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Corrigendum: Complete genome sequence of biocontrol strain *Bacillus velezensis* YC89 and its biocontrol potential against sugarcane red rot

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KEYWORDS

Bacillus velezensis, biocontrol, sugarcane red rot, genome sequencing, biocontrol mechanism

A corrigendum on

Complete genome sequence of biocontrol strain *Bacillus velezensis* YC89 and its biocontrol potential against sugarcane red rot

by Xie, L., Liu, L., Luo, Y., Rao, X., Di, Y., Liu, H., Qian, Z., Shen, Q., He, L., and Li, F. (2023). *Front. Microbiol.* 14:1180474. doi: 10.3389/fmicb.2023.1180474

In the published article, there was an error regarding the affiliations for Lufeng Liu. As well as having affiliation 2, they should also have “¹ College of Agronomy and Biotechnology, Yunnan Agricultural University, Kunming, China” and “³ Sugarcane Research Institute, Yunnan Agricultural University, Kunming, China.”

In the published article, there was an error regarding the affiliations for Yining Di. As well as having affiliations 2 and 3, they should also have “¹ College of Agronomy and Biotechnology, Yunnan Agricultural University, Kunming, China.”

In the published article, there was an error regarding the affiliations for Lilian He. As well as having affiliation 1, they should also have “³ Sugarcane Research Institute, Yunnan Agricultural University, Kunming, China.”

In the published article, there was an error regarding the affiliations for Fusheng Li. As well as having affiliation 1, they should also have “³ Sugarcane Research Institute, Yunnan Agricultural University, Kunming, China.”

A correction has been made to **Results**, “3.1. Genomic features and annotation of *Bacillus velezensis* YC89”, paragraph two. The sentence previously stated:

“Among these pathways, the most represented pathways included carbohydrate metabolism (242 genes, 6.52% of all CDS), followed by amino acid metabolism, and metabolism of cofactors and vitamin pathways (**Supplementary Figure S3**).”

The corrected sentence appears below:

“Among these pathways, the most represented pathways included carbohydrate metabolism (242 genes, 6.52% of all CDS), followed by amino acid metabolism, and metabolism of cofactors and vitamin pathways (**Supplementary Figure S2**).”

A correction has been made to **Results**, “3.2. Identification of strain YC89”, paragraph one. The sentence previously stated:

“These results indicate that YC89 is closely related to *B. velezensis* FZB42 and *B. amyloliquefaciens* 6B (**Supplementary Figure S3**). For an in-depth analysis of the taxonomic status of YC89 strain, a genomewide phylogenomic tree was constructed. The results revealed that strain YC89 formed a close genetic relationship with strain *B. velezensis* GS-1 (**Supplementary Figure S4**).”

The corrected sentence appears below:

“These results indicate that YC89 is closely related to *B. velezensis* FZB42 and *B. amyloliquefaciens* 6B (**Supplementary Figure S3A**). For an in-depth analysis of the taxonomic status of YC89 strain, a genome-wide phylogenomic tree was constructed. The results revealed that strain YC89 formed a close genetic relationship with strain *B. velezensis* GS-1 (**Supplementary Figure S3B**).”

A correction has been made to **Results**, “3.8.2. Evaluation of *Bacillus velezensis* YC89 for biocontrol potential and growth promotion under greenhouse conditions”, paragraph one. The sentence previously stated:

“Collectively, the potted results indicated that the YC89 strain could control the red rot disease of sugarcane and promote the growth of sugarcane plants (**Supplementary Figure S5**).”

The corrected sentence appears below:

