Published online 22 July 2019

Nucleic Acids Research, 2019, Vol. 47, No. 15 ***8333–8334***
doi: 10.1093/nar/gkz641

Corrigendum

Metal sensing and regulation of adaptive responses to manganese limitation by MtsR is critical for group A streptococcus virulence

Hackwon Do[1], Nishanth Makthal[1], Pete Chandrangsu[2,3], Randall J. Olsen[1,4], John D. Helmann[2], James M. Musser[1,4] and Muthiah Kumaraswami[1,*]

[1]Center for Molecular and Translational Human Infectious Diseases Research, Houston Methodist Research Institute, and Department of Pathology and Genomic Medicine, Houston Methodist Hospital, Houston, TX 77030, USA, [2]Department of Microbiology, Cornell University, Ithaca, NY 14853-8101, USA, [3]W.M. Keck Science Department, Claremont McKenna, Pitzer and Scripps College, Claremont, CA 91711, USA and [4]Department of Pathology and Laboratory Medicine, Weill Medical College of Cornell University, New York, NY 10021, USA

Nucleic Acids Research, 2019: https://doi.org/10.1093/nar/gkz524

The Authors wish to make the following corrections to their article.

In Figure 1, panel B1 (Apo MtsR) was inadvertently repeated in B5 (MtsR:Mn – non-specific probe). A new Figure 1 is provided below. The Figure has also been replaced in the published article.

*To whom correspondence should be addressed. Tel: +1 713 441 5252; Fax: +1 713 441 7295; Email: mkumaraswami@houstonmethodist.org

© The Author(s) 2019. Published by Oxford University Press on behalf of Nucleic Acids Research.
This is an Open Access article distributed under the terms of the Creative Commons Attribution Non-Commercial License (http://creativecommons.org/licenses/by-nc/4.0/), which permits non-commercial re-use, distribution, and reproduction in any medium, provided the original work is properly cited. For commercial re-use, please contact journals.permissions@oup.com

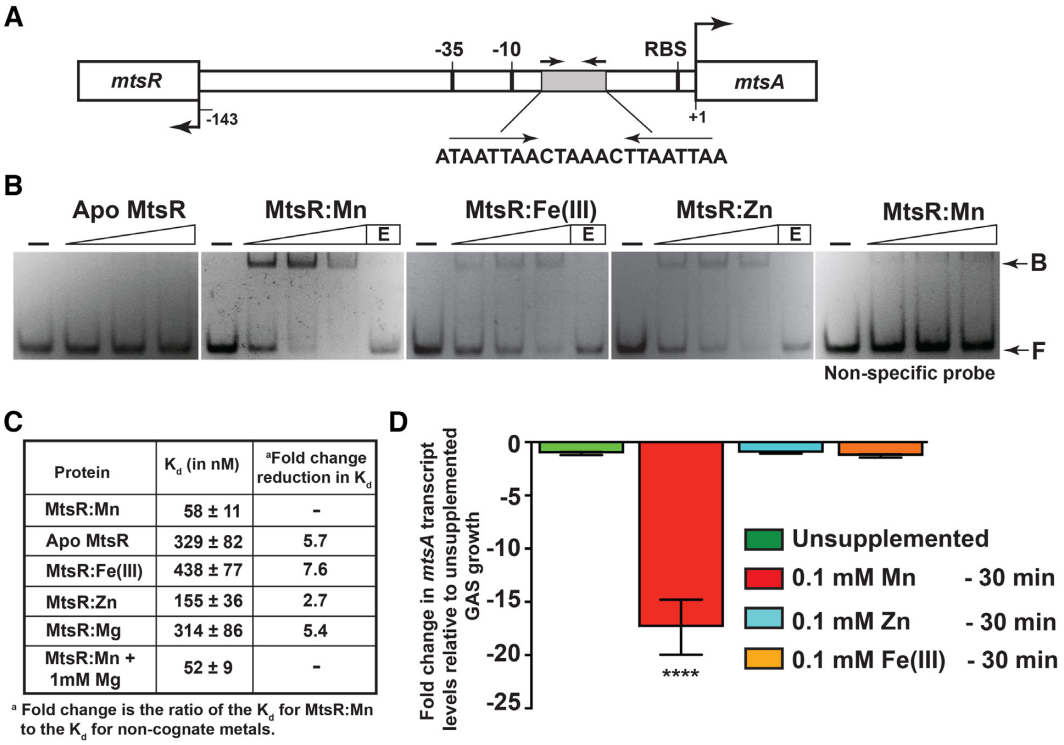

Figure 1. Transcription regulation of *mtsA* by MtsR is Mn dependent. (**A**) Genetic organization of the *mtsR* and *mtsA* gene region in GAS genome. The *mtsR* and *mtsA* genes are divergently transcribed. Numbers below the line indicate the nucleotide positions relative to the first nucleotide of the mtsA start codon. The putative –10 and –35 hexamers of the *mtsA* promoter and an inferred ribosomal-binding site (RBS) located upstream of *mtsA*labeled are marked and labeled above the line. The predicted MtsR-binding site in the *mtsA* promoter is marked by a shaded box and the pseudoinverted repeat within the MtsR-binding site is marked by arrows. The nucleotide sequence of the MtsR-binding site used in the electrophoretic mobility shift (EMSA) and fluorescent polarization (FP) analyses is shown. (**B**) The interactions between MtsR and the operator sequences in *mtsA* promoter as assessed by EMSA. Increasing concentrations (0, 100, 200 and 300 nM MtsR) of non-metallated (apo MtsR) or MtsR bound with different metals were incubated with oligoduplex containing the *mtsA* promoter sequences. The reaction mixtures were resolved on a 10% native-PAGE and the PAGE running buffer does not contain EDTA. Each indicated metal was added at a final concentration of 300 μM. The positions of free (F) and MtsR-bound (B) probes are labeled and indicated by arrows. E; indicates addition of metal chelator EDTA to the reaction mixture. (**C**) MtsR-*mts* motif binding constants assessed in the absence or presence of the indicated metals as assessed by fluorescent polarization (FP) assay. The apparent binding constants with standard deviations are shown. Each indicated metal was added at a final concentration of 10 μM and Mg was added at a final concentration of 1 mM. (**D**) Wild-type (WT) GAS was grown in THY medium to mid-exponential phase of growth (A_{600} 1.0) and incubated with 100 μM of the indicated metals for 30 min. Transcript level of *mtsA* was measured by qRT-PCR. Three biological replicates were performed and analyzed in triplicate. Data graphed are means ± standard deviation. Average values for unsupplemented samples were used as a reference and fold changes in transcript levels of the indicated samples relative to reference are shown. Statistical significance was determined by *t* test. **** indicates statistical significance with $P < 0.0001$ for the indicated samples compared to reference growth.