



Corrigendum: An Evolutionary Arms Race Between *Burkholderia* pseudomallei and Host Immune System: What Do We Know?

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A Corrigendum on

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In the original article, there was a mistake in **Figure 1** as published. The annotation of core and accessory genes in the Figure 1 was misplaced. The corrected figure appears below.

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.

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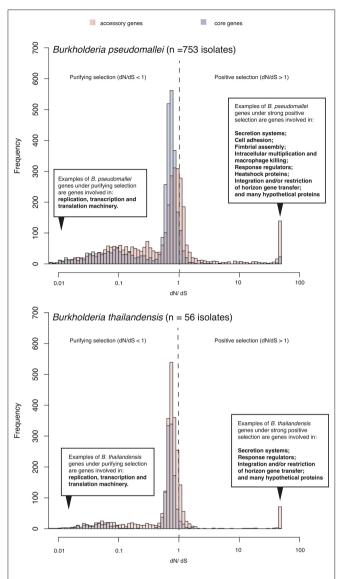


FIGURE 1 | Selection pressure acting on *B. pseudomallei* population. The histogram summarizes ranges of *dN/dS* calculated from predicted coding sequences from a collection of diverse *B. pseudomallei* population from northeast Thailand (Chewapreecha et al., 2019), and *B. thailandensis* genomes from the public database. *B. pseudomallei* and *B. thailandensis* have highly plastic genomes comprising of at least two chromosomes of ~7–8 Mb in size when combined. Using a pan-genome approach, all coding sequences could be categorized as "core" (present in all genomes) or "accessory" (variably present across studied genomes). Accessory genes display an elevated level of *dN/dS* which is signatures of positive selection or more relaxed purifying selection.