

# Book of Abstracts

## GENARA 2025



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# Global Exchange on Next-Gen Engineering and Life Sciences Research and Applications (GENARA)



Oludeniz, Turkey  
October 21-27, 2025

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PLENARY SPEAKER

Id-4

**Synthetic Biology-Based Biomanufacturing**

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**Abstract.** Synthetic biology is characterized by adopting the approach of design-build-test-learn (DBTL). One of the most recognized applications of synthetic biology is its ability to alter the metabolism of chassis cells to produce value-added products such as biofuels, plant natural products, and polymer materials. This new mode of biomanufacturing makes microorganisms as cell factories more competitive with organic chemical synthesis. In another aspect, nowadays the natural and health - enhancing functional foods play a crucial role in preventing diseases and promoting human health. The edible medicinal mushroom *Ganoderma lucidum* has been used for over 2000 years as an oral administration medicine in East Asia to treat various diseases and improve human health. Ganoderic acids (GAs), the mushroom derived lanostane-type triterpenoids, are its major bioactive metabolites with anti-cancer, hepatoprotective and cholesterol-lowering activities. Yet their biosynthetic pathway is unclear, and their biosynthesis by the native GAs-producing fungus *G. lucidum* is rather inefficient. In this lecture, after an overview of recent advances in synthetic-biology based biomanufacturing technology, a detailed research example of a synthetic biology approach to efficiently produce GAs with specific activities by engineering baker's yeast will be demonstrated. We design an GA biosynthetic pathway, and have identified key P450 enzymes catalyzing the triterpenoid structure modifications and reprogrammed the GA biosynthetic network in the yeast. For example, the P450 enzymes CYP512W2 (oxidization), CYP512W6 (hydroxylation) and CYP512A13 (a multifunctional cytochrome directly catalyzes the conversion of the carbon-carbon conjugated double bond on the lanostane skeleton) were identified and analyzed. After the steps of design-build-test, then we enter the learning step. By engineering the key enzymes, a higher titer of GAs was achieved in the yeast fermentation. By recycling the DBTL steps, an even higher titer of the targeted products was finally realized. In addition, we reveal the catalytic mechanism of related CYPs. Our work provides new insights into the post-modification of triterpenoids. We also investigated the bioactivities of GAs, e.g., the inhibition of GAT on hepatocellular carcinoma both in vitro and in vivo was found. Our work creates an efficient biomanufacturing platform for functional food key components - GAs, and it is of significant impact on the development of GAs-producing-yeast based dietary nutrition for human health.

**Keywords:** Synthetic Biology; Biomanufacturing; Cell Factory; Natural Products; Bioactive Compounds



PLENARY SPEAKER

Id-6

**Mechanism of Human Primosome Function**

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**Abstract.** The human primosome, a four-subunit complex of primase and DNA polymerase alpha (Pol $\alpha$ ), initiates DNA synthesis on both chromosome strands by generating chimeric RNA-DNA primers for loading DNA polymerases delta and epsilon (Pol $\epsilon$ ). Replication protein A (RPA) tightly binds to single-stranded DNA strands, protecting them from nucleolytic digestion and unauthorized transactions. We report here that RPA plays a critical role for the human primosome during DNA synthesis across inverted repeats prone to hairpin formation. On other alternatively structured DNA, forming a G-quadruplex, RPA does not assist primosome. A stimulatory effect of RPA on DNA synthesis across hairpins was also observed for the catalytic domain of Pol $\alpha$  but not of Pol $\epsilon$ . The winged helix-turn-helix domain of RPA is essential for an efficient hairpin bypass and increases RPA-Pol $\alpha$  cooperativity on the primed DNA template. Cryo-EM studies revealed that this domain is mainly responsible for the interaction between RPA and Pol $\alpha$ . The flexible mode of RPA-Pol $\alpha$  interaction during DNA synthesis implies the mechanism of template handover between them when the hairpin formation should be avoided. This work provides insight into a cooperative action of RPA and primosome on DNA, which is critical for DNA synthesis across inverted repeats.

