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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

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