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► To cite this version:

Ying Su, Pauline Seguinot, Isabelle Sanchez, Anne Ortiz Julien, José María Heras, et al.. Nitrogen source utilisation by non-Saccharomyces yeasts in winemaking conditions. 7. Conference on Yeasts and Filamentous Fungi, Jun 2019, Milan, Italy. . hal-02961837

HAL Id: hal-02961837

<https://hal.science/hal-02961837>

Submitted on 8 Oct 2020

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Nitrogen source utilisation by non-*Saccharomyces* yeasts in winemaking conditions

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Introduction

Non-*saccharomyces* strains are becoming more widely applied in oenological practice, however, little is known about the nitrogen preferences and utilisation mechanism by non-*Saccharomyces* strains. We tried to decipher the fate of different nitrogen sources by quantitative isotope labelling based analysis with selected nitrogen sources during fermentations conducted by *T. delbrueckii* and *M. pulcherrima* strains.

Objectives

- Explore the redistribution of ammonium, glutamine, and arginine, the three major nitrogen sources in the grape must by using ¹⁵N labelled molecules.
- Study the metabolism of the major intermediates of the Ehrlich pathway, leucine and valine by ¹³C labelled molecules.

Results

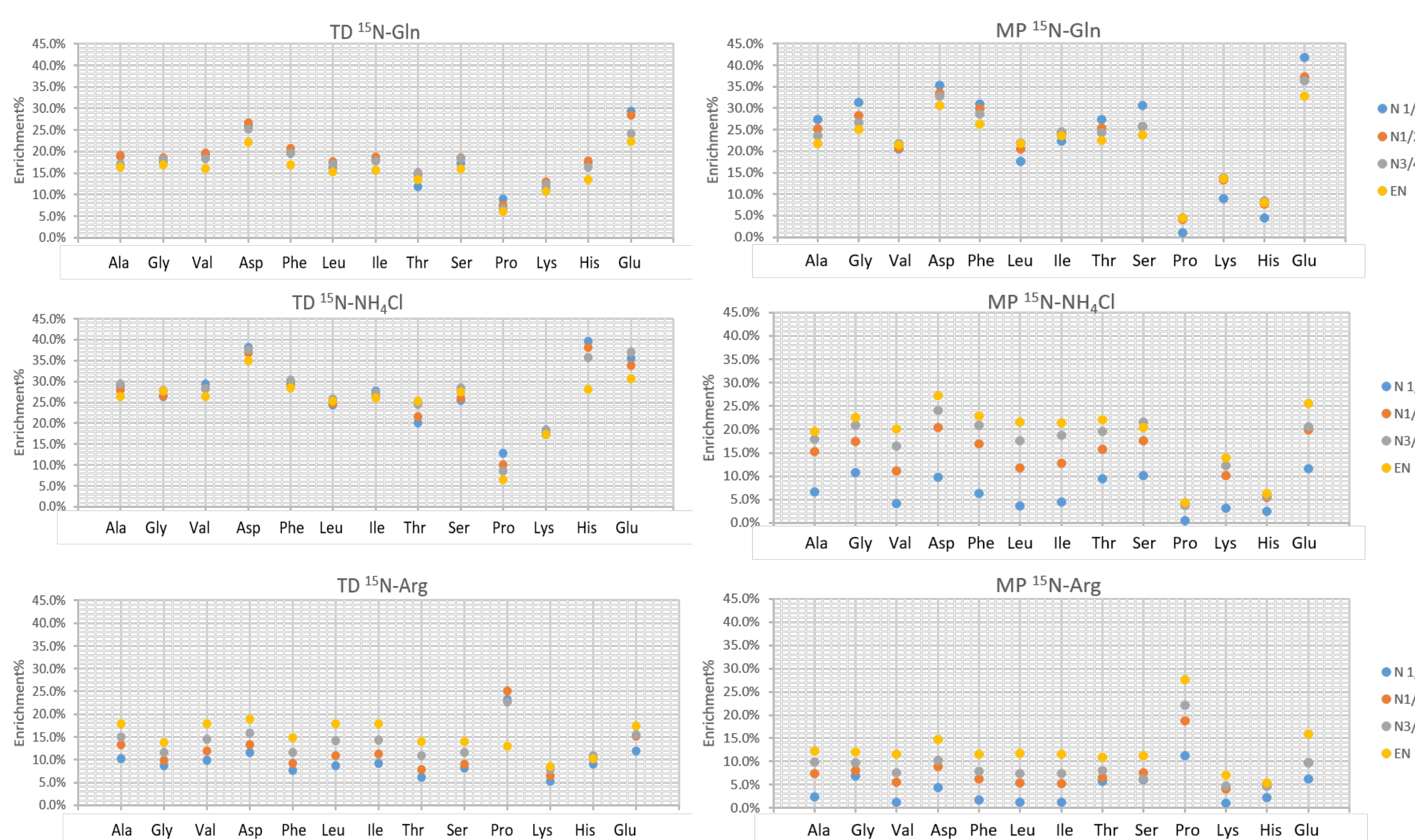


Figure 1. Enrichment of proteinogenic amino acids during fermentation with isotopic labelled amino acids.

