



GENETIC DIVERSITY OF *OENOCOCCUS OENI* STRAINS ISOLATED FROM YINCHUAN WINE REGION IN THE EAST OF HELAN MOUNTAIN, CHINA

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Abstract

Aim: This study aimed to isolate *Oenococcus oeni* in red wines from Yinchuan wine region in the East of Helan Mountain, China, and analysis their genetic diversity.

Methods and Results: *Oenococcus oeni* strains were isolated from Cabernet Sauvignon and Cabernet Gernischt wines of four representative wineries in 2016. Total 207 *O. oeni* strains were isolated and identified by species-specific PCR. Following that, 206 amplified fragment length polymorphism (AFLP) genotypes were detected, with the similarity coefficients ranging between 63% - 97%. Based on the UPGMA, two major phylogroups were deciphered at 81% similarity level. Interestingly, the strains in different phylogroups were isolated from wines of different cultivars. In addition, strains from the same winery formed a unique cluster.

Conclusions: Our results indicate there is an obvious genetic relationship of *O. oeni* with grape cultivars and their origins. Our results also support the fact that *O. oeni* is an important factor related to the wine terroir.

Significance and Impact of the Study: The Chinese wine industry has steadily grown in recent years. However, limited development and application of indigenous *O. oeni* strains would lead to homogeneity in wine quality. The outcome of this study would lay down the theoretical foundation for the development of indigenous *O. oeni* strains with regional characteristics.

Keywords: Wine, *Oenococcus oeni*, genetic diversity, AFLP

Genetic diversity of *Oenococcus oeni* strains isolated from Yinchuan wine region in the east of Helan Mountain, China



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Background

- Up to now, the studies on genetic diversity and selection promising indigenous strain of *Oenococcus oeni* (*O. oeni*) have focused on developed wine-making regions abroad, such as France, Spain, Italy, Australia, Argentina and Chile, while the research on different wine-making region of China is still scarce.

Aim

- This study aimed to isolate *O. oeni* in red wines from Yinchuan wine region in the East of Helan Mountain, China, and analysis their genetic diversity.

Method

- *O. oeni* strains were isolated from Cabernet Sauvignon and Cabernet Gernischt wines of four representative wineries in 2016 and identified by species-specific PCR.
- Amplified Fragment Length Polymorphism (AFLP) technique was used for genetic diversity analysis and phylogeny study of *O. oeni* strains.

Results

- Total 207 *O. oeni* strains were isolated and identified by species-specific PCR.

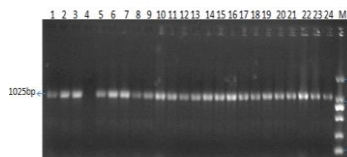


Fig. 1 Electrophoresis results of some isolated strains identified by species-specific PCR

- 206 AFLP genotypes were detected, with the similarity coefficients ranging between 63% - 97%.

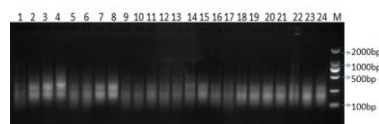


Fig. 2 Electrophoresis photograph of preamplification from some isolated strains

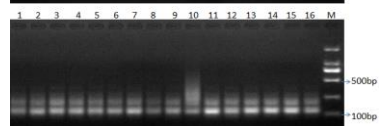
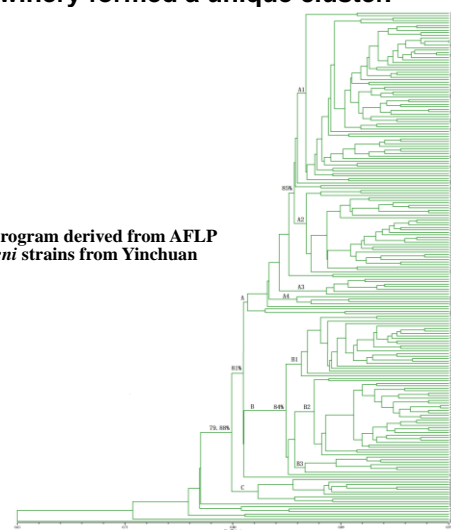


Fig. 3 Electrophoresis photograph of selective amplification from some isolated strains

- Based on the UPGMA, two major phylogroups were deciphered at 81% similarity level.
- The strains in different phylogroups were isolated from wines of different cultivars. In addition, strains from the same winery formed a unique cluster.

Fig. 4 UPGMA dendrogram derived from AFLP patterns of 207 *O. oeni* strains from Yinchuan



Conclusions

- Our results indicate there is an obvious genetic relationship of *O. oeni* with grape cultivars and their origins. Our results also support the fact that *O. oeni* is an important factor related to the wine terroir.

Acknowledgements

This work was financially supported by the National Key R&D Programs of China (2019YFD1002503 and 2016YFD0400504) and the Natural Science Basic Research Plan in Shaanxi Province of China (2019JQ-532).

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