**Keywords:** Human Primosome; DNA Polymerase Alpha; Replication Protein A; Hairpin Bypass; DNA Synthesis

INVITED SPEAKER

Id-1

**Is Ultra-Weak Photon Emission a Fast Communication Tool for DNA?**

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**Abstract.** Living cells (plants, animals, humans) have spontaneous ultraweak photon emission (UPE), which most researchers believe is directly related to reactive oxygen radicals. The emission of biophotons exhibits short, quasi-periodic bursts, similar to those used for binary data transmission over noisy channels. The situation is similar to the challenging information transmission that occurs in the "humid and noisy environment of biological systems". In recent decades, a new field of research focusing on biophotons has emerged. For example, Esmaeilpour et al. studied UPEs from neurons and observed that the intensity of UPE was higher before cell differentiation than after, suggesting that measuring UPE could be useful in assessing the effects of nanoparticles on living cells. Zapata et al. found that UPE emission varies with diseases (including diabetes, hemiparesis, protoporphyria) and changes in brain activity. They concluded that UPEs are natural and promising non-invasive spectroscopic variables that offer a wide range of diagnostic applications. UPE detection allows for maximum protection of gametes and embryos during assisted reproduction, avoiding all physical, chemical, and biological factors. Spontaneous photon emission from developing mouse embryos was detected under ideal incubation conditions, without external stimulation, using an Olympus® microscope incubator and a single-photon sensitive Hamamatsu Photonics® photon camera. By applying the second law of thermodynamics, the low entropy energy absorbed and used by the embryos can be distinguished from the higher entropy energy released and detected in their environment. To evaluate the higher entropy energy data from embryos, we developed a unique algorithm for calculating the entropy weighted spectral fractal dimension. Structure-based analyses allowed for the discrimination between live and degenerated mouse embryos, as well as between frozen and fresh embryos and background. The novel detection of ultraweak photon emission from mouse embryos may provide a basis for the development of a photon emission embryo control system (PEECS) (Bódis et al., Berke et al.). Ultraweak photon emission fingerprints of embryos can be used to select viable samples in an ideal dark environment. It is important to note that cell-to-cell communication via biophotons has also been demonstrated in plants, bacteria, animal neutrophil granulocytes, kidney cells, and neurons. Biophotons thus allow cells to interact without molecular signals, suggesting that there are intercellular processes that do not depend on molecule-receptor recognition. Potapovich et al. have found strong evidence for non-chemical intercellular signaling that triggers biological cellular responses. They observed that different cell types generate lethal signals in response to oxidative stress that can affect target cells over long distances, even in non-aqueous environments, causing morphological changes and loss of viability. These results strongly support the hypothesis that biophotons may have biological significance. It has been traditionally believed that macromolecules found in living cells, including DNA, RNA, and proteins, do not exhibit specific light emission. However, recent research challenges this concept by showing that under certain conditions and at physiological temperatures, nucleic acids exhibit spontaneous light emission. Even DNA, which does not normally fluoresce, can occasionally emit light. The natural

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fluorescence of these molecules can be even brighter than that achieved with fluorescent markers, making them ideal for imaging without the toxicity associated with staining. The photons emitted by DNA molecules offers a huge potential for observing physiological and pathological processes in cells, tissues, and developing embryos, both in vivo and in vitro. If we can decode the "photonic language", we will have a tool to intervene in biological processes. Furthermore, it could be an excellent tool for theoretical research and practical development of DNA-based molecular electronics. Ultimately, this could also open up the possibility of developing a molecular hybrid computer (DNA quantum computer) that operates at room temperature (Pietruszka et al.)

**Keywords:** Photon Emission; DNA; PEECS.

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INVITED SPEAKER

Id-16

**The Science of Self-Destruction: Smart Apoptotic Inducers Bridging Natural Products, Metal Complexes, and Nanomaterials in Cancer**

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**Abstract.** What if cancer cells could be instructed to dismantle themselves, leaving healthy tissue untouched? This question has guided our work in developing smart apoptotic inducers, a class of agents that harness the body's own machinery for programmed self-destruction. This is the vision behind smart apoptotic inducers, a new generation of therapeutics that harness the body's own program for cellular self-destruction. Why pursue apoptosis when conventional therapies already exist? Because chemotherapy and radiotherapy, though lifesaving, are often blunt tools—plagued by multidrug resistance, systemic toxicity, and poor selectivity. Apoptosis, in contrast, is precise: it turns malignant cells into architects of their own demise, reducing relapse and inflammation while sparing normal cells. Where do we find such inducers? Nature offers one pathway—marine sponges, mangroves (*Xylocarpus*, *Bruguiera*), and medicinal plants like *Vitex rotundifolia* provide scaffolds that awaken both intrinsic and extrinsic apoptotic routes. Chemistry offers another—synthetic agents such as palladium and zinc complexes, carbon dots, and Fe-based MOFs bind DNA with high fidelity, triggering apoptosis through engineered precision. How do we ensure these agents reach the right cells at the right time? Here, nanotechnology and material science enter the stage: hyaluronan-conjugated nanoparticles, paclitaxel-HA hybrids, gemcitabine-loaded carriers, and biodegradable thin films create smart delivery systems that exploit tumor-specific markers for controlled, selective release. When will this matter? In the era of precision oncology, where therapies must be patient-tailored, sustainable, and minimally toxic, these smart apoptotic inducers could redefine the landscape of cancer therapeutics. This keynote will explore how natural compounds wisdom, chemical innovation, and material science converge to turn a biological program into a therapeutic revolution.