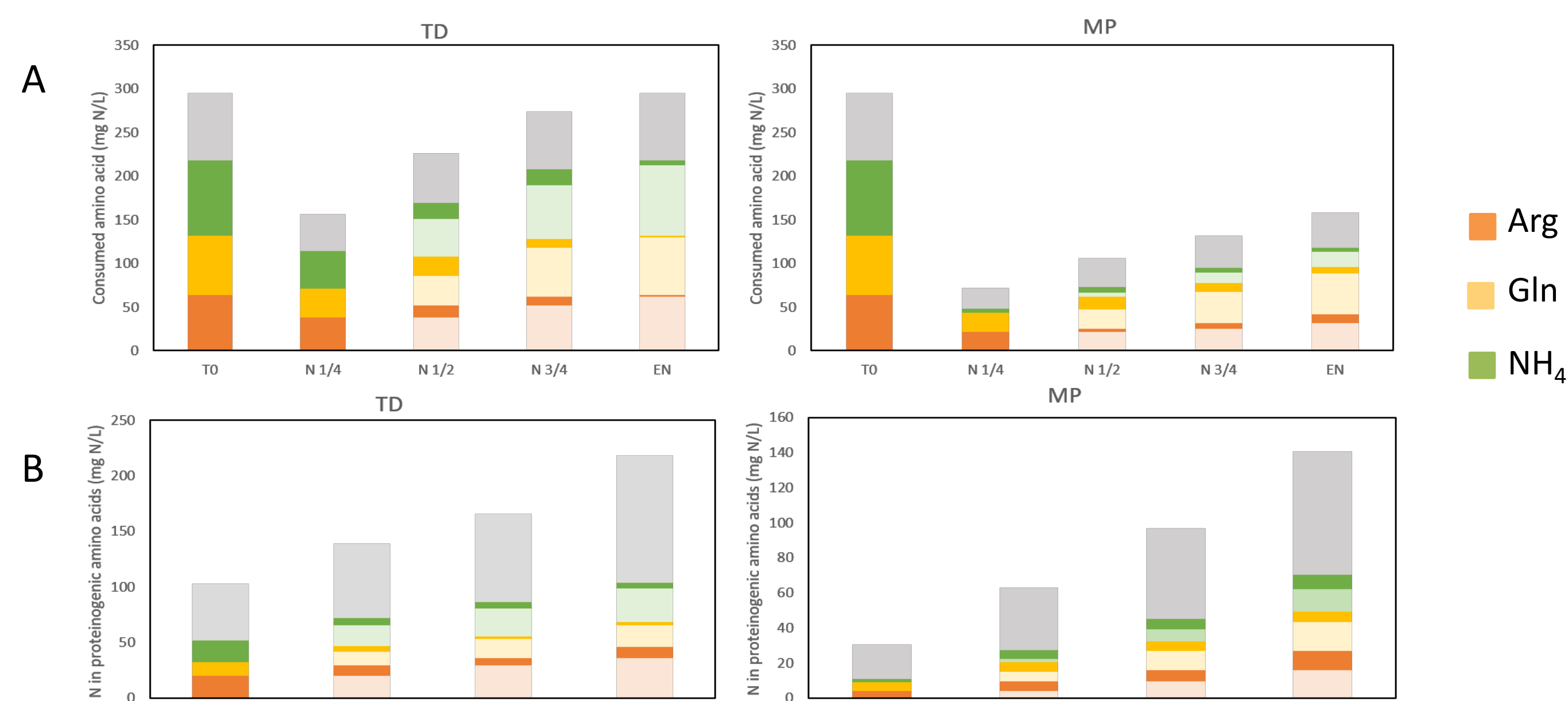


Figure 2. (A) The proportion of consumed arginine, glutamine and ammonium in total consumed nitrogen sources. T₀ represents the initial concentration supplied in the synthetic must. (B) Portion of nitrogen provided by consumed arginine, glutamine, and ammonium recovered in proteinogenic amino acids. Dark colour is the difference between the previous stage and the current stage, light colour represents the amount which has been consumed (A) or incorporated in the previous stage (B).

