

## Quesiti busta 1

- Il/La candidato/a illustri i principi generali e le principali metodologie per l'allestimento dei preparati per l'osservazione microscopica a fresco, con colorazioni positiva (differenziale e non) e negativa.
- Il/La candidato/a illustri come si imposta una sommatoria su foglio elettronico.
- Il/La candidato/a legga e traduca in italiano il seguente testo: Lichen mycobiome represents fungal community residing within lichen thalli. While it is acknowledged that factors like the host lichen species and environmental conditions influence the structure of the lichen mycobiome, the existing research remains insufficient. To investigate which factor, host genus or location, has a greater impact on the lichen mycobiome, we conducted a comparative analysis of mycobiomes within *Parmelia* and *Peltigera* collected from both Turkey and South Korea, using high-throughput sequencing based on internal transcribed spacer region amplification. Overall, the lichen mycobiome was dominated by Capnodiales (Dothideomycetes), regardless of host or location. At the order level, the taxonomic composition was not significantly different according to lichen genus host or geographical distance. Hierarchical clustering of the top 100 abundant ASVs did not clearly indicate whether the lichen mycobiome was more influenced by host genus or location. Analyses of community similarity and partitioning variables revealed that the structure of the lichen mycobiome is more significantly influenced by location than by host genus. When analyzing the core mycobiome by host genus, the *Peltigera* mycobiome contained more ASV members than the *Parmelia* mycobiome. These two core mycobiomes also share common fungal strains, including basidiomycete yeast. Additionally, we used chi-squared tests to identify host genus-specialists and location-specialists. By comparing lichen mycobiomes of the same genera across different countries, our study advances our comprehension of these microbial communities. Our study elucidates that, although host species play a contributory role, geographic distance exerts a more pronounced impact on the structure of lichen mycobiome.
- Il/La candidato/a elenchi le principali funzioni del Nucleo di Valutazione dell'Università degli Studi di Perugia, come da Art. 26 dello Statuto.

omissis

## Quesiti busta 2

- Il/La candidato/a illustri i principi generali e le principali tecniche per la valutazione dell'influenza dei parametri abiotici sullo sviluppo microbico (aerobiosi/anaerobiosi, pH, temperatura, Aw).
- Il/La candidato/a spieghi brevemente a cosa serve una macro su foglio elettronico.
- Il/La candidato/a legga e traduca in italiano il seguente testo: Here we describe recent breakthroughs in our understanding of microbial life in dry volcanic tephra ("soil") that covers much of the surface area of the highest elevation volcanoes on Earth. Dry tephra above 6000 m.a.s.l. is perhaps the best Earth analog for the surface of Mars because these "soils" are acidic, extremely oligotrophic, exposed to a thin atmosphere, high UV fluxes, and extreme temperature fluctuations across the freezing point. The simple microbial communities found in these extreme sites have among the lowest alpha diversity of any known earthly ecosystem and contain bacteria and eukaryotes that are uniquely adapted to these extreme conditions. The most abundant eukaryotic organism across the highest elevation sites is a *Naganishia* species that is metabolically versatile, can withstand high levels of UV radiation and can grow at sub-zero temperatures, and during extreme diurnal freeze-thaw cycles (e.g. - 10 to + 30 °C). The most abundant bacterial phylotype at the highest dry sites sampled (6330 m.a.s.l. on Volcán Llullaillaco) belongs to the enigmatic B12-WMSP1 clade which is related to the *Ktedonobacter/Thermosporothrix* clade that includes versatile organisms with the largest known bacterial genomes. In contrast to the extremely low diversity of dry tephra, fumaroles found at over 6000 m.a.s.l. on Volcán Socompa support very diverse microbial communities with alpha diversity levels rivalling those of low elevation temperate soils. Overall, the high-elevation biome of the Atacama region provides perhaps the best "natural experiment" in which to study microbial life in both its most extreme setting (dry tephra) and in one of its least extreme settings (fumarolic soils).
- Il/La candidato/a definisca e descriva le principali funzioni del Comitato unico di garanzia per le pari opportunità dell'Università degli Studi di Perugia, come da Art. 29 dello Statuto.

