USA). Discrete variables were tested using the chi-square test; continuous variables were tested using Mann-Whitney *U* test. An ordinal regression model was used to calculate risk for developing higher histological score. A two-tailed *P* value < 0.05 was considered statistically significant.

Availability of Nucleotide Sequences. The accession number for nucleotide sequences were deposited in DDBJ under accession number LC334483 – LC335589 and LC339076 – LC339479.

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Author Contributions

L.A.W., M.M. and Y.Y. design the study. P.S., L.A.W., T.U. and M.M. carried out the experiments. L.A.W., M.M., T.U., R.S. and Y.Y. carried out the analyzed the data. M.I.L., M.H., N.N., A.F.S., M.M., L.A.W. and Y.Y. carried out the sample acquisition and data collection. L.A.W., M.M., R.S. and Y.Y. writing and revising the manuscript.

Additional Information

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