**Keywords:** Smart Apoptotic Inducers; Targeted Cancer Therapy; Nanotechnology Drug Delivery; Intrinsic/Extrinsic Apoptosis; Precision Oncology

INVITED SPEAKER

Id-20

**Endophytic Pgp Bacteria *Bacillus Subtilis*: Physiological and Molecular Regulation of Wheat Tolerance to Multiple Abiotic Stresses**

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**Abstract.** Abiotic stresses related to climate change, such as drought, extreme temperatures, flooding, and salinity, are intensifying annually and threaten global food security. The effects of single abiotic stresses on major agricultural crops have been widely studied; however, these stressors naturally manifest in combination under field conditions, causing damage that significantly exceeds their individual effects. Physiological, metabolic, and molecular crop responses to abiotic stress combinations can differ substantially from responses to individual stresses. Understanding the mechanisms of plant responses to multiple stresses is critical to unravel the complexities of their adaptive strategies and to engineer climate-resilient crops. Beneficial strains of endophytic plant growth-promoting (PGP) bacteria, which can activate the natural defense systems of host plants without causing negative impacts on the plants themselves, the environment, or human health, represent a promising, eco-friendly biological approach for increasing crop adaptive potential and productivity under adverse environmental conditions. However, progress in studying the mechanisms of PGP bacteria-mediated tolerance in major crops, including wheat, achieved in recent years mainly concerns individual stresses, whereas data on their combined effects are scarce and fragmentary. In this context, our study focuses on investigating the effects of multiple abiotic stresses on responses of soft spring wheat (*Triticum aestivum* L.) genotypes with contrasting dehydration tolerance [tolerant Ekada109 (DT); sensitive Zauralskaya Zhemchuzhina (DS)], as well as the potential of pre-sowing seed inoculation with the endophytic bacterium *Bacillus subtilis* 10-4 (*Bs*) to mitigate these effects. The research examines changes in growth, morphology, photosynthetic activity, and stress tolerance in pot experiments under controlled conditions. The effects of combined abiotic stresses (soil drought, NaCl-induced salinity, and heat (+35°C)) on both uninoculated and *Bs*-inoculated DT and DS wheat plants will be presented. The discussion will focus on the phenotypic and morpho-physiological changes associated with stress tolerance (including growth, biomass, root system architecture, and grain yield), as well as the relationship between the efficiency of *Bs* colonization and host plants tolerance. The influence of the studied abiotic stress combinations and endophytic *Bs* inoculation on photosynthetic pigment content (chlorophylls a, b, and carotenoids), photosynthetic apparatus activity, chlorophyll fluorescence parameters (e.g., Fo, Fm, Fv/Fo, Y(NO)), leaf area, and stomatal characteristics of DT and DS wheat genotypes will also be considered. Overall, the findings shed light on the responses of DT and DS wheat genotypes to multiple abiotic stresses and highlight the potential of using endophytic *Bs* as bioinoculants. This approach offers an eco-friendly strategy to enhance wheat's adaptive potential and resilience to multiple abiotic stresses under a changing climate.

**Keywords:** Endophyte; *Bacillus subtilis*; Multiple abiotic stresses; Wheat; Stress tolerance.

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**Acknowledgment:** The study was supported by the grant of the Russian Science Foundation No. 25-16-00188, <https://rscf.ru/en/project/25-16-00188/>.

