Chemostat modeling of Escherichia coli persistence in conventionalized mono-associated and streptomycin-treated mice - DTU Orbit (11/01/2019)

**Chemostat modeling of Escherichia coli persistence in conventionalized mono-associated and streptomycin-treated mice**

We have previously shown that Escherichia coli BJ4 has similar doubling time in mice that are mono-associated (having only the inoculated E. coli BJ4) or streptomycin-treated (having mainly gram-positive bacteria plus the inoculated E. coli BJ4). We also showed that when the mice were conventionalized (fed cecum homogenate from conventional mice or ones with a complete microbial flora), the introduction of complete flora in both cases increased the in vivo doubling time, while decreasing the colony counts in fecal samples. To determine whether the increase in doubling time could explain the decrease in colony counts, we analyzed our previous results by a chemostat model. The analysis shows that the increasing doubling time alone is sufficient to explain the decrease in colony counts in mono-associated mice, but not in the streptomycin-treated mice. The observed decreasing rate in colony counts in streptomycin-treated mice is slower than predicted. Furthermore, whereas the model predicted a decrease to extinction in both mice, the E. coli persist at a frequency 10-80 times higher in streptomycin-treated mice than in mono-associated mice. Thus, while a chemostat model is able to explain some of the population dynamics of intestinal bacteria in mice, additional factors not included in the model are stabilizing the system. Because we find that E. coli declines more slowly and to a higher stabilization frequency in streptomycin-treated mice, which have a more diverse flora before conventionalization, we take these results to suggest that the persistence of E. coli populations is promoted by species diversity. We propose that a mechanism for the persistence may be the presence of new E. coli niches created by keystone species in the more diverse flora.

**General information**

State: Published  
Organisations: Center for Biomedical Microbiology, Department of Systems Biology  
Contributors: Rang, C., Midtvedt, T., Molin, S., Chao, L.  
Pages: 86-90  
Publication date: 2001  
Peer-reviewed: Yes

**Publication information**  
Journal: Canadian Journal of Microbiology  
Volume: 47  
Issue number: 1  
ISSN (Print): 0008-4166  
Ratings:  
Web of Science (2019): Indexed yes  
BFI (2018): BFI-level 1  
Web of Science (2018): Indexed yes  
BFI (2017): BFI-level 1  
Scopus rating (2017): CiteScore 1.52 SJR 0.579 SNIP 0.561  
Web of Science (2017): Impact factor 1.243  
Web of Science (2017): Indexed yes  
BFI (2016): BFI-level 1  
Scopus rating (2016): CiteScore 1.48 SJR 0.551 SNIP 0.6  
Web of Science (2016): Impact factor 1.462  
BFI (2015): BFI-level 1  
Scopus rating (2015): CiteScore 1.27 SJR 0.545 SNIP 0.585  
Web of Science (2015): Impact factor 1.335  
BFI (2014): BFI-level 1  
Scopus rating (2014): CiteScore 1.31 SJR 0.554 SNIP 0.575  
Web of Science (2014): Impact factor 1.221  
Web of Science (2014): Indexed yes  
BFI (2013): BFI-level 1  
Scopus rating (2013): CiteScore 1.25 SJR 0.532 SNIP 0.541  
Web of Science (2013): Impact factor 1.182  
ISI indexed (2013): ISI indexed yes  
BFI (2012): BFI-level 1  
Scopus rating (2012): CiteScore 1.31 SJR 0.529 SNIP 0.59  
Web of Science (2012): Impact factor 1.199  
ISI indexed (2012): ISI indexed yes  
BFI (2011): BFI-level 1