



## Reply to Mortazavi, "Acquired Antibiotic Resistance in Escherichia coli Exposed to Simulated Microgravity: Possible Role of Other Space Stressors and Adaptive Responses"

Madhan R. Tirumalai, DGeorge E. Fox

<sup>a</sup>Department of Biology and Biochemistry, University of Houston, Houston, Texas, USA

KEYWORDS Escherichia coli, antibiotic resistance, microgravity

e thank Dr. Mortazavi for pointing out the role of radiation as an important factor under microgravity conditions (1) while referring to our paper (2). We agree with Dr. Mortazavi that radiation is an important component when it comes to assessment of bacterial response to the space environment. We have previously published papers on radiation-resistant spore-producing Bacillus strains isolated from spacecraft cleanroom facilities that are of planetary protection concern (3-7). In doing this, we have observed that the bacterial adaptive response can be of two kinds: changes in gene expression in response to the environment and changes which are genomic. Overall, we agree that studies on microbial adaptation examining the long-term effects of simulated microgravity in combination with radiation would be significant. If done using simulated microgravity, such studies would avoid the significant cost of performing similar studies on bacteria in space

In fact, we have already attempted to do this with the Escherichia coli MG1655 strain exposed to both simulated microgravity and radiation. To accomplish this, a model radiation environment was produced using radioactive cobalt wires (Co-60) suspended equidistant from the center of an incubator emitting gamma rays. This work was done in collaboration with Dr. John Ford and then-student Emma Howard Schulze at the Department of Nuclear Engineering at Texas A & M University in College Station. Unfortunately, we could not complete the study due to logistical constraints that required the experiment to be terminated after only 200 generations.

Resequencing the genome of the E. coli MG1655 strain exposed to 200 generations of both microgravity and radiation resulted in the identification of only two mutations in known genes that could be related to the radiation exposure. The first gene, recD, promotes homologous recombination in the repair of double-strand DNA breaks and during bacterial conjugation, as part of the alternative end-joining (A-EJ) system (8, 9). The second gene, mrdB, encodes an inner membrane protein that is involved in the synthesis of a cylindrical peptidoglycan which plays a role in cell shape, elongation, and division (10, 11). Both these genes are also implicated in antibiotic resistance (12, 13). However, both the mutations resulted in changes in the domains of the respective protein products that do not affect their functions. Given the limited scope of the study, the results obtained are insufficient to derive a comprehensive picture.

We once again thank Dr. Mortazavi for his comments. We do recognize that such studies should be extended toward further long-term exposure to both radiation and simulated microgravity and that doing so is essential to obtain a more holistic systemslevel picture of microbial adaptation to space conditions.

Citation Tirumalai MR, Fox GE. 2019. Reply to Mortazavi, "Acquired antibiotic resistance in Escherichia coli exposed to simulated microgravity: possible role of other space stressors and adaptive responses." mBio 10:e00391-19. https://doi.org/10.1128/mBio

Copyright © 2019 Tirumalai and Fox. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license.

Address correspondence to George E. Fox,

This is a response to a letter by S. M. J. Mortazavi https://doi.org/10.1128/mBio.00165-19.

