# Writing Composition Exercise 06: Jargon, Acronyms, and Abbreviations

## Dr. Morgan Feeney, AY 2024-25

Avoid using jargon and too many abbreviations or acronyms – they add to the cognitive burden for your reader, and even commonly used abbreviations can have multiple meanings (for example, DNA can mean Deoxyribonucleic acid, Difco Nutrient Agar, Dynamic Network Analysis, Data Not Available, etc….). In some cases it may be necessary/preferable to use an acronym (e.g., for a word commonly repeated throughout the paper), but you should exercise caution whenever choosing to use one – and when using any new acronym/abbreviation for the first time, you should write it out in full (e.g., acyl-homoserine lactones (AHLs)).

Similarly, jargon can exclude readers who are outside of a particular field (or subfield, or group). While you might say, in casual conversation, that you “spun the cells down”, in formal academic writing it would be better to say that the cells were pelleted by centrifugation.

### Exercise A.

Read each example and consider the use of acronyms/abbreviation/jargon, evaluating whether they are necessary/unnecessary, and identify any places where the writing could be improved.

**Sample 6.1** 1

Non-spore-forming Gram-negative bacilli (NGNB) have been classified as non-fermentative Gram-negative bacilli (NFGNB) or fermentative Gram-negative bacilli (FGNB). Non-spore forming Gram-negative bacteria are heterogeneous and composed of many medical important species, of which *Pseudomonas aeruginosa*, *Acinetobacter baumannii, Klebsiella pneumoniae, Enterobacter* species, *Escherichia coli, and Enterococcus faecium are* a few among the list. Most of the above-listed bacteria are members of the dangerous small group of pathogens called the ESKAPE bugs, which stand for *Enterococcus faecium, Staphylococcus aureus, K. pneumoniae, A. baumannii, P. aeruginosa, and Enterobacter* species ([Rice, 2008](https://www.frontiersin.org/journals/antibiotics/articles/10.3389/frabi.2023.1155005/full#B42)). According to [Rice, 2008](https://www.frontiersin.org/journals/antibiotics/articles/10.3389/frabi.2023.1155005/full#B42), the ESKAPE bugs are extremely important bacteria as they account for the largest proportion of hospital-acquired infections, are more virulent, easily communicable, and develop resistance against most antibacterial drugs. The ubiquitous and intrinsic resistance characteristics of Gram-negative bacteria (GNB) to the commonly used antiseptics are responsible for their ability to occupy a wide range of hospital environments, including anesthesia equipment, sinks, intravenous fluids, and fomites, or the hands of medical staff, causing device-associated hospital infections ([Gales et al., 2001](https://www.frontiersin.org/journals/antibiotics/articles/10.3389/frabi.2023.1155005/full#B15); [Mellmann et al., 2009](https://www.frontiersin.org/journals/antibiotics/articles/10.3389/frabi.2023.1155005/full#B30); [Kakati et al., 2015](https://www.frontiersin.org/journals/antibiotics/articles/10.3389/frabi.2023.1155005/full#B21)). Another feature of GNB is their relative ease of acquiring plasmid-containing genes that encode for Extended Spectrum β-Lactam Enzymes (ESBLase) and other resistance genes that confer resistance to many other classes of antibiotics ([Brolund, 2014](https://www.frontiersin.org/journals/antibiotics/articles/10.3389/frabi.2023.1155005/full#B9)).

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| Necessary/unnecessary acronyms or jargon?  | Suggested improvements? |

