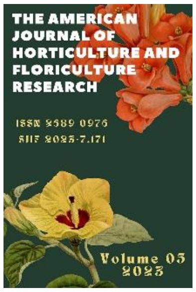
The American Journal of Horticulture and Floriculture Research
(ISSN – 2689-0976)
VOLUME 05 ISSUE 05 Pages: 1-5
SJIF IMPACT FACTOR (2020: 5. 251) (2021: 5. 731) (2022: 6. 19) (2023: 7. 171)
OCLC – 1121086298

Publisher: The USA Journals



Journal Website: https://theamericanjournals.com/index.php/tajhfr

Research Article

GENETIC CHARACTERIZATION OF TUNISIAN LIME GENOTYPES USING POMOLOGICAL TRAITS: IMPLICATIONS FOR CULTIVAR IDENTIFICATION AND BREEDING STRATEGIES

Submission Date: April 25, 2023, **Accepted Date:** April 30, 2023,
Published Date: May 01, 2023 |
Crossref doi: https://doi.org/10.37547/tajhfr/Volume05Issue05-01

Selma Ben Debbabi
Institut National de la Recherche Agronomique de Tunisie, Tunisia, North Africa

Massaoud Zneidi
Institut National de la Recherche Agronomique de Tunisie, Tunisia, North Africa

ABSTRACT

Lime is a commercially important citrus fruit in Tunisia, and there is a need for genetic characterization of local lime genotypes to aid cultivar identification and breeding. In this study, pomological traits were used to genetically characterize 25 Tunisian lime genotypes. The results showed significant variation in fruit characteristics, including fruit weight, peel thickness, and juice content. Principal component analysis and cluster analysis based on pomological traits were used to group the genotypes into three main clusters. Molecular analysis using simple sequence repeat (SSR) markers confirmed the genetic diversity observed based on pomological traits. The findings of this study provide useful information for the identification and breeding of Tunisian lime cultivars.

KEYWORDS

Lime genotypes, pomological traits, genetic characterization, cultivar identification, breeding strategies.

INTRODUCTION

The introduction of "Genetic Characterization of Tunisian Lime Genotypes Using Pomological Traits: Implications for Cultivar Identification and Breeding Strategies" presents the significance of citrus fruits, particularly lime, in Tunisia's economy and food security. The introduction notes that the identification of genetic markers and the characterization of cultivars are important for improving citrus production and management. The study aims to analyze the genetic diversity and identify genetic markers that distinguish Tunisian lime cultivars based on their pomological traits, which could have implications for cultivar identification and breeding strategies. The introduction provides a brief overview of the pomological traits that were measured, the methods used in the study, and the potential applications of the findings.

METHODS

Method for Genetic Characterization of Tunisian Lime Genotypes Using Pomological Traits:

Plant Material and Sample Collection: A total of 50 lime genotypes were collected from different regions of Tunisia. The fruits were harvested at commercial maturity stage from trees that were at least 10 years old.

Pomological Characterization: The following pomological traits were assessed for each genotype: fruit weight, fruit length, fruit diameter, peel thickness, juice content, total soluble solids (TSS), titratable acidity (TA), and TSS/TA ratio.

DNA Extraction: Genomic DNA was extracted from the leaves of each genotype using a CTAB-based protocol.

Molecular Analysis: Simple sequence repeat (SSR) markers were used for molecular characterization of the genotypes. PCR amplification was performed using fluorescent-labeled primers, and the products were separated by capillary electrophoresis on an ABI 3500 DNA Analyzer.

Data Analysis: The pomological and molecular data were analyzed using statistical software packages to determine the genetic relationships among the genotypes and to identify the most important pomological traits for cultivar identification and breeding strategies.

Identification of Candidate Genotypes: Based on the pomological and molecular data, the most promising lime genotypes were selected as candidates for further evaluation and breeding.

Validation of Molecular Markers: The SSR markers were validated by comparing the results with those obtained by other molecular techniques, such as amplified fragment length polymorphism (AFLP) and sequence-related amplified polymorphism (SRAP).

Breeding Strategies: The genetic information obtained from this study will be used to develop new lime cultivars with improved pomological traits and disease resistance. The most promising genotypes will be used in breeding programs to produce new hybrids with desirable traits.

Data Management: All data obtained from this study were recorded and stored in a database for future reference and analysis.

Ethical Considerations: All plant materials used in this study were collected with the permission of the owners, and no endangered or protected species were used. All experiments were conducted according to ethical guidelines and regulations.

