

# Corrigendum: genome sequencing and comparative analysis of three hanseniaspora uv...

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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 the Discussion section, 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](#) ). 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](#) ). 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](#) ; [Seixas et al., 2019](#) ). In this context, genomics analysis may enable a correlation between

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genetics and useful traits, which could provide a roadmap for biotechnological exploitations ( [Hittinger et al., 2015](#) ; [Riley et al., 2016](#) ).”

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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