

# [Corrigendum: genome sequencing and comparative analysis of three hanseniaspora uv...](https://assignbuster.com/corrigendum-genome-sequencing-and-comparative-analysis-of-three-hanseniaspora-uvarum-indigenous-wine-strains-reveal-remarkable-biotechnological-potential/)

[](https://assignbuster.com/)[Health & Medicine](https://assignbuster.com/essay-subjects/health-n-medicine/)

A Corrigendum on   
Genome Sequencing and Comparative Analysis of Three *Hanseniaspora uvarum* Indigenous Wine Strains Reveal Remarkable Biotechnological Potential

*by Guaragnella, N., Chiara, M., Capece, A., Romano, P., Pietrafesa, R., Siesto, G., et al. (2020). Front. Microbiol. 10: 3133. doi: 10. 3389/fmicb. 2019. 03133*

In the original article, there was an error as the extent of knowledge on genetics and physiology of the *Hanseniaspora* species was not correctly identified.

A correction has been made to theDiscussionsection, paragraph 1. The corrected sentence appears below:

“ Over the last years, the beneficial contribution of non- *Saccharomyces cerevisiae* yeast species to wine characteristics has been recognized, making the exploitation of non-conventional yeasts as a new source of biodiversity with potential biotechnological significance ( [Masneuf-Pomarede et al., 2015](#B4) ). Among these yeasts, the genus *Hanseniaspora* , which can play a critical role in the modulation of the wine sensory profile by increasing its complexity and organoleptic richness, is attracting a significant interest ( [Fleet, 2003](#B1) ). So far, the knowledge on genetics and physiology of *Hanseniaspora* species remains limited, notwithstanding some recent significant studies open new perspectives in the field, revealing species-specific properties to be explored ( [Langenberg et al., 2017](#B3) ; [Seixas et al., 2019](#B6) ). In this context, genomics analysis may enable a correlation between genetics and useful traits, which could provide a roadmap for biotechnological exploitations ( [Hittinger et al., 2015](#B2) ; [Riley et al., 2016](#B5) ).”

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

## References

Fleet, G. H. (2003). Yeast interactions and wine flavour. *Int. J. Food Microbiol.* 86, 11–22. doi: 10. 1016/s0168-1605(03)00245-9

Hittinger, C. T., Rokas, A., Bai, F. Y., Boekhout, T., Goncalves, P., Jeffries, T. W., et al. (2015). Genomics and the making of yeast biodiversity. *Curr. Opin. Genet. Dev.* 35, 100–109. doi: 10. 1016/j. gde. 2015. 10. 008

Langenberg, A. K., Bink, F. J., Wolff, L., Walter, S., von Wallbrunn, C., Grossmann, M., et al. (2017). Glycolytic functions are conserved in the genome of the wine yeast *Hanseniaspora uvarum* , and *Pyruvate Kinase* limits its capacity for alcoholic fermentation. *Appl. Environ. Microbiol.* 83: e001580-17. doi: 10. 1128/AEM. 01580-1517

Masneuf-Pomarede, I., Bely, M., Marullo, P., and Albertin, W. (2015). The genetics of non-conventional wine yeasts: current knowledge and future challenges. *Front. Microbiol.* 6: 1563. doi: 10. 3389/fmicb. 2015. 01563

Riley, R., Haridas, S., Wolfe, K. H., Lopes, M. R., Hittinger, C. T., Goker, M., et al. (2016). Comparative genomics of biotechnologically important yeasts. *Proc. Natl. Acad. Sci. U. S. A.* 113, 9882–9887. doi: 10. 1073/pnas. 1603941113

Seixas, I., Barbosa, C., Mendes-Faia, A., Guldener, U., Tenreiro, R., Mendes-Ferreira, A., et al. (2019). Genome sequence of the non-conventional wine yeast *Hanseniaspora guilliermondii* UTAD222 unveils relevant traits of this species and of the *Hanseniaspora* genus in the context of wine fermentation. *DNA Res.* 26, 67–83. doi: 10. 1093/dnares/dsy039