

RESTORE PROJECT: RECOVERY AND VALORIZATION OF TRADITIONAL SOLANUM TUBEROSUM VARIETIES AT RISK OF EXTINCTION

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Over the past five decades, human activities have had a profound impact on the ecological foundation of the biosphere, often leading to irreversible damage. The loss of biodiversity, characterized by the depletion of living organisms and habitats, as well as the simplification of landscapes, has become a critical global issue. This loss stems from both the overexploitation of natural resources and the widespread alteration of environments. Recognizing the significance of this problem, as highlighted by the "*Piano Nazionale sulla Biodiversità di Interesse Agricolo*" (National Plan for Biodiversity of Agricultural Interest) published by the Italian Ministry of Agricultural, Food and Forestry Policies, efforts to restore, preserve, and characterize genetic resources have emerged as essential for biodiversity conservation. Particularly for endangered species and ecotypes, such actions are imperative. With these considerations in mind, the "RESToRE" Project (*founded by Piedmont Region in the frame of the PSR 2014-2024 - Op. 10.2.1*) was conceived to address the specific recovery,

characterization, and sanitization needs of traditional Italian local landraces/varieties of potatoes that are at risk of extinction

The Project encompasses a set of overarching objectives, which include enhancing the phytosanitary aspects of the genotypes and preserving disease-free tubers that exhibit the characteristic traits of their respective landraces/varieties. The activities pertaining to characterization, along with the identification of appropriate sanitization strategies, will not only improve production but also foster interest among producers and promote consumer utilization. Furthermore, the valorization of the recovered, characterized, and restored genetic material may entail future assessments for their culinary suitability, which could potentially bolster the competitiveness of local genetic resources in comparison to commercially available counterparts.

In this study, our focus was specifically on a collection of 22 local Italian potato varieties, encompassing a total of about 60 accessions obtained from diverse locations across seven Italian regions. To characterize this germplasm set, we employed a next-generation sequencing (NGS) technology to generate high-throughput sequencing data, enabling the detection of numerous genetic polymorphisms. The K-seq protocol was employed, which utilizes Klenow polymerase-based PCR with short primers, designed by analyzing k-mer sets in the genome sequence. Through the fingerprinting process, duplications, synonymies, and similarities among different accessions of traditional Italian varieties were identified. In the next phase of the project, these findings will be compared with a selection of European potato varieties derived from the core collection established within the framework of the EU-funded project "*G2P-SOL: Linking genetics resources, genomes and phenotypes of solanaceous crops*" (www.g2p-sol.eu).