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EFFECT OF MICROBIAL STRAINS ON HEXANAL

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OBJECTIVE



Plant-based protein consumption → many positive effects. Disadvantages : beany off-flavors¹.
Hexanal is a well-known contributor².

Study the potential of microorganisms to metabolize the off-flavor by reducing the amount of hexanal.

MATERIAL & METHODS

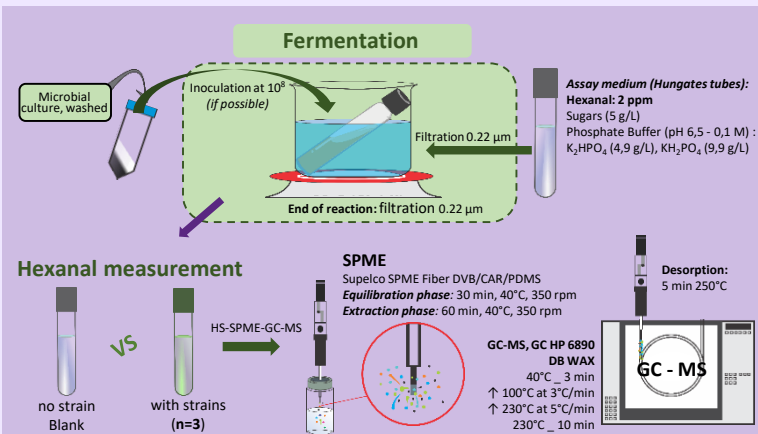


Table 1: Strains labels and inoculum (LAB = Lactic Acid Bacteria)

Strains type	N°	(UFC/mL)
<i>Lactobacillus</i> (Homo LAB)	1, 3, 4, 5	10 ⁸
<i>Lactococcus</i> (Homo LAB)	8	10 ⁸
<i>Pediococcus</i> (Homo LAB)	10	10 ⁸
<i>Streptococcus</i> (Homo LAB)	9	10 ⁸
<i>Lactobacillus</i> (HeteroF LAB)	2, 7	10 ⁸
<i>Lactobacillus</i> (HeteroO LAB)	6, 15	10 ⁸
<i>Leuconastoc</i> (HeteroO LAB)	11	10 ⁸
Yeasts (Alcoholic fermentation)	13, 14	10 ⁷ / 10 ⁵
Acetic acid bacteria	12	10 ⁸
<i>Bacillus subtilis</i>	16	10 ⁷

RESULTS

Hexanal converted to hexanol by ADH, Fig 1.
Generally, high decrease in hexanal => high increase in hexanol.

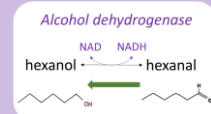


Figure 1: ADH mechanism

Different strains (Tab. 1) applied on hexanal.
All strains impact hexanal: with different levels of reduction (Fig. 2).

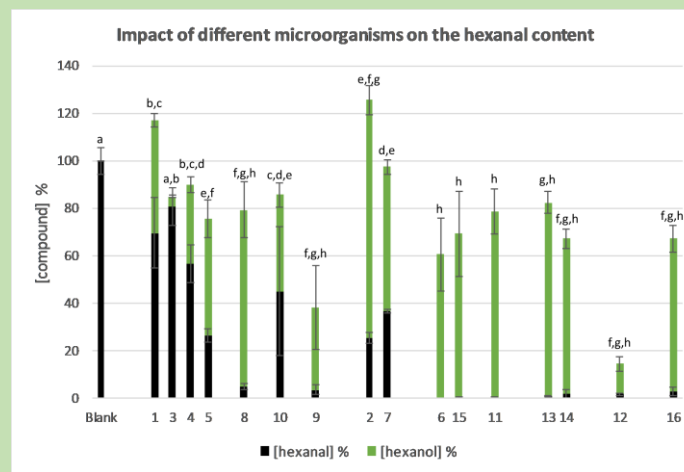


Figure 2: Impact of different microorganisms on the hexanal content
^{a,b,c}: Statistical analysis on hexanal, ANOVA and Tukey's ($\alpha = 0.05$)

Most efficient : 8, 9, 6, 15, 11, 13, 14, 12, 16

WHY ?

REFERENCES

- Rackis, J. J. et al. (1979). *JAACS*, 56, 262-271
- Warner, K. et al. (1978). *JAACS*, 55, 252-256
- Caplice, E. and Fitzgerald, G. F. (1999). *Int J Food Microbiol.*, 50(1-2), 131-149
- Garrigues, C. et al. (1997). *J Bacteriol.*, 179:6, 5282-5287
- Faria-Oliveira, F. et al. (2013). *Food Industry, Intech*, 23, 519-547
- Cruz Ramos, H. et al. (2000). *J Bacteriol.*, 182(11), 3072-3080
- Lynch, K. M. et al. (2019). *Compr Rev Food Sci Food Saf.*, 18(3), 587-625

INTERPRETATIONS

Location of ADH (Fig 3).

- Homo and HeteroF**: inducible enzymes.
- HeteroO**: constitutive enzymes.
- Alcoholic**: at least 5 ADHs, constitutive enzymes.
- AAB**: ADH + ALDH, less hexanol production.
- Bacillus**: ADH in fermentation.

Constitutive enzymes = more efficient for hexanal decrease

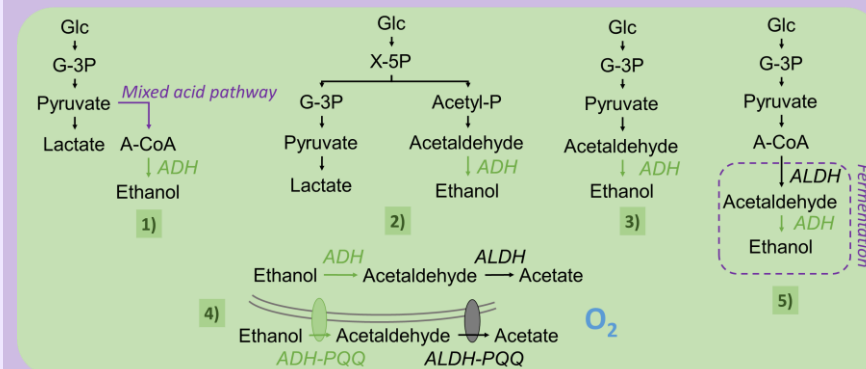


Figure 3: ADH in the primary metabolism of 1) homofermentative LAB^{3,4}, 2) heterofermentative LAB³, 3) yeast alcoholic fermentation⁵, 4) acetic acid bacteria⁷ 5) *Bacillus subtilis*⁶.
Carbon dioxide is not represented in metabolic pathways 2) and 3).

CONCLUSION

Best candidates : obligatory heterofermentative strains of LAB, AAB, yeasts, *B subtilis*, partly due to their constitutive enzymes.
Through the impact of the ADH, microorganisms have the ability to convert green notes aldehydes into their corresponding alcohols. So on, microorganisms have the potential to reduce the "beany" off-flavor and improve the overall flavor of vegetable protein.