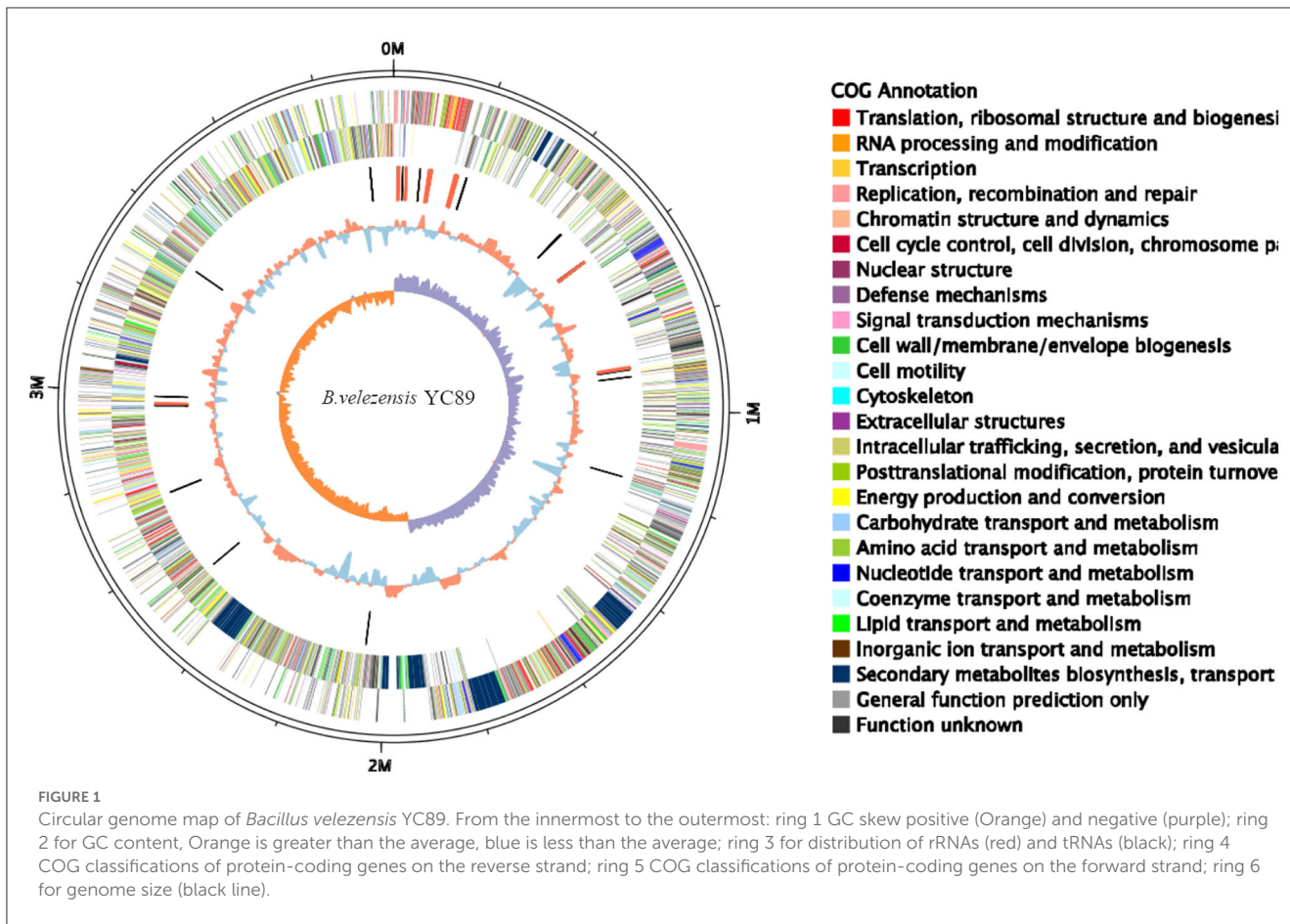
“Collectively, the potted results indicated that the YC89 strain could control the red rot disease of sugarcane and promote the growth of sugarcane plants (**Supplementary Figure S4**).”

