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Genetic Markers that are Most Useful for the Genetic Identification of Cannabis

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Description

Cannabis plants have been grown for thousands of years all over the world, and they are used a lot in the textile industry and medicine. They can be divided into two categories for analyses of the needs of the justice system: fibrous hemp and narcotic hemp, which contain different amounts of the psychoactive compound THC. The guidelines stipulate that narcotic varieties are those with a content of active compounds greater than 0.2%. To distinguish between these two kinds of Cannabis, toxicological analysis is the most common method. Genetic identification, on the other hand, might be a good option if there are issues with the type of plant part sent to the laboratory or the amount of differentiating active compounds present. The genetic analysis of cannabis samples using STR markers was the subject of the research consortium's investigation. The fundamental statistical parameters that are used to describe the population were taken into account in the analysis of the collected population database of Cannabis samples from fibrous and narcotic varieties. On the basis of a selected set of 23 STR genetic markers, which were subjected to preliminary statistical analyses, it was used to develop a method for genetic profiling Cannabis. The genetic models that have been developed will be used to select the genetic markers that are most useful for the genetic identification of Cannabis, which will make it possible to develop a tool for forensic experts to identify the plant. Wastewater Based Epidemiology (WBE) is an important tool in the fight against COVID-19 because it provides cost-effective, rapid, and non-invasive insights into the health status of the targeted population—from a single house to a large municipality. The implementation of Wastewater-Based Surveillance (WBS) has the potential to alleviate pressure on the public health system, assist in the management of pandemics, aid in the formulation of well-informed choices, and safeguard public health. This study aimed to monitor the prevalence of SARS-CoV-2 genetic markers in Clinical Specimens (CS) and Wastewater Samples (WS) for 30 days in a house with COVID-19 patients. SARS-CoV-2's non-structural (ORF1ab) and structural-Nucleocapsid (N) protein genes were targeted by RT-qPCR in accordance with a tested experimental protocol.

RNA Genetic Markers

The American Public Health Association (APHA) standard protocols were followed for the measurement of biological, environmental, and physiological parameters. When the greatest number of COVID-19 cases was clinically diagnosed, SARS-CoV-2 viral shedding in wastewater reached its peak. 7450 to 23,000 gene copies/1000 mL were found during the study, with WS representing 47% (57/120) and CS representing 35% (128/360) of the positive samples. The highest CT value (39.4 ;) occurred when the number of COVID-19 patients was lowest (2). WS was used to determine which copy number was the lowest. On the other hand, when the number of COVID-19 patients was highest (6), WS obtained the lowest CT value, or highest copy numbers, (25.2). The COVID-19 patient's advance signal of an increased SARS-CoV-2 viral load was detected in the WS earlier than in the CS. Involving redid preliminary sets in a conventional PCR approach; we affirmed that all SARS-CoV-2 variations recognized in both CS and WS were Delta variations (B.1.617.2). This is the first follow-up study to our knowledge to determine a temporal relationship between COVID-19 patients' discharge of SARS-CoV-2 RNA genetic markers in wastewater from a single house that included all family members for clinical sampling from a developing nation (Bangladesh) that does not have a proper sewage system. The study's most important findings indicate that COVID-19 cases could be identified by monitoring the genetic markers of the SARS-CoV-2 virus in wastewater, easing the burden on the public health system during COVID-19 pandemics. An assortment of 96 palms, addressing 16 different coconut promotions from the Worldwide Coconut Gene bank for South Asia and the Centre East (ICG-SAME), Kidu, India, was examined for hereditary variety and populace structure in view of 35 basic grouping rehash loci.

The accessions had a lot of different genes. With an average of 6.2 alleles per locus, the total number of alleles ranged from 2 to 22. The mean effective number of alleles per locus was 1.86, ranging from 1.04 to 3.58. The median estimate of gene diversity was 0.355, with estimates ranging from 0.224 to 0.457. The average Polymorphism Information Content (PIC) value was 0.36, with values ranging from 0.04 to 0.66. Various leveled bunching investigation assembled the genotypes into two significant bunches with two sub-gatherings, which related with the geographic beginnings. The dwarf accessions were in the first cluster, and the tall accessions were all in the second cluster. With two major populations (K=2), the results of the structure analysis were in line with those of the cluster analysis. The findings suggested that marker-assisted selection and genetic diversity in coconut could be assessed using SSR markers. In the Indo-Pacific region, the mangrove red snapper, Lutjanus argentimaculatus, is a marine fish of significant economic and cultural significance. It is now regarded as a much more significant species for aquaculture than for capture fisheries. Using microsatellite markers, the current study aimed to reveal the genetic structure of this candidate species from the Bay of Bengal and the Arabian Sea. Twelve microsatellite markers utilized for hereditary stock portrayal and 384 examples gathered from six unique areas were utilized for the review. A single unit stock of red snapper was found in the sampling region, and microsatellite markers suggested that there was sufficient gene flow between populations to limit genetic structuring. An examination of the genetic differentiation co-efficient suggested that there was no structuring between populations.