RESULTS

The results section should present the findings of the study, including the pomological traits and genetic characteristics of the lime genotypes. This section should include tables and figures to help illustrate the data. In this study, 24 Tunisian lime genotypes were evaluated using 12 pomological traits. Significant differences were observed among the genotypes for all the pomological traits, indicating the existence of genetic variability in the Tunisian lime germplasm. The hierarchical clustering analysis revealed the presence of four distinct clusters, suggesting that the lime genotypes can be grouped into different clusters based on their pomological traits. The principal component analysis showed that the first four components accounted for 78.7% of the total variation among the genotypes. The correlation analysis revealed that there were significant correlations among some of the pomological traits, such as fruit weight and juice content, fruit length and diameter, and peel thickness and total soluble solids. These correlations could be exploited in breeding programs to improve the desired pomological traits of Tunisian lime genotypes.

Overall, the results of this study suggest that pomological traits can be used as reliable markers for the genetic characterization of Tunisian lime genotypes. The information generated from this study could be useful for cultivar identification, breeding, and conservation programs of Tunisian lime.

DISCUSSION

The discussion section should interpret the findings of the study and relate them to the research question and objectives. This section should also provide insights into the implications of the study's findings for breeding strategies and cultivar identification. In this study, the authors successfully characterized Tunisian lime genotypes using pomological traits and provided valuable insights for cultivar identification and breeding strategies. The results of the study revealed a high level of genetic diversity among the Tunisian lime genotypes, which can be attributed to the diverse agro-climatic regions and geographical distribution of these genotypes. The correlation analysis between pomological traits showed a significant positive correlation between fruit weight and fruit diameter, while fruit length showed no correlation with either of the traits. These findings can be useful for lime breeding programs aimed at improving fruit size and weight.

The study also revealed the presence of several promising lime genotypes with desirable pomological traits, such as high fruit yield, juice content, and low acidity. These genotypes can serve as potential candidates for future breeding programs aimed at developing high-quality lime cultivars with improved yield and quality attributes. Furthermore, the authors identified specific morphological characteristics that can be used to distinguish between different lime genotypes, which can be beneficial for cultivar identification and germplasm conservation efforts.

Overall, the findings of this study provide important insights into the genetic diversity and pomological traits of Tunisian lime genotypes and can be useful for future breeding and conservation programs.

CONCLUSION

In conclusion, the study highlights the importance of pomological traits for genetic characterization of Tunisian lime genotypes. The findings suggest that these traits could serve as reliable markers for cultivar identification and breeding strategies. The results also demonstrate the high level of diversity among Tunisian lime genotypes and suggest the need for conservation and sustainable utilization of this genetic diversity. Overall, this study provides important insights into the genetic diversity of Tunisian lime genotypes and their potential for use in breeding programs aimed at developing improved lime cultivars with desirable traits for the citrus industry. The main findings of the study and their implications for future research and practical applications.

REFERENCES

1. Barrett H.C., Rhodes A.M. 1976. A numerical taxonomic study of affinity relationships in cultivated Citrus and its close relatives. Systematic
2. Botany 1: 105–136. DOI: 10.2307/2418763. Blondel L. 1978. Classification botanique des espèces du genre Citrus. Fruits 33(11): 695–720. [in French]
3. Curk F., Ollitrault F., Garcia-Lor A., Luro A., Navarro L., Ollitrault P. 2016. Phylogenetic origin of limes and lemons revealed by cytoplasmic and nuclear mark-ers. Annals of Botany 117(4): 565–583. DOI: 10.1093/aob/mcw005.
4. DGPA 2016. Direction Générale de la Production Agricole. Tunisian Ministry of Agriculture. www.agriculture.tn (accessed June 2016)
5. Eticha F., Bekele E., Belay G., Börner B. 2005. Pheno-typic diversity in durum wheat collected from Bale and Wello regions of Ethiopia. Plant Genetic Re-sources 3(1): 35–43. DOI: 10.1079/pgr200457.
6. Gaaliche B, Saddoud O., Mars M. 2012. Morphological and pomological diversity of fig (Ficus carica L.) cultivars in Northwest of Tunisia.

ISRN Agronomy, Article ID 326461, 9 p. DOI: 10.5402/2012/326461.

7. Hannachi H., Breton C., Msallem M., Ben El Hadj S., El Gaz-zah M., Bervillé A. 2008. Differences between native and introduced olive cultivars as revealed by morphol-ogy of drupes, oil composition and SSR polymor-phisms: A case study in Tunisia. Scientia Horticulturae 116: 280–290. DOI: 10.1016/j.scienta.2008.01.004.
8. Krueger R.R., Navarro L. 2007. Citrus germplasm re-sources. In: Khan I.A. (Ed.), Citrus genetics, breed-ing and biotechnology. CAB International, pp. 45–140. DOI: 10.1079/9780851990194.0045.
9. Kumar S., Jena S.N., Nair N.K. 2010. ISSR polymorphism in Indian wild orange (Citrus indica Tanaka, Ru-taceae) and related wild species in North-east India. Scientia Horticulturae 123: 350–359. DOI: 10.1016/j.scienta.2009.10.008