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Correction: Elucidation of the RamA Regulon in *Klebsiella pneumoniae* Reveals a Role in LPS Regulation

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The authors would like to correct Fig 4 and Fig 7, as errors were made in the preparation of these figures for publication. In Fig 4B, the existing panels for the gene promoters yrbF and ybhT are the wrong EMSA images for these promoters. The authors have provided a corrected version of Fig 4 here. In Fig 7B, the panel for Ecl8ΔramA was a replication of the image shown for the wild type strain *K. pneumoniae* Ecl8. The authors have provided a corrected Fig 7 here.

The authors confirm that these changes do not alter their findings. The authors have provided raw, uncropped blots for Fig 4B as Supporting Information.
**Fig 4.**

**A:** Quantitative real-time RT-PCR validation of differentially expressed genes in Ecl8ΔramR. All qPCR experiments were performed as outlined in materials and methods. Expression levels were normalized to 16S levels, and fold change values were generated by calibrating against Ecl8ΔramA. Genes designated BN373_36191, BN373_39031, BN373_03291 encode a putative membrane protein, oxidoreductase family and conserved hypothetical protein respectively. All data is a mean of 3 experiments.

**B:** Electrophoretic Mobility Shift Assay (EMSA) using purified RamA protein. Following PCR amplification, each promoter region was end-labelled with 32P-γ ATP. Purified RamA (200 nM) and the different labelled DNA probes (2 nM) were incubated on ice. All reactions were performed on ice prior to electrophoresis on 7.5% native gel. Lane 1 of each panel indicates the labelled DNA probe only, Lane 2 is the BSA control and Lane 3 contains RamA+DNA.

**C:** Transcription in vitro assay of different promoters using the purified RamA protein. The test DNA (2 nM- *yrbF*, *ybhT*, *yhbW*, *acrA*, *nfnB*, *lpxCD* and *lpxC*) with the control template (*gnd*) were incubated for transcription *in vitro* [32P]α-UTP with (+) or without (-) 200 nM purified RamA. Samples were fractionated by polyacrylamide/urea gel electrophoresis prior to drying and exposure to the phosphorimager. Relative fold increase was determined using densitometric analysis as described previously [55], by first normalizing all test transcription levels to the control promoter (*gnd*) prior to comparison to the no protein control. Statistics was done using One way ANOVA (P value < 0.05) where transcription levels were found to be statistically significant in the presence of purified RamA compared to the no protein control.

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Supporting Information

S1 Fig. Uncropped blots for Fig 4B. Raw data phosphor image scan for the EMSA analyses on the ybhT and yrbF promoters. The experimental setup was as described previously in Fig 4. Briefly, Electrophoretic Mobility Shift Assay (EMSA) using purified RamA protein. Following PCR amplification, each promoter region was end-labelled with $^{32}$P-$\gamma$ ATP. Purified RamA (200 nM) and the labelled DNA probes (2 nM) were incubated on ice. All reactions were performed on ice prior to electrophoresis on 7.5% native gel. Lane 1 of each panel indicates the labelled DNA probe only, Lane 2 is the BSA control and Lane 3 contains RamA+DNA. The

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dried gel was scanned after overnight exposure to the phosphor screen under default settings on the phosphorimager Typhoon FLA7000IP (GE Healthcare).

(PDF)

Reference