INVITED SPEAKER

Id-25

Engineering of Microbial Strains for Steroid Biotechnology

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**Abstract.** Microbial conversion of natural sterols currently forms the technological basis for the production of steroids used in the pharmaceutical, food, and veterinary industries, including corticoids, neurosteroids, sex hormones, bile acids, and other terpenoid lipids. Fast-growing saprotrophic actinobacteria of the genus *Mycolicibacterium*, such as *M. neoaurum*, *M. smegmatis*, and *M. fortuitum*, efficiently metabolize natural sterols due to their efficient hydrophobic substrate transport systems, multienzyme steroid catabolism systems, and high metabolic flexibility. Modification of the primary catabolic pathway of actinobacteria, the so-called 9(10)-secopathway of sterol degradation, not only improves the biocatalytic properties of industrial strains by suppressing undesirable activities that lead to byproduct formation, but also redirects metabolic fluxes within the cell toward the formation of target steroid products. Thus, a deletion in the *kstD* gene, encoding 3-ketosteroid-1-dehydrogenase, in the *M. neoaurum* strain NRRL B-3805 reduces the undesirable formation of androstadienedione (ADD) and other 1-dehydrosteroids during androstenedione (AD) production. Knockout of the *fadD3* gene in the *M. smegmatis* mc2 155 strain promotes the accumulation of valuable indane compounds used in progestin synthesis. Inactivation of the *fabG* gene in *M. neoaurum* and its derivatives enables the efficient production of valuable C22 steroids, such as 20-hydroxymethylpregnenone. A promising direction is the creation of transgenic mycolicibacteria based on heterologous expression of foreign steroidogenesis systems, which ensure the selective formation of valuable compounds from phytosterols in one biotechnological stage. For example, co-expression of the genes encoding 17 $\beta$ -hydroxysteroid dehydrogenase from the fungus *Cochliobolus lunatus* and the glucose-6-phosphate dehydrogenase from *Mycobacterium tuberculosis* in *M. neoaurum* VKM Ac-1816D cells ensures efficient production of the male sex hormone testosterone from phytosterol. Expression of genes coding for the initial stage the mammalian steroidogenesis within the tricistronic operon (CYP11A1-Ad-AdR) in *M. smegmatis* cells enables the production of the highly sought-after hormone progesterone from cholesterol in a single biotechnological step. The strains capable of effective regio- and stereoselective hydroxylation of androstanes have been created using heterologous expression of the genes encoding mutant bacterial cytochrome P450 BM3 LG23 from *Priestia megaterium*. The results presented in the report demonstrate the high potential of actinobacteria as a microbial chassis for creating effective industrial producers of sought-after steroid compounds. The problems and prospects of using genetically modified strains and biotechnologies in the industry are discussed. This work was carried out within the framework of the State Contract of the Ministry of Science and Higher Education of the Russian Federation No. 125041005029-5 on the topic FMRM-2025-0032 "Development of Genome-Based Technologies and Metabolic Engineering Methods for the Creation of High-Yield Bacterial Producers and Multispecies Consortia for Biotechnology, Agro-Industrial Complex, and Food Industry."

**Keywords:** Microbial Steroid Bioconversion; *Mycolicibacterium* Engineering; Sterol Catabolic Pathway; Metabolic Flux Redirection; Industrial Steroid Production.

