

O. polymorpha from pentose sugars and enabled L-lactic acid production from lignocellulosic substrates. Metabolic engineering of *C. famata* resulted in strains with increased riboflavin production from xylose, lignocellulosic hydrolysates, and crude glycerol. The obtained strains provide a basis for further development of yeast-based production processes using lignocellulosic sugars and glycerol as carbon sources.

Keywords: *Ogataea polymorpha*, *Candida famata*, bioethanol, L-lactic acid, riboflavin, metabolic engineering.

Production of the bioethanol and high-value chemicals from lignocellulosic hydrolysates has important economic and environmental issues. We study ethanol, lactic acid and riboflavin synthesis by the industrially important non-conventional yeasts *Ogataea polymorpha* and *Candida famata*. Using approaches of metabolic engineering and classical selection, strains of the thermotolerant yeast *O. polymorpha* have been constructed accumulating more than 20 g/L of ethanol from abundant lignocellulosic sugar xylose which 50 times exceeded ethanol production by the wild-type strain. Ethanol production from another important pentose sugar L-arabinose was also increased. Constructed strains also accumulated increased amounts of ethanol in lignocellulosic hydrolysates. The strains of *O. polymorpha* producing enhanced amounts of ethanol from pure and crude glycerol also have been isolated.

Recombinant strains of *O. polymorpha* producing lactic acid in lignocellulosic hydrolysates were constructed. Yeast *C. famata* is capable of riboflavin overproduction under iron starvation. Previously, robust genetically stable *C. famata* riboflavin overproducers in iron-rich glucose media have been isolated. Using metabolic engineering approaches, the strains of *C. famata* accumulating elevated amounts of riboflavin from xylose, lignocellulosic hydrolysates and crude glycerol (by-product of biodiesel production) have been constructed. Future prospects of the current research and possible industrial implementation will be discussed.

This work was supported by the National Research Foundation of Ukraine (Grant No. 2025.07/0152).

<https://doi.org/10.30970/apmicro.2026.28>

Sylchuk A., Loboda M.

WHOLE-GENOME SEQUENCING, BIOACTIVITY, ADAPTIVE POTENTIAL AND PHYTOSTIMULATORY PROPERTIES OF *AMYCOLATOPSIS ROODEPOORTENSIS* Y13 ISOLATED FROM WAR-IMPACTED SOIL

Department of General and Soil Microbiology, D. K. Zabolotny Institute of Microbiology and Virology of the National Academy of Sciences of Ukraine, 154 Akademika Zabolotnoho St., Kyiv, 03143, Ukraine
e-mail: andriisylchuk@imv.org.ua

Abstract. The actinomycete strain *Amycolatopsis roodepoortensis* Y13, isolated from war-impacted soil, was subjected to whole-genome sequencing, biosynthetic gene clusters for secondary metabolites together with resistance determinants for heavy metals were detected in the genome. The strain tolerated elevated concentrations of copper and zinc as well as increased salinity, displayed high sensitivity to aminoglycosides and vancomycin, and exhibited antagonistic activity against several

phytopathogenic fungi, including *Sclerotinia sclerotiorum*, *Bipolaris sorokiniana*, *Alternaria arborescens*, *Fusarium graminearum* and *Aspergillus niger*. In a *Triticum aestivum* L. germination bioassay, strain Y13 significantly ($p < 0.001$) stimulated root and stem growth, increasing primary root length by 18.0 % and stem length by 27.4 %. These findings indicate that *A. roodepoortensis* Y13 combines multi-stress resistance with antimicrobial and phytostimulatory potential.

Keywords: *Amycolatopsis roodepoortensis*; whole-genome sequencing; heavy metal resistance; antagonistic activity; phytostimulation.

Actinomycetes remain the most prolific bacterial source of agriculturally valuable secondary metabolites, and genome-based approaches continue to uncover previously hidden biosynthetic potential within this group (Cibichakravarthy & Jose, 2021). They synthesise a wide range of bioactive substances, including siderophores, antibiotics and phytohormones: their secondary metabolites neutralise the effects of heavy metals, their antibiotics are actively used against phytopathogenic fungi, and their phytohormones improve plant growth and yield. Therefore, the aim of this work was to perform whole-genome sequencing of strain Y13, to determine its resistance to heavy metals, elevated salinity and antibiotics, to study its antagonistic activity against phytopathogenic fungi, and to determine its phytostimulatory effect.

Strain Y13 was isolated from soil in Kryvyi Rih, Ukraine, near the “Kryvorizhstal” plant (47°28'26.53"N, 33°38'57.62"E), a territory impacted by a ballistic missile strike. The 16S rRNA gene was sequenced by the Sanger method, and the whole genome was sequenced using Illumina NovaSeq. A neighbour-joining tree was constructed in MEGA 12.1.1 with the bootstrap method (1,000 replications) (Kumar et al., 2024). Genome annotation was performed with the DFAST and RAST pipelines, and taxonomic identification was confirmed by average nucleotide identity (ANI) analysis using DFAST_QC (Elmanzalawi et al., 2025). Biosynthetic gene clusters (BGCs) responsible for secondary metabolite production were identified with antiSMASH 8.0 (Blin et al., 2025). Antagonistic activity was assessed by the agar double-layer technique. Resistance to heavy metals was assessed by growth on potato glucose agar (PGA) supplemented with heavy metals, and salt tolerance was determined on PGA with a NaCl gradient (0, 0.1, 2, 5 and 7 %). Antibiotic sensitivity was tested by the modified Kirby-Bauer disc-diffusion method on glucose yeast medium (GYM). The phytostimulatory effect of strain Y13 was tested in a germination bioassay with *Triticum aestivum* L. cv. ‘MIP Valencia’ (Aramis LLC).