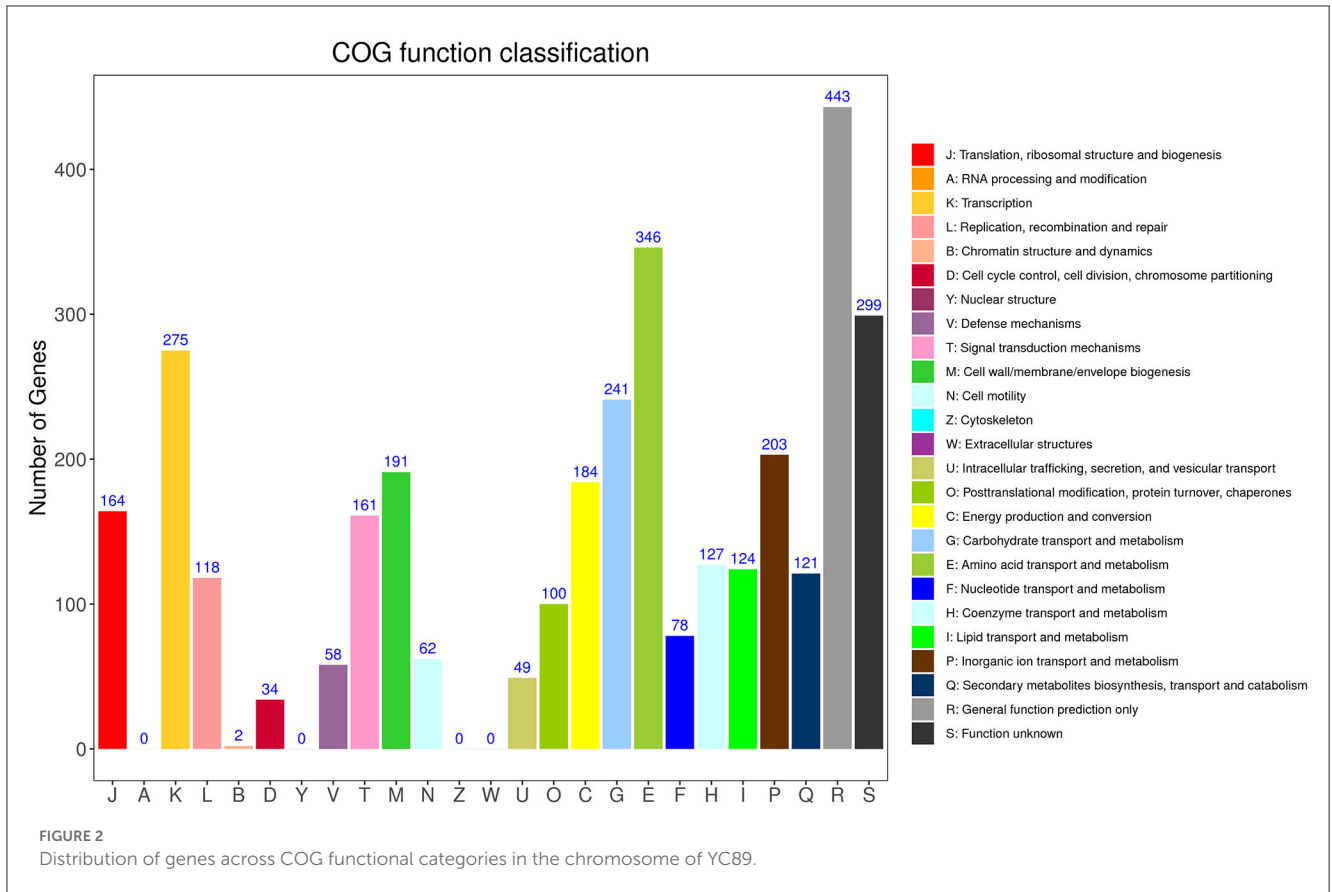
In the published article, there were errors in **Figures 1–6** as published. The order of images was incorrect, such that the captions appeared alongside the wrong images. The corrected **Figures 1–6** and their captions appear below.

The authors apologize for these errors and state that they do not change the scientific conclusions of the article in any way. The original article has been updated.