ORAL PRESENTATION

Id-24

**3-Methoxymethyl Esters of Sterols for Microbial Production of Pregnenolone**

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**Abstract.** Steroids form a large class of organic compounds that include important biologically active substances such as sterols, sex hormones, adrenal cortex hormones, cardiac glycosides, gluco- and mineralocorticoids, sapogenins, some alkaloids, and many others. Progesterone (pregn-4-ene-3,20-dione) and pregnenolone (pregn-5-en-3 $\beta$ -ol-20-one) are steroid hormones widely used in medicine and veterinary. Progesterone plays a crucial role in female fertility, maintaining pregnancy, reducing the negative effects of menopause and various gynecological pathologies. Pregnenolone is a neurosteroid, which is used in the therapy of a number of psychosomatic disorders as a neuromodulator and is also a precursor to a range of other valuable hormones. cDNA copies of the bovine *AdR*, *Adx* and *CYP11A1* genes encoding mature forms of enzymes of cholesterol hydroxylase/C20-C22 lyase system (CH/L) were combined with acetamidase promoter in the plasmid generating an artificial tricistronic operon. Using this construct, a recombinant strain of the actinobacterium *Mycolicibacterium smegmatis* expressing the system of the initial step of mammalian steroidogenesis was created and is used for the bioconversion of chole- and phytosterols to produce progesterone. However, the oxidation of C3-OH-group by the own enzymes of the recipient strain resulted in the formation of cholestenone and phytosterones, which prevented the progesterone accumulation. 3-keto-4-ene-sterones were not the appropriate substrates for eukaryotic CYP11A1. Methoxymethylation at C3 of a gonane ring was applied as a promising method for preventing the formation of cholestenone and phytosterones. The esterification reaction to produce MOM derivatives of chole- and phytosterols occurred with a molar yield of 92-96%. The created recombinant whole-cell catalyst is capable of transforming MOM-cholesterol and, to a lesser extent, MOM-phytosterol to MOM-pregnenolone (yields 20 and 60% mol., respectively) with impurities of MOM-dehydroepiandrosterone (2.5-14.0% mol.) - the final product of  $\beta$ -side chain oxidation of MOM-cholesterol. Multiple additions of the inducer (acetamide) to the bioconversion medium provided high expression of the genes coding for mammalian CH/L. As a result of bioconversion conditions optimization, it was shown that with a daily feeding of fructose as an additional carbon source, using methyl- $\beta$ -cyclodextrin in a molar ratio to the substrate of 5 : 1, and changing a mode of the substrate addition MOM-cholesterol addition schedule (started at 24 hours since inoculation) the maximum molar yield of MOM-pregnenolone was achieved - 70-80% (mol.) or the titer of 0.7-1.8 g/l from 1-3 g/l of MOM-cholesterol. The maximum titer of 2.9 g/L was obtained from 6 g/l of cholesterol, which was added in three doses every 12 hours starting from 24 hours of the growth. The efficiency of MOM-pregnenolone isolation from the culture broth was 65-70%, and that of the MOM group hydrolysis was 94-97%. The total efficiency of the biotechnology under developed was 40% (mol.). The results open the prospects for the biotechnological application of the new whole-cell microbial biocatalysts for the pregnenolone production from



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MOM-substituted cholesterol. This work was carried out within the framework of the State Contract of the Ministry of Science and Higher Education of the Russian Federation No. 125041005029-5 on the topic FMRM-2025-0032 "Development of Genome-Based Technologies and Metabolic Engineering Methods for the Creation of High-Yield Bacterial Producers and Multispecies Consortia for Biotechnology, Agro-Industrial Complex, and Food Industry."

**Keywords:** Steroid Bioconversion; *Mycolicibacterium smegmatis*; MOM-Cholesterol; Pregnenolone Production; Mammalian CYP11A1 System

POSTER PRESENTATION

Id-18

**Targeting Apoptosis Mechanisms: Synergistic Cytotoxic Effects of Pd(II) Complexes and Curcumin in MCF-7 Breast Cancer Cells**

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**Abstract.** Cancer continues to be a significant cause of death globally, with breast cancer being the most common type among women. Despite advancements in treatment, challenges such as drug resistance, systemic toxicity, and insufficient selectivity persist in obstructing therapeutic success. This necessitates innovative approaches that integrate effectiveness with enhanced safety. Transition metal complexes are increasingly recognized as viable alternatives to platinum-based drugs, owing to their varied mechanisms and reduced toxicity. Palladium (Pd) complexes demonstrate significant cytotoxic effects, whereas curcumin, a natural polyphenol derived from *Curcuma longa*, has shown effective anticancer properties. In this study, we investigated the synergistic anticancer effects of Pd(II) complexes in combination with curcumin against MCF-7 breast cancer cells. The cytotoxic and apoptotic effects of Pd(II) complexes, curcumin, and their combinations on MCF-7 breast cancer cells. Cytotoxicity was evaluated using the MTT assay, and the IC<sub>50</sub> and Selectivity Index (SI) values were established. The evaluation of drug interactions was conducted utilizing the Chou–Talalay method. Apoptosis was assessed through Annexin V/PI staining, TUNEL assay, and the activity of caspase-3/7, caspase-8, and caspase-9, along with the expression levels of Bax, Bcl-2, and p53. Both Pd complexes and curcumin exhibited cytotoxicity that was dependent on both dose and time, demonstrating a selectivity index greater than 3 in cancer cells compared to normal Vero cells. Combination treatments significantly improved cytotoxicity, leading to reduced IC<sub>50</sub> values (S5+Curcumin: 7.23 µM; S7+Curcumin: 13.48 µM) and exhibiting synergism (CI < 1). Apoptotic assays demonstrated increased apoptosis, notable caspase activation, upregulation of Bax/p53, and downregulation of Bcl-2 in the combination groups. Consequently, Pd–curcumin combinations demonstrate significant synergistic anticancer effects in MCF-7 cells, presenting a promising therapeutic strategy with enhanced efficacy and selectivity.