**Sample 6.2.** 2

The combined-culture technique involves co-culturing actinomycetes with mycolic acid-containing bacteria (MACB); e.g., *Tsukamurella pulmonis* TP-B0596, which has been used to stimulate SM production in actinomycetes ([Onaka et al., 2011](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2024.1422977/full#B33); [Asamizu et al., 2015](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2024.1422977/full#B3); [Kato et al., 2022](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2024.1422977/full#B24)). This method yielded significant success and resulted in the isolation of 44 new SMs from 15 different actinomycetes so far ([Supplementary Table S1](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2024.1422977/full#SM1)). In a previous study, we documented the creation of a mutant library of *S. coelicolor* JCM4020 using a carbon ion (12C5+) beam to screen for mutants displaying varying levels of undecylprodigiosin (RED) production ([Yanagisawa et al., 2022](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2024.1422977/full#B57)). This approach was used to identify the genes responsible for RED production during interactions with *T. pulmonis*, which could contain a yet-unknown regulation system. Out of ~152,000 irradiated spores, we identified 86 mutants that exhibited a phenotype characterized by decreased RED production while maintaining apparent normal growth on minimal medium ([Yanagisawa et al., 2022](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2024.1422977/full#B57)). We analyzed point mutations induced by carbon-ion beam irradiation in 16 randomly selected mutants and revealed that the inactivation of genes such as *gltB* (glutamate synthase, *sco2026*), *fusA* (elongation factor G, *sco4661*), and *sarA* (a hypothetical membrane protein, *sco4069*) led to reduced RED production ([Yanagisawa et al., 2022](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2024.1422977/full#B57)). Additionally, further investigation of remaining mutants revealed that inactivation of *sco1718* (a TetR family transcriptional regulator, TFR) leads to reduced production of SMs, including RED, which is caused by overexpression of adjacent *sco1719-20* genes encoding ATP-binding cassette (ABC) transporters ([Lei et al., 2023](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2024.1422977/full#B27)). Furthermore, we also found two other TFR-ABC transporter gene sets (*sco4358-4360* and *sco5384-5382*) in the genome that can affect SM production ([Lei et al., 2023](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2024.1422977/full#B27)). In this study, we used a forward genetics approach to further investigate the acquired mutants and identified *ccr1* (*sco1842*) as the causative factor behind the observed reduction in RED production. We report the impact of *ccr1* on SM production in two *Streptomyces* species: *S. coelicolor* A3(2) and *S. nigrescens* HEK616.

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| Necessary/unnecessary acronyms or jargon?  | Suggested improvements? |

**Sample 6.3.** 3

In recent years, polymyxin has been used as a last-resort therapy for carbapenem-resistant bacterial infections. The emergence of heteroresistance (HR) to polymyxin hampers the efficacy of polymyxin treatment by amplifying resistant subpopulation. However, the mechanisms behind polymyxin HR remain unclear. Small noncoding RNAs (sRNAs) play an important role in regulating drug resistance. The purpose of this study was to investigate the effects and mechanisms of sRNA on polymyxin B (PB)-HR in carbapenem-resistant *Klebsiella pneumoniae*. In this study, a novel sRNA PhaS was identified by transcriptome sequencing. PhaS expression was elevated in the PB heteroresistant subpopulation. Overexpression and deletion of PhaS were constructed in three carbapenem-resistant *K. pneumoniae*strains. Population analysis profiling, growth curve, and time-killing curve analysis showed that PhaS enhanced PB-HR. In addition, we verified that PhaS directly targeted phoP through the green fluorescent protein reporter system. PhaS promoted the expression of *phoP*, thereby encouraging the expression of downstream genes *pmrD*and*arnT*. This upregulation of *arnT* promoted the 4-amino-4-deoxyL-arabinosaccharide (L-Ara4N) modification of lipid A in PhaS overexpressing strains, thus enhancing PB-HR. Further, within the promoter region of PhaS, specific PhoP recognition sites were identified. ONPG assays and RT-qPCR analysis confirmed that PhaS expression was positively modulated by PhoP and thus up-regulated by PB stimulation. To sum up, a novel sRNA enhancing PB-HR was identified and a positive feedback regulatory pathway of sRNA-PhoP/Q was demonstrated in the study. This helps to provide a more comprehensive and clear understanding of the underlying mechanisms behind polymyxin HR in carbapenem-resistant *K. pneumoniae*.

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| Necessary/unnecessary acronyms or jargon?  | Suggested improvements? |

### Exercise B.

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Look at your introduction thus far (or any other piece of writing). Go through it, and examine your use (or lack of use) of acronyms and jargon. Consider how your writing can be improved and make the appropriate edits.

### References

1. Desalegn, Y., Bitew, A., & Adane, A. (2023). A spectrum of non-spore-forming fermentative and non-fermentative Gram-negative bacteria: multi-drug resistance, extended-spectrum beta-lactamase, and carbapenemase production. *Frontiers in Antibiotics*, *2*. <https://doi.org/10.3389/frabi.2023.1155005>
2. Lei, Y., Onaka, H., & Asamizu, S. (2024). Transcriptionally induced nucleoid-associated protein-like ccr1 in combined-culture serves as a global effector of *Streptomyces* secondary metabolism. *Frontiers in Microbiology*, *15*. https://doi.org/10.3389/fmicb.2024.1422977
3. Zhao, Z., Yang, T., Xiang, G., Zhang, S., Cai, Y., Zhong, G., Pu, J., Shen, C., Zeng, J., Chen, C., & Huang, B. (2024). A novel small RNA PhaS contributes to polymyxin B-heteroresistance in carbapenem-resistant *Klebsiella pneumoniae*. *Emerging Microbes & Infections*, *13*(1). https://doi.org/10.1080/22221751.2024.2366354