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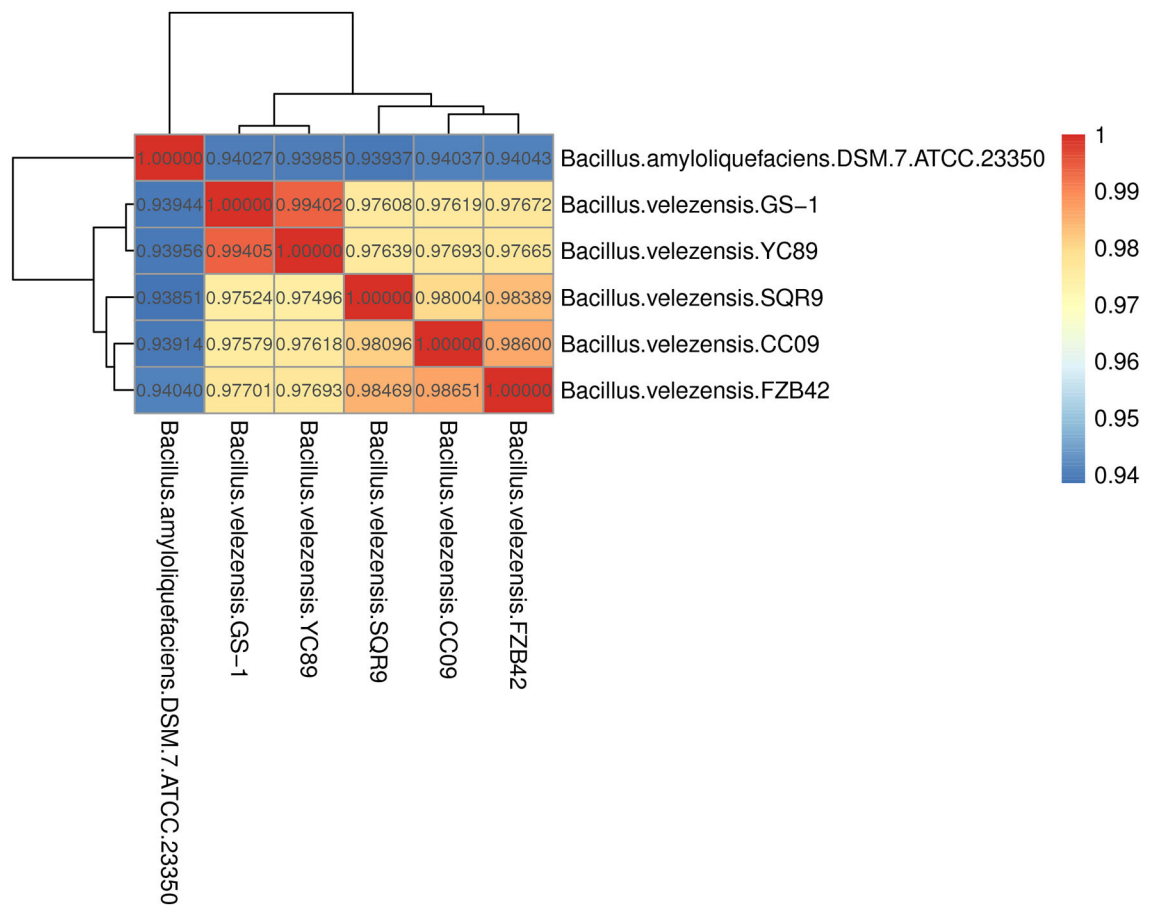
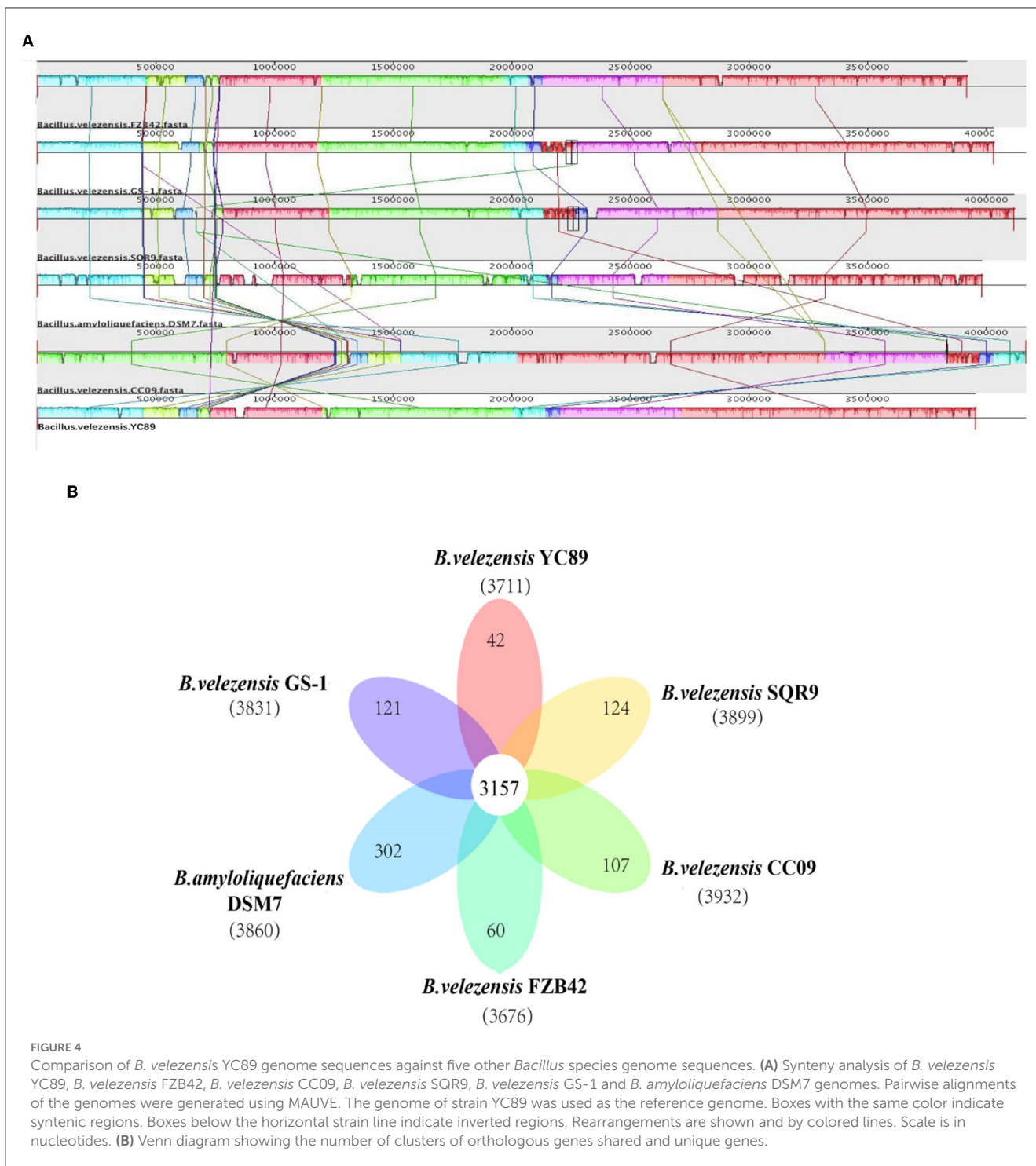
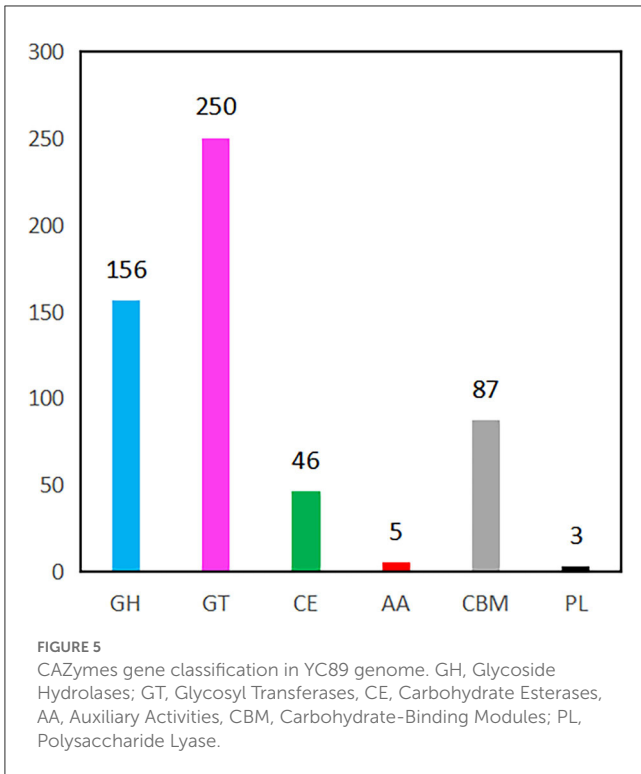