Based on 16S rRNA gene phylogenetic analysis, strain Y13 belongs to the genus *Amycolatopsis* and forms a clade with *A. roodepoortensis* ZEL 1. The whole-genome sequence was deposited in the NCBI database (BioProject PRJNA1215024). The ANI value relative to the reference genome of *A. roodepoortensis* DSM 46661 was 96.63 %, confirming the identification of strain Y13 as *A. roodepoortensis*. The genome comprises approximately 8.87 million base pairs across 55 sequences, with a GC content of 69.1 %, and encodes auxin biosynthesis (10 subsystems) together with resistance determinants for mercury (1), arsenic (4), cobalt-zinc-cadmium (20) and copper (15), as well as thiazole-oxazole-modified microcin (TOMM) synthesis (2). BGCs with high homology corresponded to erythromycin-related clusters (Ery-3 to Ery-9), geosmin, ectoine, mirubactin, albachelin, 2-methylisoborneol, citrulassin, ristomycin and ϵ -poly-L-lysine.

Strain Y13 grew actively at 600 mg/L of copper and zinc but was inhibited at 500 mg/L of chromium and 300 mg/L of nickel, and it tolerated up to 5 % NaCl. It showed the highest sensitivity to aminoglycosides (gentamicin, 11.3 mm; kanamycin, 10.3 mm; amikacin, 8.3 mm; streptomycin, 7.3 mm) and to vancomycin (8.7 mm). Fluoroquinolones produced no complete inhibition zone but a less-dense lawn (5–7 mm), indicating a bacteriostatic effect, while the strain was insensitive to β -lactams, cephalosporins and carbapenems, and

unaffected by polyenes and polymyxin B — a pattern typical of *Amycolatopsis* spp. due to endogenous β -lactamase production and/or low-affinity target proteins.

Strain Y13 exhibited antagonistic activity against *Sclerotinia sclerotiorum* SSC21 (7 mm), *Bipolaris sorokiniana* TR1 (7.7 mm), *Alternaria arborescens* TR1 (5 mm), *Fusarium graminearum* DSM 21727 (11 mm) and *Aspergillus niger* ATCC 6275 (6 mm); the biomass extract inhibited *B. sorokiniana* TR1 (9 mm), while the culture-liquid supernatant was slightly more active (13.7 mm). In the *Triticum aestivum* L. germination bioassay, all measured morphometric parameters increased significantly ($p < 0.001$): primary root length rose from 107.83 to 127.23 mm (+18.0 %), the first lateral root from 94.53 to 116.07 mm (+22.8 %), the second lateral root from 81.63 to 105.00 mm (+28.6 %, the largest gain), and stem length from 58.87 to 75.00 mm (+27.4 %).

The isolated strain *A. roodepoortensis* Y13 combines resistance to several adverse factors with promising antimicrobial and phytostimulatory properties, indicating its potential for biotechnological application, including the reclamation of war-impacted soils.

References

1. Blin, K., Shaw, S., Vader, L., Szenei, J., Reitz, Z. L., Augustijn, H. E., Cediél-Becerra, J. D. D., de Crécy-Lagard, V., Koetsier, R. A., Williams, S. E., Cruz-Morales, P., Wongwas, S., Segurado Luchsinger, A. E., Biermann, F., Korenskaia, A., Zdouc, M. M., Meijer, D., Terlouw, B. R., van der Hooft, J. J. J., ... Weber, T. (2025). antiSMASH 8.0: Extended gene cluster detection capabilities and analyses of chemistry, enzymology, and regulation. *Nucleic Acids Research*, 53(W1), W32–W38. <https://doi.org/10.1093/nar/gkaf334>
2. Cibichakravarthy, B., & Jose, P. A. (2021). Biosynthetic potential of *Streptomyces* rationalizes genome-based bioprospecting. *Antibiotics*, 10(7), 873. <https://doi.org/10.3390/antibiotics10070873>
3. Elmanzalawi, M., Fujisawa, T., Mori, H., Nakamura, Y., & Tanizawa, Y. (2025). DFAST_QC: Quality assessment and taxonomic identification tool for prokaryotic genomes. *BMC Bioinformatics*, 26(1), 3. <https://doi.org/10.1186/s12859-024-06030-y>
4. Kumar, S., Stecher, G., Suleski, M., Sanderford, M., Sharma, S., & Tamura, K. (2024). MEGA12: Molecular evolutionary genetic analysis version 12 for adaptive and green computing. *Molecular Biology and Evolution*, 41(12), msae263. <https://doi.org/10.1093/molbev/msae263>

<https://doi.org/10.30970/apmicro.2026.29>

Trufanova N.¹, Trufanov O.², Raievska I.³, Petrenko O.^{1,3}

BIFIDOBACTERIUM BIFIDUM LVA-3 FERMENTATE AS AN ANTIBACTERIAL AND PRECONDITIONING AGENT FOR MESENCHYMAL STEM CELLS

¹*Institute for Problems of Cryobiology and Cryomedicine of the National Academy of Sciences of Ukraine, 23 Pereiaslavskaya St., Kharkiv, 61016, Ukraine*

²*National Scientific Center «Hon. Prof. M. S. Bokarius Forensic Science Institute», 8-A Zolochivska St., Kharkiv, 61177, Ukraine*

³*V. N. Karazin Kharkiv National University, 4 Maidan Svobody, Kharkiv, 61022, Ukraine*
e-mail: natalia_trufanova@cryonas.org.ua

Abstract. The therapeutic efficacy of adipose tissue-derived mesenchymal stem cells (AD-MSCs) can be compromised by local inflammation and microbial infections at wound sites. Preconditioning MSCs with probiotic postbiotics offers a dual strategy to prime stem cell function and provide local antibacterial