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On-Site Trial Study of Denitrification to Suppress Sulfate-Reducing Bacteria (SRB) in Polymer Flooding Wastewater

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Abstract: Sulfate-reducing bacteria (SRB) is a common group of harmful bacteria in oilfield production, capable of reducing oxidized sulfur compounds such as sulfates (SO_4^{2-}, SO_3^{2-}) to sulfide ions using various organic materials including petroleum and natural gas as carbon sources. This metabolic process by SRB poses significant hazards to oilfield operations: SRB-induced corrosion by removing hydrogen ions from metal cathodes; safety risks due to the production of hydrogen sulfide; and a decrease in polymer viscosity in polymer flooding oilfields, affecting the effectiveness of polymer flooding. The current effective method to mitigate the hazards of SRB is biological suppression through the introduction or activation of nitrate-reducing bacteria (NRB), leveraging inter-species competition. This paper conducted an on-site trial at a polymer flooding station in Shengli Oilfield, achieving satisfactory results.

Keywords: Sulfate-reducing Bacteria; Nitrate-Reducing Bacteria; Biological Suppression; On-site trial.

1. On-Site Trial Process

The trial process is shown in Figure 1. An anti-nitrification suppression device for SRB was added in front of the existing water injection station buffer tank. By introducing functional bacterial solutions and biological suppressants, SRB was suppressed while simultaneously eliminating sulfides and increasing polymer viscosity.

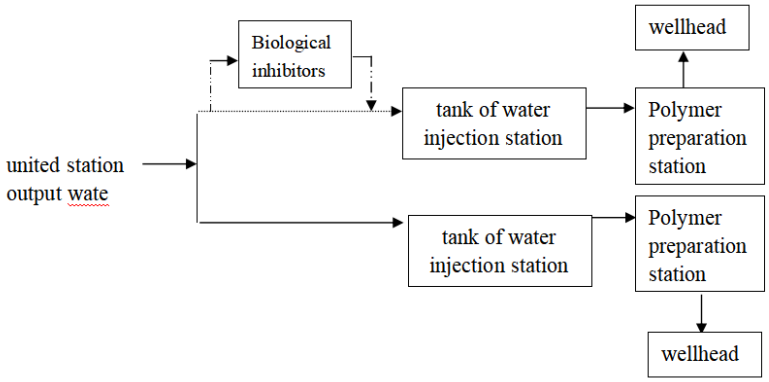


Fig 1. Flow chart of biological inhibition on SRB for polymer wastewater

2. Changes in Community Structure After On-Site Implementation

2.1. Microbial Community Diversity

Diversity analysis was conducted on samples taken from the output water of the joint station, waste water before and after anti-nitrification suppression of SRB. The results are shown in Table 1. From the joint station output to the water injection station, bacterial diversity increased, and after anti-nitrification suppression of SRB, the diversity index decreased. This indicates that after treatment by the joint station's wastewater treatment system and during transportation to the injection station, due to environmental changes (various chemicals added during wastewater treatment, changes in pH, temperature, etc.) and contamination along the way, microbial species became more abundant. However, the anti-nitrification suppression of SRB, due to the addition of suppressants, selectively activated nitrate-reducing bacteria in the wastewater. During the growth and reproduction process of NRB, through competition for nutrients, intermediate product inhibition, and alteration of the system's oxidation-reduction potential (ORP), some microorganisms were inhibited, leading to a decrease in microbial diversity [1-3].

Table 1. The variation of microbial diversity index before and after denitrification inhibition

sample	sobs	chao	ace	shannon	simpson
Outlet water	336	344.611111	351.609108	2.749799	0.134692
Before inhibition	364	369.571429	377.507746	3.007974	0.101377
After inhibition	251	263.857143	272.595211	2.283789	0.173195

To further verify the changes in microbial community structure before and after biological suppression of SRB, a Venn diagram was used to analyze the overlap of OTUs among samples. A total of 951 OTUs were identified across three samples, with 207 OTUs common to all three samples. There were 291 OTUs shared between the external input water and the pre-suppression sample, while the post-suppression sample shared 221 OTUs with the pre-suppression sample and 220 OTUs with the external input water. This indicates that after the addition of NO_3^- for denitrification to suppress SRB, the nitrate-reducing bacteria in the wastewater were activated, leading to a significant change in community structure.

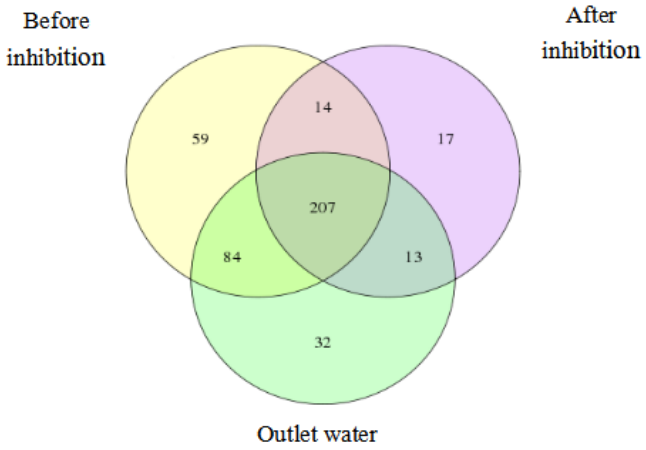


Fig 2. Venn diagram of samples OTU before and after denitrification inhibition

Further analysis of the microbial community structure was conducted using Principal Component Analysis (PCA), as shown in Fig. 3. The microbial community structure changed significantly after denitrification suppression of SRB, with the pre- and post-suppression samples clearly separated along the first axis (PC1), which explained 90.8% of the variance. The microbial community structure also changed during the transportation process from the joint station to the injection station, showing a 9.2% difference along the second axis (PC2) [4].