FIGURE 3
Heatmap of pairwise average nucleotide identity (ANI) values for whole genomes of YC89 and five other *Bacillus* species.





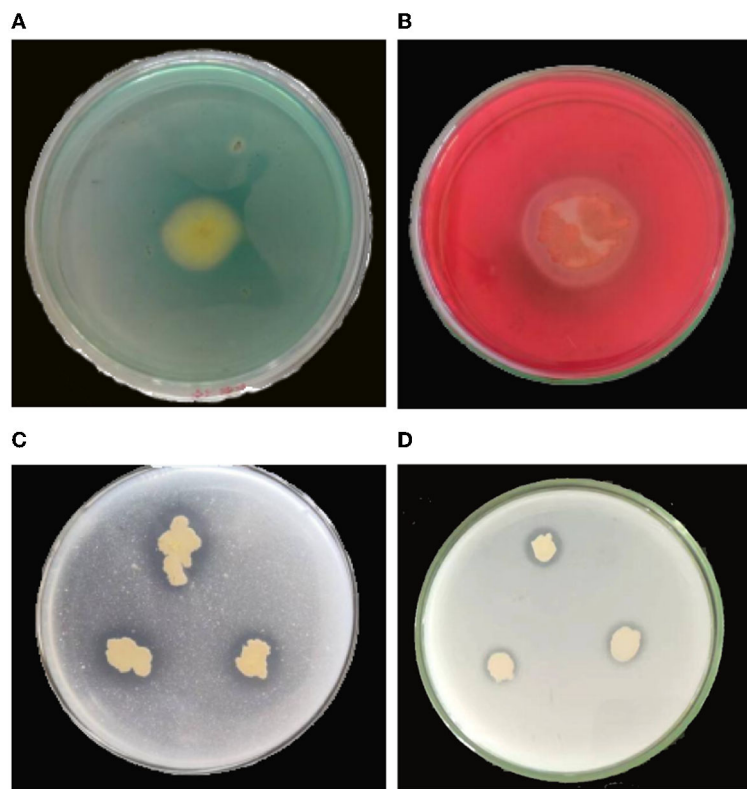


FIGURE 6
Determination of biological activity of *B. velezensis* YC89. (A): siderophore, (B): cellulase, (C): Monkina, (D): NBRIP.