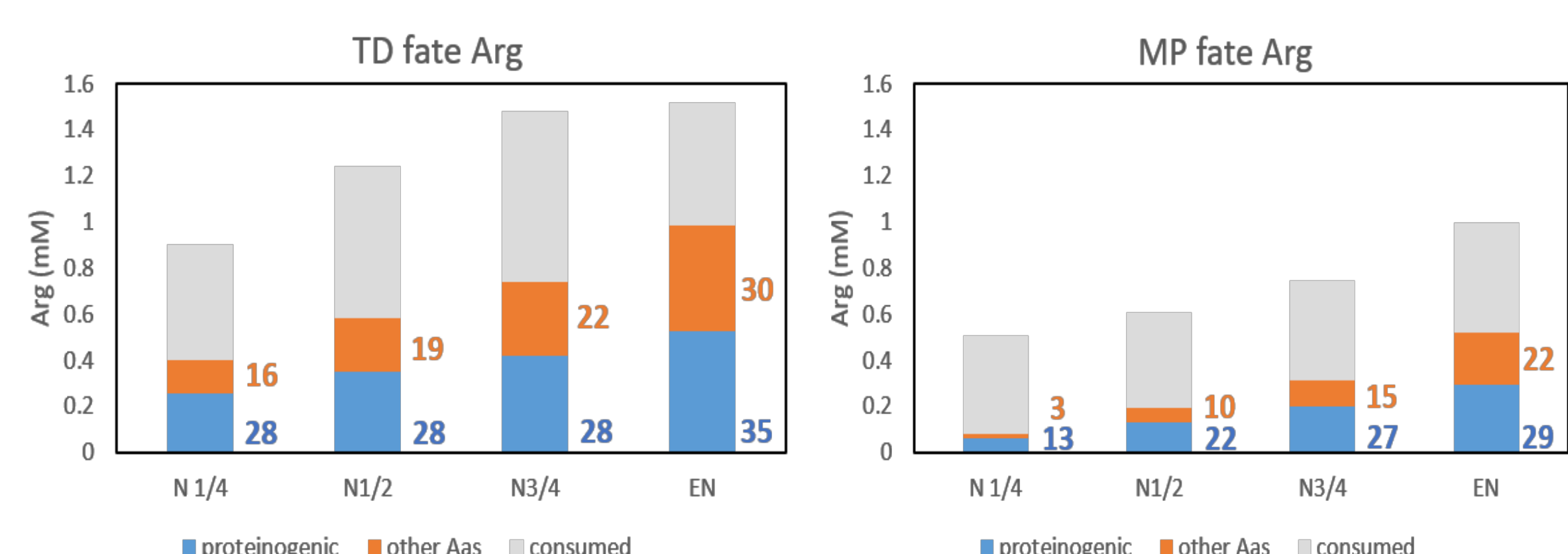


Figure 3. Fate of arginine during fermentation. Blue bar represents the consumed arginine directly incorporated into proteinogenic arginine. Orange bar represents the consumed arginine were catabolised to form other amino acids. The numbers in blue and orange indicate the ratio (in percentage) of arginine incorporated to proteinogenic arginine or catabolised to the total consumed arginine.