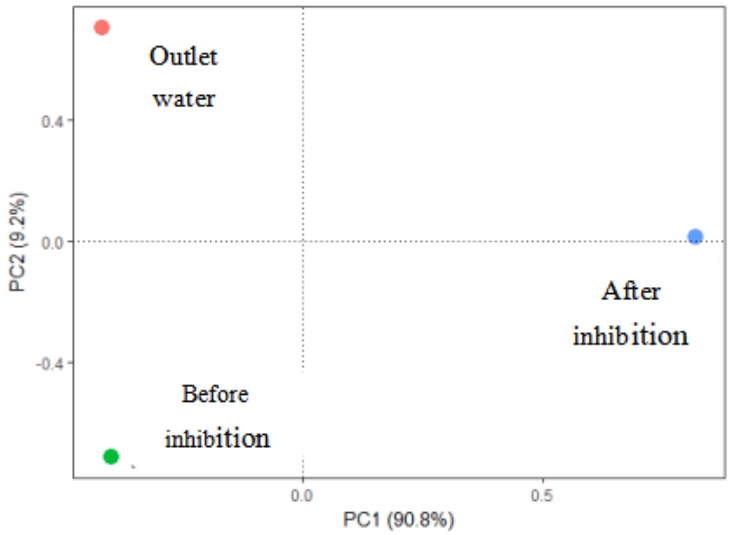


Fig 3. PCA of microbial community

The DNA extracted from the external input water, pre-suppression, and post-suppression wastewater samples was sent to BGI Gene Company for Illumina high-throughput sequencing. The corresponding bioinformatics analysis of the community structure changes is shown in Fig. 4.

From the community structure analysis, it is evident that the dominant bacteria in the external input water and pre-suppression wastewater were Desulfovibrio, Desulfotomaculum, and Geobacter species with sulfate-reducing functions, with an increase in abundance from the joint station to the injection station. The samples also detected a certain abundance of Pseudomonas (a type of Pseudomonad), Hydrogenophilus, and Flexistipes. After denitrification suppression, the dominant bacteria became Chelatococcus (23.3%), Thauera (16.0%), and Marinobacter (3.5%), which have denitrification functions. The addition of the regulator increased the competitive advantage of the denitrifying bacteria and gradually replaced SRB as the dominant bacterial group. It was also found that the abundance of Hydrogenophilus, Flexistipes, and Pseudomonas decreased, indicating that the addition of NO3- activated the denitrifying bacteria in the wastewater, affecting the activity of microorganisms using petroleum hydrocarbons as a carbon source [5,6].

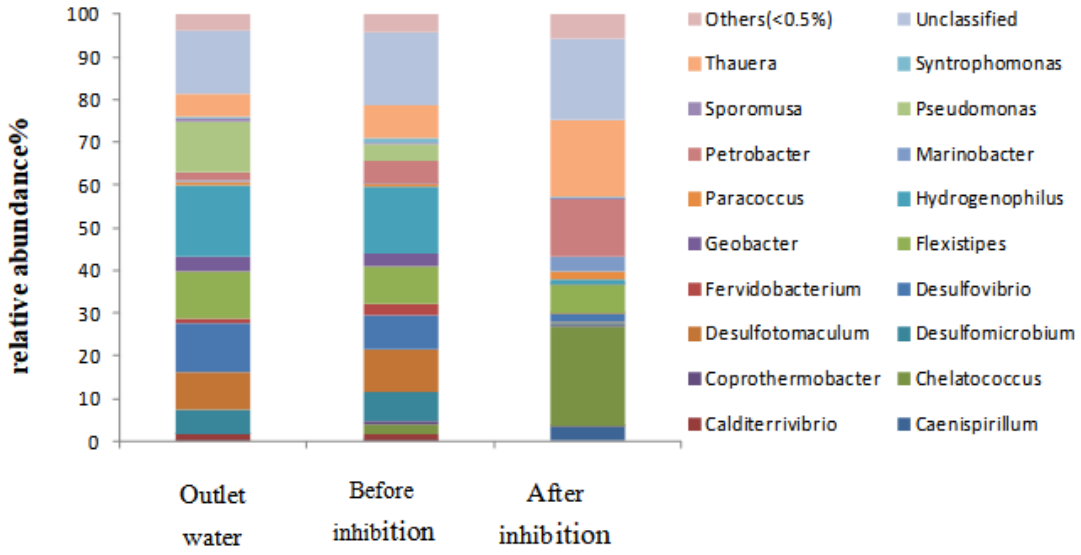


Fig 4. The bacterial communities of polymer station waste water before and after denitrification inhibition

