Species of the soft rot Pectobacteriaceae are an important group of plant pathogens and are known to co-infect potato tubers. The authors tried to get insight into the dynamics of co-infection by creating synthetic communities made of 6 strains (3 strains from two species each). They inoculated liquid cultures and potatoes and observed the outcome of the co-infections using amplicon sequencing (of the gapA gene), bacterial population sizes, and symptoms on potato tubers. The obtained results suggest that there is competition among strains of the same species, there is cooperation through trophic interaction, and there is toxicity interference.

Overall, the manuscript describes a clear hypothesis and a well-designed experiment to answer it and results are described well and discussed objectively. I have no major concerns about the study but I list comments that I hope can improve the manuscript. Also, there are minor English language issues throughout the manuscript that need to be fixed since they distract from the science.

L107 The authors should explain here or at the beginning of the results section the rationale for creating synthetic communities of 6 strains with 3 strains per species. Moreover, the authors need to explain how strains were chosen and what is known about the strains. Some strains could be distinguished from each other using gapA sequencing but others could not. This suggests that some strains are closely related (possibly identical) to each other while other strains in other species are more divergent. Do the authors have a phylogenetic tree of the strains that could be shown as a Supplementary Figure? How these strains are related to each other could be an important factor contributing to the outcome of the entire experiment so the authors definitely need to provide more information about the chosen strains.

L327 That is too bad that a CFU to OD analysis was not made ahead of time in order to have a ratio closer to 50%. Also, did the authors make sure that the ration of species based on cfu corresponded to the ratio based on gapA sequence counts? It is unlikely but it is possible that there would be some amplification/sequence bias.

L334 In the extreme case where P. aquaticum represented 79% to start with, going to 90% would be really minimal. Would it be helpful to represent the data as a change in ration instead or besides a percentage. In other words: show how species changed in ratio in the different synthetic communities so you could conclude independently of the absolute percentages which species outcompeted the other species in which communities.

L373 Consider changing "coexistence between the two species twice was more frequent" to "the frequency of co-existence was twice as high in TSB medium compared to withing potato tubers:

L385-386 Is it known which cell wall degrading enzymes are encoded in the genome of P. aquaticum compared to the other species? In other words, is the genetic basis of this phenotype known?

L524 either "bacterial community" or "microbial community"

L459 instead of saying "more numerous" maybe say "had a higher percentage" since it is the percentage that is reported and not the absolute CFUs.

L468 Since in L467, you point out a single strain, I expected here to see the specific strain of P. parmentieri listed instead of just the species.

L493 should it be BRASI 3230 since it says CFBP3230?