



UVIDI U RAZVOJ NOVIH SOJEVA PIVSKOG KVASCA KROZ ADAPTIVNU LABORATORIJSKU EVOLUCIJU

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Sažetak:

Industrija zanatskog piva sve više istražuje alternativne sirovine kako bi stvorila nove stilove piva. Heljda, pseudožitarica bez glutena, bogata linalima i bioaktivnim jedinjenjima, predstavlja obećavajuću opciju. Međutim, fermentacija heljdine sladovine predstavlja izazove, posebno u pogledu performansi kvasca. U ovoj studiji izalovali smo divlje sojeve *Saccharomyces cerevisiae* izolovane iz slavenačke fermentacije kao i iz prirodnog okruženja, a na osnovu skrininga odabrali smo soj koji je dodatno prilagođen za fermentaciju heljde i ječmene sladovine u stresnim uslovima pivarstva korišćenjem adaptivne laboratorijske evolucije (A.pE). Preko 30 uzastopnih fermentacija, populacije kvasca su bile izložene hidrostatičkom pritisku i CO₂ stresu, simulirajući industrijske uslove. Genomske analize su otkrile značajne događaje gubitka heterozigotnosti (LOH) i aneuploidiju kod evoluiranih klonova, posebno na manjim hromozomima, što sugerise da su ove promene igrale ključnu ulogu u poboljšanju iskorišćenja maltoze i maltatrioze, posebno u heljdinoj sladovini. Štaviše, klonovi prilagođeni heljdi pakazali su veću hromozomsku nestabilnost, uključujući gubitak mitohondrijske DNK, što je rezultiralo fenotipovima sa respiratornim nedostatkom. Studija naglašava složene genomske mehanizme koji su u osnovi adaptacije kvasca na alternativne supstrate za pivare, nudeći uvid u razvoj sojeva kvasca optimizovanih za proizvodnju piva bez glutena.

Ključne reči: heljdin slad, autohtoni kvasci, adaptivna laboratorijska evolucija (ALE), genomika

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INSIGHTS INTO THE DEVELOPMENT OF NOVEL BREWING YEAST STRAINS THROUGH ADAPTIVE LABORATORY EVOLUTION

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Summary:

The craft beer industry is increasingly exploring alternative raw materials to create novel beer styles. Buckwheat, a gluten-free pseudocereal rich in minerals and bioactive compounds, presents a promising option. However, fermenting buckwheat wort poses challenges, especially regarding yeast performance. In this study, we isolated wild *Saccharomyces cerevisiae* strains isolated from Slovenian fermentations as well as from natural environments, and based on screening we selected a strain that was further adapted for buckwheat and barley wort fermentations under stressful brewing conditions using adaptive laboratory evolution (ALE). Over 30 successive fermentations, yeast populations were exposed to hydrostatic pressure and CO₂ stress, simulating industrial conditions. Genomic analyses revealed significant loss-of-heterozygosity (LOH) events and aneuploidy in evolved clones, particularly on smaller chromosomes, suggesting that these changes played a key role in improving maltose and maltotriose utilization, especially in buckwheat wort. Furthermore, clones adapted to buckwheat exhibited higher chromosomal instability, including mitochondrial DNA loss, resulting in respiratory-deficient phenotypes. The study highlights the complex genomic mechanisms underlying yeast adaptation to alternative brewing substrates, offering insights into the development of yeast strains optimized for gluten-free beer production.

Keywords: buckwheat wort, autochtoneous yeasts, adaptive laboratory evolution (ALE), genomics

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