3. Functional Gene Quantitative Analysis

Fluorescence quantitative PCR technology was used to conduct quantitative detection of functional genes in the polymer flooding wastewater samples. The results are shown in Figure 5. The changes in the number of functional bacteria can be observed. Before anti-nitrification suppression of SRB, the number of nitrate-reducing bacteria in the polymer flooding wastewater was relatively low, with very little nirS gene content, while the sulfate-reducing bacteria were abundant, with dsr gene content reaching 105 copies/μL. After anti-nitrification suppression treatment, the nirS gene in the polymer flooding wastewater increased to over 108 copies/μL, and the dsr gene expression dropped to below 102 copies/μL, indicating that before anti-nitrification suppression, the sulfate-reducing reaction dominated the system, and after implementation, the nitrate-reducing reaction of nitrate-reducing bacteria had a significant inhibitory effect on the sulfate-reducing reaction.

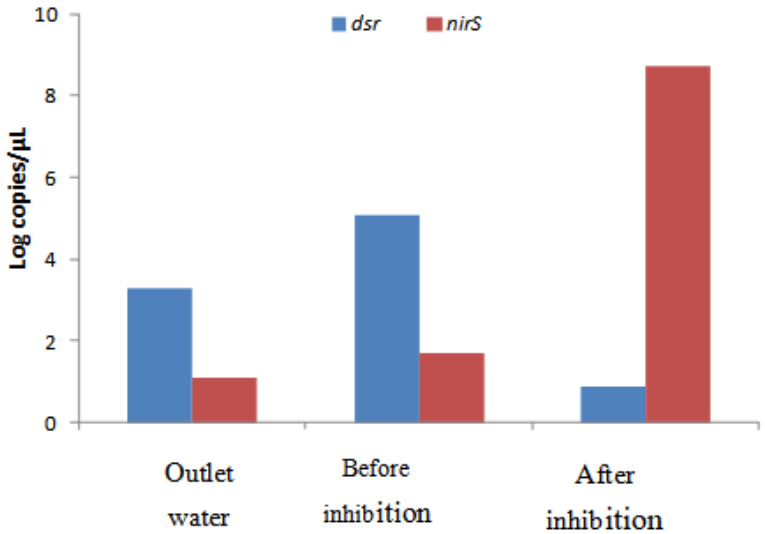


Fig 5. Comparison of functional gene copies before and after denitrification inhibition

4. Impact of Anti-Denitrification Suppression of SRB on Wastewater Viscosity

After implementing anti-nitrification suppression of SRB by adding biological regulators, the average wellhead viscosity increased from about 17 mPa.s to over 35 mPa.s. It can be seen that after the removal of sulfides, the viscosity of the polymer solution was significantly improved.

5. Oilfield Development Status

After the implementation of anti-nitrification suppression of SRB, the development status of the test area oilfield is shown in Figure 6. It can be seen from the figure that due to the significant increase in the viscosity of the polymer solution, the comprehensive water cut of the test area block decreased slightly, and the daily oil level increased.

6. Conclusion

The results of the on-site study of anti-nitrification suppression of SRB indicate that the addition of anti-nitrification suppressants, by activating NRB, not only eliminated the already produced H_2S but also suppressed the re-generation of H_2S. The concentration of H_2S in the system was reduced to below 0.2 mg/L, and the viscosity of the injection polymer well increased from 17.5 mPa.s to over 35.0 mPa.s. The problem of polymer solution viscosity loss was effectively solved, and the viscosity stability was also improved.

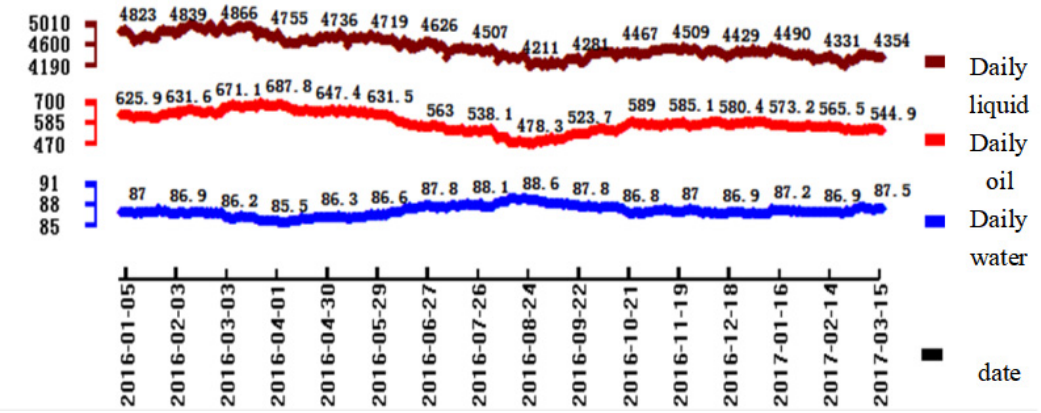


Fig 6. Development situation of test block during denitrification inhibition process

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