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### Quesiti busta 3

- Il/La candidato/a illustri i principi generali e le principali tecniche per la conservazione *ex-situ* dei microrganismi, evidenziando vantaggi e svantaggi di ciascuna di esse, aiutandosi con alcuni esempi.
- Il/La candidato/a spieghi come si calcola l'errore standard di una media su foglio elettronico.
- Il/La candidato/a legga e traduca in italiano il seguente testo: In view of the high responsiveness of polar ecosystems to the global climate change, the research of Antarctic microorganisms has become a topical issue. The unique ecosystems that have developed under the severe climate conditions of the continent lack flowering plants but are dominated by soil mycobiota. Antarctic fungi form the basis of local communities, e.g., endoliths and microbial mats. Furthermore, Antarctic fungi are a major force that mediates transformation of rock minerals in situ and makes biologically significant elements available for other organisms. For these reasons, mycobiota plays a central role in the maintenance of ecological equilibrium in Antarctica. The dominant fungal division on the continent is Ascomycota (77.1%), and not Basidiomycota (9.1%), as it is the case on other continents. For a number of reasons, yeasts and yeast-like micromycetes (mainly basidiomycetes) are more tolerant to extreme conditions in various Antarctic biotopes than filamentous fungi. Substantial evidence suggests that filamentous fungi and yeasts are better adapted to existence in ecosystems with extremely low temperatures than other microorganisms. Due to the long-term isolation of Antarctica from other continents, local biota has been evolving largely independently, which led to emergence of multiple endemic fungal taxa. This review discusses the current state of research on the structure of fungal communities of Antarctic subaerial and subaquatic biotopes, the ecological role of yeast-mycelial dimorphism in Antarctic fungi, the problem of endemism of Antarctic mycobiota, as well as the ecological and physiological adaptations of fungi to low temperatures; it also justifies the relevance of research into secondary metabolites of psychrophilic micromycetes.
- Il/La candidato/a illustri il Collegio dei Revisori dei conti, come da Art. 25 dello Statuto.

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#### Quesiti busta 4

- Il/La candidato/a illustri i principi generali e le principali tecniche per la verifica della produzione di metaboliti extracellulari nei microrganismi (es. enzimi, acidi organici, antibiotici).
- Il/La candidato/a spieghi che formato indica in un file l'estensione ".csv"
- Il/La candidato/a legga e traduca in italiano il seguente testo: This study explored the degradation potential of a yeast strain, *Meyerozyma caribbica*, alone and in combination with *Bacillus velezensis* and *Priestia megaterium*, found novel for lindane biodegradation. Isolated from hexachlorocyclohexane (HCH)-contaminated sites, *M. caribbica*, *B. velezensis*, and *P. megaterium* demonstrated lindane reduction efficiencies of 86.5%, 78.6%, and 77.5%, respectively, at 750 mg L<sup>-1</sup> within 10-day incubation period. Kinetic analysis revealed that *M. caribbica* followed the first-order degradation ( $r^2 = 0.991$ ;  $T_{1/2} = 4.3$  days). Notably, *M. caribbica* exhibited the highest dechlorinase activity (9.27 U mL<sup>-1</sup>) in the cell supernatant. Co-cultivation as the mixed culture of *M. caribbica* and *P. megaterium* achieved maximum lindane reduction (90%) and dechlorinase activity (9.93 U mL<sup>-1</sup>). Whereas the mixed culture of *M. caribbica* and *B. velezensis* resulted in 80.9% reduction at 500 mg L<sup>-1</sup> lindane with dechlorinase activity of 6.77 U mL<sup>-1</sup>. Growth kinetics, modelled using the Monod equation, showed a maximum specific growth rate of 0.416 h<sup>-1</sup> for the mixed culture of *M. caribbica* and *P. megaterium* at 750 mg L<sup>-1</sup> lindane. GC-MS analysis confirmed the presence of intermediate metabolites, viz.,  $\gamma$ -pentachlorocyclohexane, 1,2,4-trichlorobenzene, 1,4-dichlorobenzene and maleyl acetate, validated successive dechlorination and oxidative-reduction processes during lindane biodegradation. The findings of the study highlighted the potential of these novel microbial strains and their mixed cultures for effective bioremediation of lindane-contamination.
- Il/La candidato/a illustri la durata in carica, elettorato passivo, modalità di elezione e cessazione dalla carica di Rettore, come da Art. 11 dello Statuto.

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## Quesiti busta 5

- Il/La candidato/a illustri i principi generali della norma europea ISO 20387, recepita a livello nazionale come UNI EN ISO 20387:2020, in merito ai requisiti generali per il biobanking di collezioni biologiche.
- Il/La candidato/a spieghi l'utilizzo di incolla Valori quando si copia e incolla il contenuto di più celle su foglio elettronico.
- Il/La candidato/a legga e traduca in italiano il seguente testo: In the current study, we compared the production of extracellular lignocellulose degrading enzymes and bioethanol from the spent mushroom substrate (SMS) of *Calocybe indica* and *Volvariella volvacea*. From SMS at different stages of the mushroom development cycle, ligninolytic and hydrolytic enzymes were analysed. The activities of lignin-degrading enzymes, including lignin peroxidase (LiP), laccase, and manganese peroxidase (MnP) were maximal in the spawn run and primordial stages, while hydrolytic enzymes including xylanase, cellobiohydrolase (CBH), and carboxymethyl cellulase (CMCase) showed higher activity during fruiting bodies development and at the end of the mushroom growth cycle. SMS of *V. volvacea* showed relatively lower ligninase activity than the SMS of *C. indica*, but had the maximum activity of hydrolytic enzymes. The enzyme was precipitated with acetone and further purified with the DEAE cellulose column. The maximum yield of reducing sugars was obtained after hydrolysis of NaOH (0.5 M) pretreated SMS with a cocktail of partially purified enzymes (50% v/v). After enzymatic hydrolysis, the total reducing sugars were  $18.68 \pm 0.34$  g/l (SMS of *C. indica*) and  $20.02 \pm 0.87$  g/l (SMS of *V. volvacea*). We observed the highest fermentation efficiency and ethanol productivity (54.25%, 0.12 g/l h) obtained from SMS hydrolysate of *V. volvacea* after 48 h at  $30 \pm 2$  °C, using co-culture of *Saccharomyces cerevisiae* and *Pachysolen tannophilus*.
- Il/La candidato/a elenchi la composizione del Consiglio di Amministrazione dell'Università degli Studi di Perugia, come da Art. 21 dello Statuto.