Published 26 March 2019



## **REFERENCES**

- Mortazavi SMJ. 2019. Acquired antibiotic resistance in Escherichia coli exposed to simulated microgravity: possible role of other space stressors and adaptive responses. mBio 10:e00165-19. https://doi.org/10.1128/ mBio.00165-19.
- Tirumalai MR, Karouia F, Tran Q, Stepanov VG, Bruce RJ, Ott CM, Pierson DL, Fox GE. 2019. Evaluation of acquired antibiotic resistance in Escherichia coli exposed to long-term low-shear modeled microgravity and background antibiotic exposure. mBio 10:e02637-18. https://doi.org/10.1128/mBio.02637-18.
- Gioia J, Yerrapragada S, Qin X, Jiang H, Igboeli OC, Muzny D, Dugan-Rocha S, Ding Y, Hawes A, Liu W, Perez L, Kovar C, Dinh H, Lee S, Nazareth L, Blyth P, Holder M, Buhay C, Tirumalai MR, Liu Y, Dasgupta I, Bokhetache L, Fujita M, Karouia F, Eswara Moorthy P, Siefert J, Uzman A, Buzumbo P, Verma A, Zwiya H, McWilliams BD, Olowu A, Clinkenbeard KD, Newcombe D, Golebiewski L, Petrosino JF, Nicholson WL, Fox GE, Venkateswaran K, Highlander SK, Weinstock GM. 2007. Paradoxical DNA repair and peroxide resistance gene conservation in Bacillus pumilus SAFR-032. PLoS One 2:e928. https://doi.org/10.1371/journal.pone.0000928.
- Tirumalai MR, Rastogi R, Zamani N, O'Bryant Williams E, Allen S, Diouf F, Kwende S, Weinstock GM, Venkateswaran KJ, Fox GE. 2013. Candidate genes that may be responsible for the unusual resistances exhibited by Bacillus pumilus SAFR-032 spores. PLoS One 8:e66012. https://doi.org/ 10.1371/journal.pone.0066012.
- Tirumalai MR, Fox GE. 2013. An ICEBs1-like element may be associated with the extreme radiation and desiccation resistance of Bacillus pumilus SAFR-032 spores. Extremophiles 17:767–774. https://doi.org/10.1007/ s00792-013-0559-z.
- Stepanov VG, Tirumalai MR, Montazari S, Checinska A, Venkateswaran K, Fox GE. 2016. Bacillus pumilus SAFR-032 genome revisited: sequence update and re-annotation. PLoS One 11:e0157331. https://doi.org/10 .1371/journal.pone.0157331.

- Tirumalai MR, Stepanov VG, Wunsche A, Montazari S, Gonzalez RO, Venkateswaran K, Fox GE. 2018. Bacillus safensis FO-36b and Bacillus pumilus SAFR-032: a whole genome comparison of two spacecraft assembly facility isolates. BMC Microbiol 18:57. https://doi.org/10.1186/ s12866-018-1191-y.
- Amundsen SK, Taylor AF, Chaudhury AM, Smith GR. 1986. recD: the gene for an essential third subunit of exonuclease V. Proc Natl Acad Sci U S A 83:5558–5562. https://doi.org/10.1073/pnas.83.15.5558.
- Chayot R, Montagne B, Mazel D, Ricchetti M. 2010. An end-joining repair mechanism in Escherichia coli. Proc Natl Acad Sci U S A 107:2141–2146. https://doi.org/10.1073/pnas.0906355107.
- Meeske AJ, Riley EP, Robins WP, Uehara T, Mekalanos JJ, Kahne D, Walker S, Kruse AC, Bernhardt TG, Rudner DZ. 2016. SEDS proteins are a widespread family of bacterial cell wall polymerases. Nature 537:634–638. https://doi .org/10.1038/nature19331.
- Cho H, Wivagg CN, Kapoor M, Barry Z, Rohs PD, Suh H, Marto JA, Garner EC, Bernhardt TG. 2016. Bacterial cell wall biogenesis is mediated by SEDS and PBP polymerase families functioning semi-autonomously. Nat Microbiol 2016:16172. https://doi.org/10.1038/nmicrobiol.2016.172.
- Tamaki S, Matsuzawa H, Matsuhashi M. 1980. Cluster of mrdA and mrdB genes responsible for the rod shape and mecillinam sensitivity of Escherichia coli. J Bacteriol 141:52–57.
- Wilkinson M, Troman L, Wan Nur Ismah WA, Chaban Y, Avison MB, Dillingham MS, Wigley DB. 2016. Structural basis for the inhibition of RecBCD by Gam and its synergistic antibacterial effect with quinolones. Elife 5:e22963. https://doi.org/10.7554/eLife.22963.
- Tirumalai MR, Karouia F, Tran Q, Stepanov VG, Bruce RJ, Ott CM, Pierson DL, Fox GE. 2017. The adaptation of Escherichia coli cells grown in simulated microgravity for an extended period is both phenotypic and genomic. Npj Microgravity 3:15. https://doi.org/10.1038/s41526-017-0020-1.