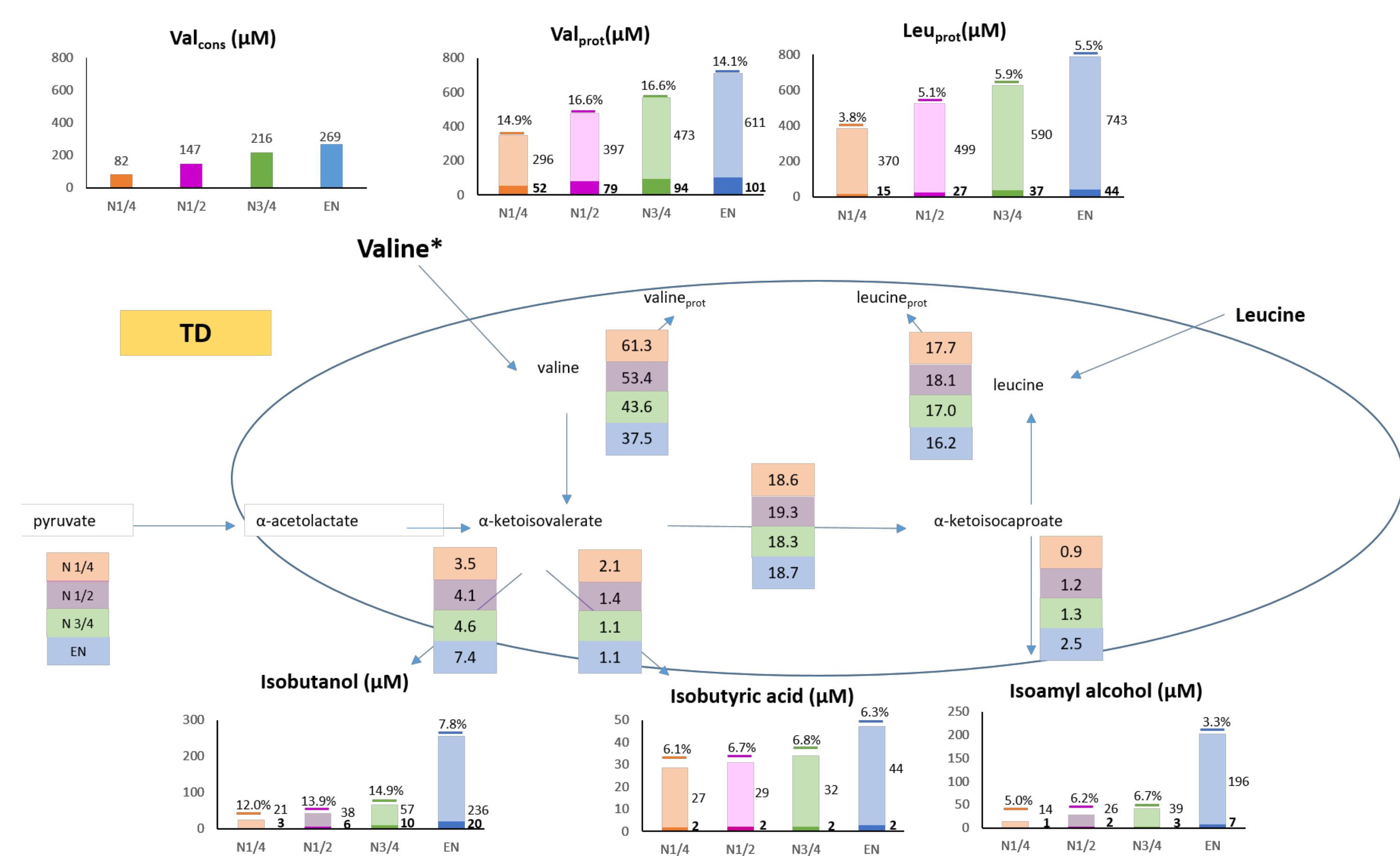


Figure 3. The redistribution of labelled valine in *Torulaspora delbrueckii*. Labeled compounds were showed in bars with darker colour. The numbers on the top of each bar are the percentage of the labelled compound in the total amount of the compound at each stage. The values in the coloured boxes in the metabolic schema represent the percentage of consumed amino acids that is used in the pathway.

