

	Yes	Can be improved
Does the introduction provide sufficient background and include all relevant references?	(x)	()
Are all the cited references relevant to the research?	(x)	()
Is the research design appropriate?	()	(x)
Are the methods adequately described?	()	()
Are the results clearly presented?	()	()
Are the conclusions supported by the results?	(x)	()

Comments and Suggestions for Authors

This article described the isolation of PHA storing MMC from cheese whey using a SBR-based domestication method. PHA production is a hot topic thus this article would attract interests from readers.

1. The text in section 2.3 and 2.4 are in italic. The text has been changed.
2. The analytical methods in section 2.3 should be briefly described instead of simply citing references. Details of the analytical method have been briefly provided, as suggested.
3. Fig 1 showed the SBR cycle on day 22, which should be described in the figure legend. The cycle number should also be explained. The information has already been included in the figure legend following the recommendation.
4. The font in the legend of Fig 3, which was wrongly labelled as Fig 1, should be modified. Changes in the figure legend were done.
5. What does X/S stand for? It means the growth yield of the biomass. In PHA selecting reactors is a quite important parameter as indicates the amount of substrate that is being directed towards cell growth. It can be considered opposite to storage yield, the higher the amount of storage yield, the lesser the growth and vice versa. Conclusively, the performance of the selection stage is optimized when the biomass converts more substrate to PHA storage and less substrate to biomass growth
6. Figure 4, 500bp. Why there were bands in lane B and C not analyzed? The representative species should be labelled with the bands on the figure. According to the comment, changes were done, and a modified figure is now included in the manuscript.

Regarding the question, as it has been explained in the text (lines 331 and 332) all the bands of the gel (no exceptions) were analyzed. However, at the sequencing stage, few bands turned out to be into a no concluding result, i.e., a proper sequence to be uploaded into the NCBI database and, therefore, there is a lack of information for that specific bands. That is why there are missing bands not included in the figure and mentioned in the text.

7. How the results shown in line 405-410 obtained? How were the fitted curve shown in Fig 5 obtained? How were the kinetics parameters determined? The abovementioned results were obtained through the calculation of substrate uptake rate ($-q_s$) and PHA production rate (q_{PHA}) at every pulse for each of the PHA accumulation batch tests. By these calculations we were able to see that, at the beginning of the PHA accumulation tests, $-q_s$ and q_{PHA} were higher, while at the end, the rate of both was lower.

The curves are basically a tendency line to allow readers to see clearly how the PHA storage evolve along the PHA accumulations tests. They were done using one of the tools of MS Office. They are not based on any mathematical model.

8. Did the authors try to isolate the PHA producing strains based on the DGGE result? It would be interesting to understand the diversity of the MMC and the contribution to PHA production, which could be discussed in the article.

Unfortunately, we did not perform the isolation of the PHA producing strain identified through the DGGE for this work. Although I completely agree with Reviewer 2 that it will enhance the relevance of the present work, the topic is currently being under consideration in our research group for future experiments. It would be nice, for example, for the determination of the maximum potential of each of the strains to accumulate PHA. Additionally, it will also allow to have a deeper knowledge about how the different strains will behave in different matrixes (apart from acidified cheese whey) and different VFA profiles, Regarding the last point it will be interesting to investigate their ability to use longer chain fatty acids such as hexanoic acid to synthesize hydroxyhexanoate (HH), which is a hot topic right now.