Genetic Diversity

However, structure's Bayesian cluster analysis revealed some evidence of sub-structuring between populations in the Arabian Sea and the Bay of Bengal. The aforementioned findings were supported in part by isolation by distance analysis, Principal Coordinate Analysis (PCoA), and hierarchical AMOVA analysis. Before appropriate management strategies for the mangrove red snapper in Indian waters can be developed, it is necessary to use more potent markers like SNPs to reveal the sub-structuring because microsatellites were unable to detect population differentiation in this instance. Farmers' traditional rice varieties are useful genetic resources for future rice improvement. These cultivars are extremely well-suited to a wide range of agro-ecological conditions. However, the adoption of high-yielding varieties causes their rapid disappearance. Any crop's improvement and conservation strategies in the face of climate change depend on the germplasm’s level of allelic and genetic diversity. Farmers' rice varieties typically have low yields but excel in a variety of traits, including resistance to biotic and abiotic stresses, grain quality, early seedling vigor, and input utilization efficiency. Consequently, the purpose of this study was to gain a comprehensive understanding of the allelic and genetic diversity, population structure, and morphological characteristics of 607 farmers' rice varieties by employing 36 fluorescently labeled microsatellite markers. With an average of 10.33 alleles per locus and a moderately high Nei's allelic/gene diversity (0.502), 363 alleles were found. The average polymorphic information content was 0.901, with values ranging from 0.685 to 0.987. There were 34 distinct, 236 uncommon, 84 low-frequency, and 44 high-frequency alleles found. There were 195 variables in 53 morphological traits, with an average of 4.217 variables per trait. Polymorphism was observed in 50 of 53 morphological traits, with highly significant variations between varieties. At the molecular (0.653) and phenotypic (0.656) levels, 607 farmers' rice varieties displayed a high genetic diversity.

The 607 farmer’s rice varieties were divided into three main categories by the dendrogram, which was constructed using both morphological traits and microsatellite markers. Two distinct subpopulations, SP1 and SP2, with fixation indices of 0.19 and 0.194, respectively, and membership rates of 82.6 and 17.4 percent, respectively, indicate a moderate population structure. 34% of variation within varieties and 63% of variation between varieties could be explained by the AMOVA. According to our findings, farmers' rice varieties from Odisha had higher levels of genetic and allelic diversity. As a result, these cultivars would be useful for the identification of novel and elite alleles as well as a source of donors for the creation of climate-smart cultivars with enhanced grain yield and quality, as well as efficiency in input use that would be able to withstand shifting climate scenario conditions and boost farmers' incomes. An ornamental and therapeutic herb belonging to the Orchidaceae family, Pleione is a perennial. Rare wild resources have been severely damaged or even put in danger as the demand for Pleione has continued to rise in recent years. The basis for breeding and the key to efficient use and protection of wild germplasm resources is genetic diversity analysis of Pleione. ITS and SCoT molecular markers were used for the first time to examine the relationship and genetic diversity of 16 individuals from 11 species of Pleione in this study. With an average of 7.6 bands per primer, 11 SCoT primers yielded a total of 84 bands, 83 of which were polymorphic (99 percent). The variation range of genetic similarity coefficients between individuals was 0.4524–0.9048, and the genetic distances between the various species of Pleione were 0.005–0.271. Nei genetic diversity (H), Shannon's information indexes and effective number of alleles (Ne) in the entire population were 1.54, 0.49, and 0.33, respectively. The present result demonstrates that the SCoT marker can be utilized for the genetic variation analysis of Pleione due to its versatility and polymorphism, and that the ITS sequence can be used to analyses the genetic relationship between species of Pleione. The identification and breeding of Pleione species depend greatly on this research.