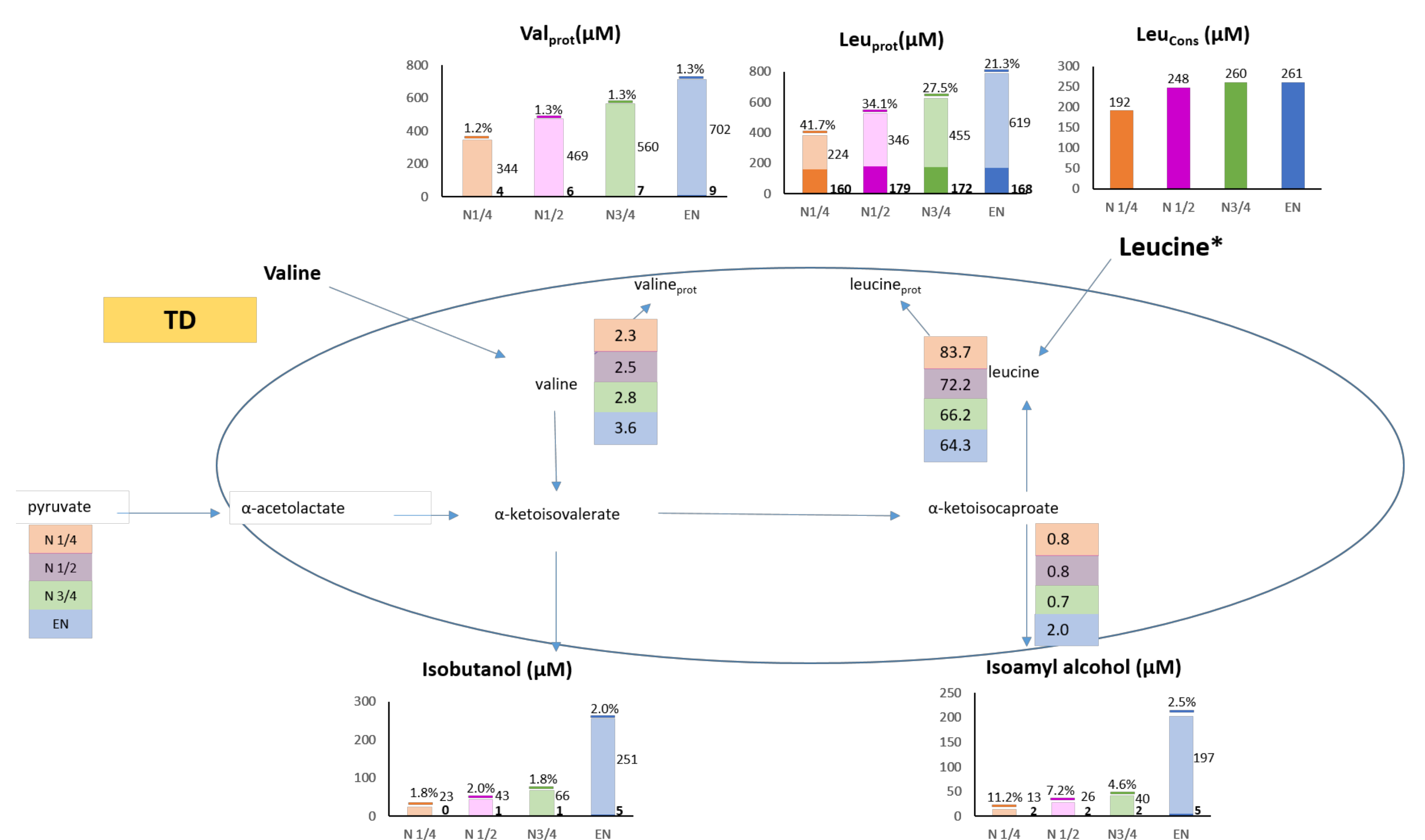


Figure 4. The redistribution of labelled leucine in *Torulaspora delbrueckii*.

Conclusions

- ❖ TD early consumes Gln and ammonium and then followed by Arg. MP first assimilates Gln, while ammonium and Arg were later consumed.
- ❖ For both strains not all the consumed amino acids is directly incorporated into proteins, although they were sometimes supplied in low concentration.
- ❖ Catabolism of nitrogen sources plays a minor role in volatile compounds formation.
- ❖ Comparing with SC (Crépin et al., 2017; Rollero et al., 2017), less amounts of consumed Val and Leu were used for volatile compounds synthesis.

Acknowledgement

The strains of this project are provided by Lallemand. The author also wants to thank Lallemand for financial support. YS thanks FEMS for granting the conference bursary.

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