

Management of walnut genetic resources to improve the efficiency of the breeding process in the South of Russia

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Abstract. Walnut is one of the main nut crops of world importance. Conservation and efficient use of genetic resources is one of the fundamental principles of breeding work. The most efficient way to work with genetic resources is to create core collections that include most of the genetic diversity with the least number of samples in the collection. There are several different approaches to the creation of core collections, differing in the criteria for the selection of characters and the number of samples in the collection. This article provides an overview of the most effective approaches to creating walnut core collections in southern Russia. Of course, both genetic and phenotypic diversity should be taken into account. Microsatellite markers or SNPs may be the most appropriate tools for assessing genetic diversity, depending on the objectives and sample sizes. The article also provides an overview of the most valuable traits from the point of view of walnut breeding in the North Caucasus.

1 Introduction

Walnut is one of the most widespread crops in the world [1]. The largest walnut-producing countries are the USA and China [2]. The volume of walnuts production in the world is increasing annually. This is due to both the growth of the world's population and the growing needs of the population for nut crops with high nutritional value.

The basis for effective crop cultivation is assortment, the diversity and relevance of which is supported by breeding programs. Of course, artificial selection carried out by breeders can significantly reduce the genetic diversity of a culture, which negatively affects the potential of genetic collections as sources of new traits and their combinations [3].

Breeders in an effort to improve the phenotypic properties of genotypes rely on the genetic diversity of forms in collections. It can be concluded that genetic collections should be as large as possible. However, maintaining large collections is associated with high costs, phenotypic assessment of large collections is a laborious process that requires high labor costs of highly qualified specialists [3]. The most justified way is to create core

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Characterization Genetic Breeding Resources Russia

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Table of Contents Characterization Genetic Breeding Resources Russia

1. Understanding the eBook Characterization Genetic Breeding Resources Russia
 - The Rise of Digital Reading Characterization Genetic Breeding Resources Russia
 - Advantages of eBooks Over Traditional Books
2. Identifying Characterization Genetic Breeding Resources Russia
 - Exploring Different Genres
 - Considering Fiction vs. Non-Fiction
 - Determining Your Reading Goals
3. Choosing the Right eBook Platform
 - Popular eBook Platforms
 - Features to Look for in an Characterization Genetic Breeding Resources Russia
 - User-Friendly Interface
4. Exploring eBook Recommendations from Characterization Genetic Breeding Resources Russia
 - Personalized Recommendations
 - Characterization Genetic Breeding Resources Russia User Reviews and Ratings

- Characterization Genetic Breeding Resources Russia and Bestseller Lists
- 5. Accessing Characterization Genetic Breeding Resources Russia Free and Paid eBooks
 - Characterization Genetic Breeding Resources Russia Public Domain eBooks
 - Characterization Genetic Breeding Resources Russia eBook Subscription Services
 - Characterization Genetic Breeding Resources Russia Budget-Friendly Options
- 6. Navigating Characterization Genetic Breeding Resources Russia eBook Formats
 - ePub, PDF, MOBI, and More
 - Characterization Genetic Breeding Resources Russia Compatibility with Devices
 - Characterization Genetic Breeding Resources Russia Enhanced eBook Features
- 7. Enhancing Your Reading Experience
 - Adjustable Fonts and Text Sizes of Characterization Genetic Breeding Resources Russia
 - Highlighting and Note-Taking Characterization Genetic Breeding Resources Russia
 - Interactive Elements Characterization Genetic Breeding Resources Russia
- 8. Staying Engaged with Characterization Genetic Breeding Resources Russia
 - Joining Online Reading Communities
 - Participating in Virtual Book Clubs
 - Following Authors and Publishers Characterization Genetic Breeding Resources Russia
- 9. Balancing eBooks and Physical Books Characterization Genetic Breeding Resources Russia
 - Benefits of a Digital Library
 - Creating a Diverse Reading Collection Characterization Genetic Breeding Resources Russia
- 10. Overcoming Reading Challenges
 - Dealing with Digital Eye Strain
 - Minimizing Distractions
 - Managing Screen Time
- 11. Cultivating a Reading Routine Characterization Genetic Breeding Resources Russia
 - Setting Reading Goals Characterization Genetic Breeding Resources Russia
 - Carving Out Dedicated Reading Time
- 12. Sourcing Reliable Information of Characterization Genetic Breeding Resources Russia
 - Fact-Checking eBook Content of Characterization Genetic Breeding Resources Russia
 - Distinguishing Credible Sources

13. Promoting Lifelong Learning
 - Utilizing eBooks for Skill Development
 - Exploring Educational eBooks
14. Embracing eBook Trends
 - Integration of Multimedia Elements
 - Interactive and Gamified eBooks

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