Letter to the Editor

Staphylococcus lugdunensis Is the Likely Origin of the Ornithine Decarboxylase Operon in *Staphylococcus epidermidis* 2015B[▽]

We read with interest the recent paper by Coton and colleagues (1) on the origin of the putrescine-producing ability of *Staphylococcus epidermidis* 2015B. As noted in the paper, Gram-positive bacteria generally do not exhibit ornithine decarboxylation. However, we would like to draw attention to a major exception, *Staphylococcus lugdunensis*, which is related to *S. epidermidis* but not mentioned in the original article. Ornithine decarboxylase (ODC) activity is present in virtually all *S. lugdunensis* strains (2, 4) and represents one of the key tests for identification of the species (3). This example is distinct from the other examples, *S. epidermidis* and *Oenococcus oeni*, for which ODC activity is present in only a small minority of strains.

As our group had recently completed the first reference genome sequence of *S. lugdunensis* (5), the presence of the *odc* and *potE* genes was examined in light of the findings reported by Coton et al. The two genes (locus tags SLGD_00246 and SLGD_00247; GenBank accession no. NC_013893) were arranged in an operon with structural similarity to those found in *S. epidermidis* 2015B and *O. oeni* RM83. However, unlike the other two bacteria, *S. lugdunensis* shows no evidence of recent horizontal gene transfer in the form of transposases, integrases, or other remnants of mobile genetic elements around

the ODC operon, which argues against the acquisition of the operon through recent horizontal gene transfer (HGT). This argument is also reflected in the ubiquity of ODC activity in *S. lugdunensis* strains.

We also updated the phylogenetic analysis of the putrescine-ornithine antiporter (PotE) with the inclusion of additional *S. lugdunensis* sequences, which showed phylogenetic relatedness to PotE of *S. epidermidis* 2015B (Fig. 1). Whereas *S. epidermidis* 2015B ODC and PotE showed only 65 and 69% sequence identities to the homologues in *O. oeni* RM83, they showed 83 and 88% sequence identities to the homologues in *S. lugdunensis* HKU09-01. Further analysis revealed additional similarities between the putrescine production pathways of the two *Staphylococcus* species, like the presence of a *cep* gene homologue downstream of the ODC operon and the lack of an N-terminal extension compared to the *O. oeni* ODC.

Taken together, these results strongly suggested that the putrescine production pathway of *S. epidermidis* 2015B originated from *S. lugdunensis* and that this pathway had been conserved in the genome of the latter for a significantly longer period. Identifying the biological role of the pathway in *S. lugdunensis* may help elucidate its significance in *S. epidermidis* and other Gram-positive bacteria.

FIG. 1. Neighbor-joining trees showing the phylogenetic relationships of ornithine decarboxylase homologues (A) and putrescine-ornithine antiporter homologues (B) in selected bacteria. Isolates 1 to 11 are additional *S. lugdunensis* clinical isolates included in this study. Bootstrap values obtained from 1,000 replicates are shown as percentages.

FIG. 1—Continued.

Nucleotide sequence accession numbers. Additional *S. lugdunensis* sequences corresponding to PotE have been deposited in GenBank under accession no. HQ424132 to HQ424153.

REFERENCES

1. Coton, E., N. Mulder, M. Coton, S. Pochet, H. Trip, and J. S. Lolkema. 2010. Origin of the putrescine-producing ability of the coagulase-negative bacterium *Staphylococcus epidermidis* 2015B. *Appl. Environ. Microbiol.* **76**:5570–5576.
2. Freney, J., Y. Brun, M. Bes, H. Meugnier, F. Grimont, P. A. D. Grimont, C. Nervi, and J. Fleurette. 1988. *Staphylococcus lugdunensis* sp. nov. and *Staphylococcus schleiferi* sp. nov., two species from human clinical specimens. *Int. J. Syst. Bacteriol.* **38**:168–172.
3. Tan, T. Y., S. Y. Ng, and J. He. 2008. Microbiological characteristics, presumptive identification, and antibiotic susceptibilities of *Staphylococcus lugdunensis*. *J. Clin. Microbiol.* **46**:2393–2395.
4. Tang, Y. W., J. Han, M. A. McCormac, H. Li, and C. W. Stratton. 2008. *Staphylococcus pseudolugdunensis* sp. nov., a pyrrolidonyl arylamidase/ornithine decarboxylase-positive bacterium isolated from blood cultures. *Diagn. Microbiol. Infect. Dis.* **60**:351–359.
5. Tse, H., H. W. Tsoi, S. P. Leung, S. K. Lau, P. C. Woo, and K. Y. Yuen. 2010. Complete genome sequence of *Staphylococcus lugdunensis* strain HKU09-01. *J. Bacteriol.* **192**:1471–1472.

Hoi-Wah Tsoi

Herman Tse*

Department of Microbiology
The University of Hong Kong
Pokfulam Road
Hong Kong

*Phone: 852 2255 4822

Fax: 852 2855 1241

E-mail: htse@hkucc.hku.hk

† The authors of the published article did not feel that a response was necessary.