



Corrigendum: The Stand-Alone PilZ-Domain Protein MotL Specifically Regulates the Activity of the Secondary Lateral Flagellar System in *Shewanella putrefaciens*

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A Corrigendum on

The Stand-Alone PilZ-Domain Protein MotL Specifically Regulates the Activity of the Secondary Lateral Flagellar System in *Shewanella putrefaciens*

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In the original article, there was a mistake in **Figure 1** as published. **The alignment shown in 1D for DgrA was not correct. We also updated the signature motif for the c-di-GMP-binding motif of PilZ domains with a more recent one.** The corrected **Figure 1** appears below.

In the original article, there was an error. **In the text appeared an older version of the c-di-GMP-binding motif within PilZ domains. We have updated the information along with the corresponding reference.**

A correction has been made to **Results, Identification of a flagellar motor effector protein in *Shewanella putrefaciens*, 2nd paragraph:**

Sputcn32_3446, annotated as a PilZ domain, is located 34 bp downstream of *motB* and transcribed in the same direction (**Figure 1B**). The gene is 435 bp in length and encodes a protein of 144 aa with an estimated molecular mass of 16.6 kDa and a theoretical pI of 5.94. The protein is thus much smaller than YcgR (244 aa), FlgZ (263), and MotI (217aa) as an N-terminal YcgR domain is not present (**Figure 1C**). The predicted c-di-GMP-binding motifs (**RxxxRhxh, DhSxxG; Galperin and Chou, 2020**) are fully conserved (**Figure 1D**). The protein is conserved in a number *Shewanella* species that possess dual flagellar systems, and the gene it is always located downstream of *motB*. Potential homologs of Sputcn32_3446 are also present in some species of *Aeromonas* and *Vibrio*, but absent from the well-characterized *V. parahaemolyticus* and *V. alginolyticus*, which also possess two distinct flagellar systems. We henceforth referred to the protein as MotL, relating to its location within the lateral flagellar gene operon and its differences to YcgR, FlgZ, and MotI with respect to the protein sequence and absence of further domains.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

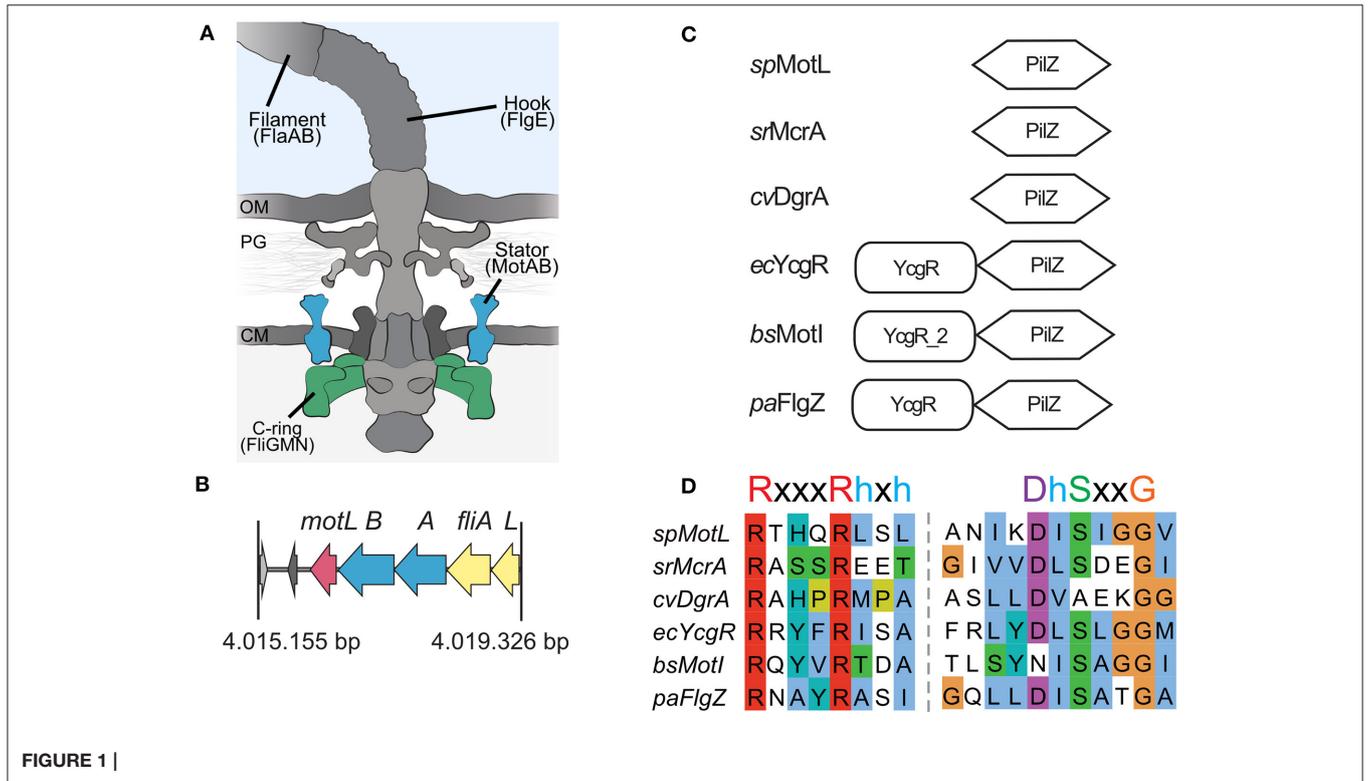


FIGURE 1 |

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Galperin, M. Y., and Chou, S. H. (2020). Structural conservation and diversity of PilZ-related domains. *J. Bacteriol.* 202:e00664-19. doi: 10.1128/JB.00664-19

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