Для впровадження цього методу в Україні, враховуючи необхідність мати 1 мільйон дійних корів у великотоварному виробництві, потрібно збільшити їх поголів'я на 600 тисяч, тобто у 2,5 рази, що є значним обсягом. Потрібно враховувати, що метод відтворення що пропонується, доцільно використовувати тільки на високопродуктивному маточному поголів'ї.

В Європі середній рівень продуктивності становить понад 10 тисяч кг молока на корову, в Ізраїлі та Нідерландах — понад 12 тисяч кг. В Україні варто почати з рівня понад 8 тисяч кг на корову і таких високопродуктивних корів в Україні налічується понад 100 тисяч голів. Протягом року використання цього методу можна вийти на рівень до 90% виходу теличок, тобто отримувати біля 90 тисяч теличок, що на 45 тисяч більше, ніж при звичайному штучному осіменінні. Таким чином 600 тисяч додаткових нетелів можна отримати за 14-15 років, доволі тривалий час.

З надходженням високопродуктивних первісток до молочних стад можна подвоїти кількість корів, на яких використовується сексована сперма, за 5-6 років. Таким чином, через 10 років після початку програми, в Україні може бути 1 мільйон дійних корів, що є цілком прийнятним терміном.

На завершення, хочу зазначити суму економічного ефекту, яку можна досягти, впровадивши цю програму у молочне скотарство України. Наші розрахунки показують, що завдяки скороченню та повному заміщенню імпорту нетелів, економія становитиме 330 мільйонів євро. Крім того, від продажу надлишкових теличок можна отримати 10 мільйонів євро на кожні 10 тисяч голів, а завдяки додатковій молочній продукції можна буде заробляти 7,5 тисячі євро на одну дійну корову. Загальний економічний ефект від використання сексованої сперми у розведенні молочної худоби та збільшення поголів'я корів до 1 мільйона у великотоварному виробництві складе приблизно 7 мільярдів євро.

APPLICATION OF QUANTITATIVE PCR FOR THE DETECTION FUNGAL ABUNDANCE

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Fungi, pervasive microorganisms, play pivotal roles in diverse ecosystem processes, notably organic matter decomposition. They coexist and interact with bacteria across various environments, forming interdependent consortia with both antagonistic and cooperative behaviours. Despite evolutionary, physiological, and metabolic disparities, these consortia collectively drive ecologically significant functions.

Within biological plants, fungi constitute part of the intricate microbiota of activated sludge. Yet, analyses of microbial communities in these engineered settings often prioritize bacteria, leaving the abundance and functions of other microbial groups relatively unexplored. These organisms contribute to biomass degradation, emerging contaminant removal, denitrification, and stabilization of activated sludge aggregates.

Traditionally, the methodology for isolating and identifying microorganisms from various materials in our cultural heritage involved cultivation methods and/or microscopy. Classical cultivation techniques offered numerous advantages, allowing the acquisition of living microorganisms for further physiological studies. Additionally, these methods facilitated both quantitative and qualitative assessments of the examined environment. Quantitative analyses were conducted through plate counts and activity determination via colony-forming unit (CFU) assays, both relying on microbial growth on selective media. However, these techniques are now recognized to have several limitations (e.g., requiring substantial sample amounts, extensive time investment, only capturing a fraction of cultivable microorganisms present in samples, etc.), resulting in an underestimation of cell numbers and failing to provide a comprehensive overview of the inhabiting microbiota.

In recent decades, several culture-independent molecular DNA and phylogenetic techniques have emerged, offering numerous advantages over traditional cultivation approaches. Molecular techniques capitalize on the specificity of nucleic acid sequences for microorganism identification and their independence from the need to culture microorganisms. Various genotyping techniques, primarily PCR-based, have been developed and adapted for fingerprinting microbial communities.

In recent years, molecular methods have revolutionized our understanding of microbial diversity and functions in various environments. Real-time PCR (qPCR) has emerged as a valuable tool for directly quantifying target microorganisms using environmental DNA. Despite this, only a limited number of studies have utilized qPCR to explore the total mycobiota size in environmental samples from soil, sediments, bioaerosols, or freshwaters. The majority of investigations into fungal populations have relied on cultivation-dependent approaches, overlooking the full extent of fungal diversity and abundance.