**Keywords:** Palladium Complexes; Curcumin; Synergistic Anticancer Activity; MCF-7 Breast Cancer Cells; Apoptosis

POSTER PRESENTATION

Id-23

**Genotype-Dependent Endophytic PGP Bacteria *Bacillus Subtilis* Inoculation Efficiency in Wheat: Relationship with Seeds Endophytic Microbiome and Field Response**

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**Abstract.** *Triticum aestivum* L. (wheat) is a major global cereal crop threatened by climate change-induced abiotic stresses. While endophytic plant growth-promoting (PGP) bacteria represent a promising, eco-friendly approach to enhance crop growth and stress tolerance, the functional mechanisms of the native wheat microbiome and their interactions with inoculated endophytes remain unclear. This study investigated the effects of endophytic bacterial *Bacillus subtilis* 10-4 (BS) pre-sowing seed inoculation on the growth of two wheat genotypes [dehydration-tolerant (DT) Ekada109 and dehydration-sensitive (DS) Zauralskaya Zhemchuzhina] under field conditions. Concurrently, we analyzed the structure and diversity of the seed endophytic microbiome via 16S rRNA and internal transcribed spacer (ITS) sequencing. A small-scale field trial was conducted at the Experimental Farming of the Chishminsky Breeding Center, Russia (54°34'16" N 55°22'11" E) during the 2025 growing season, which was characterized by extreme weather conditions, including excessive rainfall, high humidity, and significant temperature fluctuations. The results revealed genotype-specific responses: BS-inoculated DS plants showed enhanced growth, root development, and grain yield under high-humidity field conditions, contrasting with previous studies under drought where DT plants performed better in growth/yield. Metagenomic analysis revealed a fundamental disparity in the endophytic (bacterial and fungal) communities between the two genotypes. The DT genotype seeds harbored a significantly more diverse endophytic microbiome (alpha-diversity) than the DS genotype. Specifically, 75 bacteria taxa were identified in the DT seed microbiome, compared to 48 in the DS seed microbiome, with 16% and 14.6% representing uncultured species, respectively. While 17 bacterial taxa were common for both genotypes, 49 were unique to DT seeds and 28 were unique to DS seeds. The dominant genera in the DT seeds included *Chryseobacterium*, *Pedobacter*, *Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium*, *Curtobacterium*, *Pseudomonas*, *Sphingomonas*, *Stenotrophomonas*, *Sanguibacter*, *Pantoea*, *Luteibacter*, *Paenibacillus*, and *Massilia*. In contrast, the DS seed microbiome was primarily represented by *Ralstonia* and uncultured members of *Carnimonas* and *Sericytochromatia*. Fungal community analysis further highlighted the disparity in microbiome complexity. A total of 46 fungal taxa were detected in the DT seeds, compared to only 11 in the seeds of the DS genotype. Within the DT seeds microbiome, 27 fungi were identified to species level (dominated by *Aspergillus ruber*, *Alternaria* spp.), 7 were identified to genus level only, and one remained unclassified. In contrast, the DS seeds microbiome contained only 4 species-level identifications, dominated by *Alternaria alternata* and *A. oregonensis*, with one unclassified taxon. Six fungal taxa were common to both genotypes. Notably, 38 were unique to the DT seeds, while only 3 were unique to the DS seeds. This study demonstrates the genotype- and environmental-specific nature of inoculation efficacy and highlights the stress context-dependent nature of microbiome benefits:

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taxonomic richness provides tolerance to target stresses (e.g., drought) but may not provide advantages under conditions for which the system was not evolved. These findings emphasize the need for further multi-season studies to decode microbial inheritance rules to develop next-generation, stress context-tailored biologicals for sustainable agriculture.

**Keywords:** Seed microbiome; Wheat; High humidity; Bioinoculant; Stress Tolerance.

**Acknowledgment:** The study was supported by the grant of the Russian Science Foundation No. 25-16-00188, <https://rscf.ru/en/project/25-16-00188/>.

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