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## Quesiti busta 6

- Il/La candidato/a illustri i principi generali e le tecniche utilizzate per la valutazione dell'attività antimicrobica di principi attivi di varia origine.
- Il/La candidato/a spieghi a cosa serve la funzione "filtro" in un foglio elettronico.
- Il/La candidato/a legga e traduca in italiano il seguente testo: Since food spoilage by yeasts causes high economic losses, fast and accurate identifications of yeasts associated with food and food-related products are important for the food industry. In this study the efficiency of the matrix assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS) to identify food related yeasts was evaluated. A CBS in-house MALDI-TOF MS database was created and later challenged with a blinded test set of 146 yeast strains obtained from food and food related products. Ninety eight percent of the strains were correctly identified with log score values >1.7. One strain, *Mrakia frigida*, gained a correct identification with a score value <1.7. Two strains could not be identified at first as they represented a mix of two different species. These mixes were *Rhodotorula babjevae* with *Meyerozyma caribbica* and *Clavispora lusitaniae* with *Debaryomyces hansenii*. After separation, all four species could be correctly identified with scores >1.7. Ambiguous identifications were observed due to two incorrect reference mass spectra's found in the commercial database BDAL v.4.0, namely *Candida sake* DSM 70763 which was re-identified as *Candida oleophila*, and *Candida inconspicua* DSM 70631 which was re-identified as *Pichia membranifaciens*. MALDI-TOF MS can distinguish between most of the species, but for some species complexes, such as the *Kazachstania telluris* and *Mrakia frigida* complexes, MALDI-TOF MS showed limited resolution and identification of sibling species was sometimes problematic. Despite this, we showed that the MALDI-TOF MS is applicable for routine identification and validation of foodborne yeasts, but a further update of the commercial reference databases is needed.
- Il/La candidato/a illustri la Composizione del Senato Accademico, come da Art. 17 dello Statuto.

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## Quesiti busta 7

- Il/La candidato/a illustri i principi generali del trattato di Budapest in materia di deposito di risorse biologiche coperte da brevetto ai fini della protezione della proprietà intellettuale.
- Il/La candidato/a spieghi cosa si intende per trasposizione dei dati quando si copia e incolla il contenuto di più celle su foglio elettronico.
- Il/La candidato/a legga e traduca in italiano il seguente testo: *Yarrowia lipolytica* is an oleaginous yeast species that has attracted attention as a model organism for synthesis of single cell oil. Among over 50 isolates of *Y. lipolytica* identified, only a few of the strains have been studied extensively. Furthermore, 12 other yeast species were recently assigned to the *Yarrowia* clade, and most are not well characterized in terms of cell growth and lipid accumulation, especially in industrially relevant conditions. In the present study, we investigated biomass and lipid production by 57 yeast isolates, representing all 13 species in the *Yarrowia* clade, on a non-detoxified dilute acid-pretreated switchgrass hydrolysate under highly aerobic conditions. The objective was to compare yeast physiology during growth in an abundant, low-cost biomass feedstock and to expand diversity of genetically tractable, oleaginous yeasts available for lipid research. Screening of 45 *Y. lipolytica* isolates demonstrated considerable variation within the species in terms of lipid accumulation (min = 0.1 g/L; max = 5.1 g/L; mean = 2.3 g/L); three strains were especially promising for cellulosic biomass conversion with average improvements of 43.57, and 64%, respectively, in final lipid titer as compared to control strain W29. Subsequently, evaluation of strains from 13 distinct species in the *Yarrowia* clade identified *Candida phangngensis* PT1-17 as the top lipid producer with a maximum titer of 9.8 g/L lipid, which was over twofold higher than the second-best species in the clade (*Candida hollandica* NRRL Y-48254). A small set of the most promising strains from the screenings was further characterized to evaluate inhibitor tolerance, lipid production kinetics, and fatty acid distribution. We expect that the results of this study will pave the way for new biotechnological applications involving previously overlooked and under-characterized strains within the *Yarrowia* clade.
- Il/La candidato/a elenchi le principali funzioni del Direttore Generale dell'Università degli Studi di Perugia, come da Art. 24 dello Statuto.

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