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Letters to the Editor

Relationship between J-Western CagA Subtype and the *vacA* m2 Region of *Helicobacter pylori*▽

Yamazaki et al. examined the full-length sequences of the *vacA* and *cagA* genes of *Helicobacter pylori* isolated from Okinawa, Japan (4). Among 20 Okinawan strains examined, 7 had East Asian-type CagA and 13 had Western-type CagA, in agreement with previous studies (3). Okinawa, located in the southern islands of Japan, was governed by the United States from the end of World War II until 1972, and even today there is a large U.S. population in Okinawa. The data suggest that transmission of *H. pylori* between different populations may not be a rare event. However, Truong et al. confirmed that 12 of 13 Western-type CagA strains in Okinawa form a cluster of strains that are different from strains isolated from Western countries (2). They therefore proposed that there is a Japanese subtype in the Western CagA type (J-Western CagA). These data suggest that all the Western-type CagA strains in Okinawa might not have derived from those in modern Western people and may have come to Japan long ago, as we speculated previously (3). Further studies will be necessary to test this hypothesis.

By focusing on these J-Western CagA strains, we noticed that they all harbored the *vacA* m2 type, which is believed to be less virulent than the m1 type (1). To further confirm the relationship between J-Western CagA and the *vacA* m2 type, we examined 61 strains of the Western, J-Western, and East Asian CagA types whose *vacA* genotypes have been deposited in GenBank by their group (20 from Okinawa, 13 from Fukui, Japan, 22 from Vietnam, and 6 reference strains) (2, 4). We found that all 12 Okinawan J-Western CagA strains of the *vacA* m2 type had a 12-bp insertion in the 3′ region from position 619 in reference Western CagA strain 26695 (Table 1). Six Western CagA strains of the *vacA* m1 type did not have the insertion, whereas one, the J99 strain, did have the insertion. According to phylogenetic analysis, strain J99 belongs to the cluster of J-Western CagA strains; however, the reason was unclear (4). None of the 18 East Asian CagA strains from Okinawa and Fukui had the insertion, irrespective of the *vacA* status. Two strains (strain 147A [GenBank accession no. AY884088] and strain 147C [AY884089]) from the United States belonged to the J-Western CagA cluster, as described by Truong et al. (2), and also had the insertion (Table 1). In a BLAST search of positions 590 and 661 in strain OK107 (GenBank accession no. AB090086), a 12-bp insertion was found in 15 J-Western CagA strains, including strains J99, 147A, and 147C. These 3 strains were submitted to GenBank under accession no. FJ428215 (Russia), GQ161099 (China), and AY330642 (Sweden), respectively. However, their *vacA* status was not determined. We suggest that this insertion may be specific for J-Western CagA strains. A large number of Western CagA strains harboring *vacA* type m2 are needed to clarify the hypothesis that J-Western CagA strains are associated with the 12-bp insertion in the *cagA* gene. It is also important to study whether the 12-bp insertion is associated with clinical outcomes.

TABLE 1. Prevalence of the 12-bp insertion

CagA type	*vacA* type[a]	No. of CagA/*vacA* strains	No. of strains examined from:			Reference	Strains with the 12-bp insertion	
			Okinawa	Fukui	Vietnam		No.	%
J-Western CagA	m1	1	0	0	0	1	1 (strain J99)	100
	m2	12	12	0	0		12	100
	NA	2	0	0	0	2	2 (strains 147A and 147C)	100
Western CagA	m1	6	1	2	0	3	0	0
	m2	0	0	0	0		0	0
	NA	1	0	0	1		0	0
East Asian CagA	m1	17	6	11	0		0	0
	m2	1	1	0	0		0	0
	NA	21	0	0	21		0	0
Total		61	20	13	22		15	

[a] NA, not analyzed.

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