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Short communication

Molecular genetic analysis as a tool for Cannabis quality control

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Introduction

The rapid expansion of the global cannabis industry and the continuous introduction of new cultivars, hybrids, and chemovars have created increasing challenges regarding the authenticity, consistency, traceability, and safety of *Cannabis sativa*-derived products. The growing medical and commercial demand for cannabis has been accompanied by extensive breeding activities, large-scale clonal propagation, and the development of proprietary strains with distinct phytochemical profiles, further increasing the complexity of cannabis standardization and quality control (QC). In parallel, inconsistent strain labeling, genetic drift during propagation, and variability between cultivation batches have become important concerns for manufacturers, regulators, and consumers, particularly in the medicinal cannabis sector where product reproducibility and therapeutic consistency are essential.

Conventional vs molecular QC methods

Conventional quality control of cannabis is primarily based on morphological examination and chemical profiling of cannabinoids and terpenes using chromatographic techniques. Although these approaches are essential for potency assessment and regulatory compliance, they may be insufficient for reliable cultivar identification, detection of genetic instability, or identification of biological contaminants, since phytochemical composition can be strongly influenced by environmental conditions, cultivation practices, harvesting stage, storage conditions, and post-harvest processing. Unlike conventional QC methods, molecular analysis provides direct information on the genetic makeup of cannabis plants and can support quality control at multiple stages of production. These approaches are particularly useful for verification of cultivar identity in mother plants and propagation material, assessment of clonal fidelity during micropropagation, detection of genetic drift in breeding programs, authentication of commercial products, early prediction of cannabinoid

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chemotypes, and detection of pathogen and viroid infections, including Hop latent viroid (HLVd).

Molecular genetic techniques in cannabis QC

The principal molecular genetic techniques currently applied in cannabis analysis include amplified fragment length polymorphism (AFLP), random amplified polymorphic DNA (RAPD), inter-simple sequence repeat (ISSR) analysis, short tandem repeat/simple sequence repeat (STR/SSR) markers, single nucleotide polymorphism (SNP) analysis, quantitative polymerase chain reaction (qPCR), DNA barcoding, and whole genome sequencing (WGS). STR/SSR markers have shown high discriminatory power for differentiating hemp and drug-type cannabis, forensic identification, and assessment of intra- and inter-varietal genetic diversity (Dufresnes et al., 2017). In addition, considerable genetic inconsistencies were observed among samples marketed under the same strain name, emphasizing the need for standardized genetic verification systems within the cannabis industry (Schwabe et al., 2019). Recent studies combining STR profiling with multivariate statistical analysis and machine learning further demonstrated associations between specific molecular markers and cannabinoid composition, supporting the potential use of molecular markers for chemotype prediction and breeding of cannabis varieties with targeted cannabinoid profiles (Cisiana et al, 2024; Stoilkovska Gjorgievska et al., 2025). Furthermore, DNA marker systems targeting THCA synthase genes enabled discrimination of low-THC from high-THC cultivars, supporting the selection and authentication of suitable medicinal and industrial cannabis materials.

Pathogen detection with molecular methods

Molecular genetic techniques have become increasingly important for the detection of pathogens, viroids, and microbial contaminants affecting *Cannabis sativa* quality and safety. Hop latent viroid (HLVd), one of the most significant emerging threats in cannabis cultivation, has been associated with reduced plant vigor and decreased cannabinoid production (Adkar-Purushothama et al., 2023). Molecular approaches such as qPCR, RT-PCR, and next-generation sequencing (NGS) enable rapid and sensitive detection of latent infections and microbial contaminants, including toxigenic fungi such as Aspergillus and Fusarium species that may compromise the safety of medicinal cannabis products, particularly those intended for inhalation, thereby improving pathogen surveillance and overall cannabis quality control (McKernan et al., 2016). In addition, early molecular detection may help prevent large-scale propagation of infected plant material and reduce economic losses during cannabis production.

Conclusion

Molecular methods enable genetic fingerprinting, cultivar authentication, chemotype prediction, sex determination, and sensitive detection of pathogens and microbial contaminants. The integration of molecular analysis into cannabis quality control may therefore improve standardization, traceability, and product safety in breeding programs, propagation systems, pharmaceutical cannabis production, forensic investigations, and QC laboratories.

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