In numerous studies, molecular methodologies were consistently applied for precise identification of bacterial or fungal genera or exact strains. Additionally, traditional microbiological techniques, like culturing, were integrated into investigations to enable comparative analyses with molecular methods. Fungal strain identification primarily relied on culture in most studies, with only a few utilizing molecular methods.

While the aforementioned methods are commonly employed to assess the abundance and diversity of individuals within a community, there's often a need to determine the abundance of the entire target population within that community. Previous research has demonstrated the utility of quantitative PCR in assessing the abundance of specific phylogenetic groups of microorganisms in soil and other environmental samples. qPCR was developed to address a fundamental limitation of classical PCR technology, which cannot directly quantify amplicon amounts or accurately measure low DNA concentrations. Unlike classical end-point PCR, qPCR utilizes the fluorescence of a reporter molecule (such as SYBR green) to monitor the increase in PCR product during each amplification cycle. This allows for the comparison of samples during the exponential phase of amplification, before reaction saturation occurs, leading to more precise determination of starting template quantities.

Monitoring of forest biodiversity

Baseline Assessment: Before any significant event such as a war, establishing a baseline assessment of forest biodiversity is crucial. This includes conducting comprehensive surveys to document the diversity of flora and fauna, including fungi, within the forest ecosystem.

Long-Term Monitoring: Biodiversity monitoring should be conducted over the long term, ideally spanning several years or decades, to capture natural fluctuations and trends in forest biodiversity. Consistent monitoring allows for the detection of changes and helps distinguish between natural variability and impacts caused by external factors like war.

Multi-level Assessment: Biodiversity monitoring should occur at multiple levels, from species diversity to genetic variation within populations. This multi-level approach provides a more comprehensive understanding of ecosystem health and resilience.

Integrated Methods: Combining various monitoring methods, including field surveys, remote sensing, and molecular techniques like qPCR, enhances the accuracy and reliability of biodiversity assessments. Integrated approaches allow for the detection of changes across different spatial and temporal scales.

Monitoring Forest Biodiversity During and After Hostilities

Safety Considerations: During hostilities, ensuring the safety of researchers and conservationists is paramount. Monitoring efforts may need to be adjusted or postponed depending on the level of conflict and accessibility to study sites.

Rapid Assessments: In situations where conducting comprehensive surveys is not feasible due to ongoing hostilities, rapid biodiversity assessments can provide valuable initial insights into the status of forest ecosystems. These assessments may involve quick field surveys, remote sensing, and available data sources.

Adaptive Monitoring: Flexibility and adaptability are essential in post-hostility monitoring efforts. Rapid changes in environmental conditions and human activities may necessitate adjustments to monitoring protocols and priorities.

Community Engagement: In post-hostility scenarios, involving local communities in biodiversity monitoring can foster collaboration, build trust, and provide valuable local knowledge about forest ecosystems and species distributions.

Comparing Forest Biodiversity Before and After Hostilities

Direct Impacts: Hostilities can directly impact forest biodiversity through activities such as bombing, landmines, and military operations. Comparing biodiversity data before and after hostilities can reveal the extent of direct habitat destruction and mortality of flora and fauna.

Indirect Impacts: Indirect effects of hostilities, such as displacement of human populations, changes in land use patterns, and disruption of ecosystem services, can have significant implications for forest biodiversity. Monitoring these indirect impacts helps understand the full extent of biodiversity changes.

Degradation and Fragmentation: Hostilities often result in habitat degradation and fragmentation, which can isolate populations, reduce genetic diversity, and increase vulnerability to extinction. Comparing forest structure and connectivity before and after hostilities provides insights into the impacts on population.

Human-Wildlife Conflict: Hostilities can exacerbate human-wildlife conflicts, as displaced populations may encroach upon forest habitats for resources, leading to increased poaching, habitat destruction, and disturbances. Monitoring changes in human-wildlife interactions is essential for mitigating conflicts and conserving biodiversity.

Post-conflict Conservation: Post-hostility periods present opportunities for implementing conservation initiatives and restoring degraded forest ecosystems. Comparing biodiversity data over time helps evaluate the effectiveness of conservation interventions and prioritize restoration efforts in areas most affected by hostilities.

Social and Economic Factors: Understanding the social and economic drivers of biodiversity change is critical in post-hostility contexts. Monitoring changes in land tenure, livelihoods, and resource use patterns provides insights into the underlying drivers of biodiversity loss or recovery.