

A Review on Genetic History of Spinach (*Spinacia oleracea* L.)

Swati Kharade and Shamsunnisa Darzi

Department of Botany

Anjuman Islam Janjira Degree College of Science, Murud-Janjira, Raigad, Maharashtra, India

Abstract: Spinach (*Spinacia oleracea* L. $2n=2x=12$) is a widely consumed leafy vegetable known for its nutritional benefits. It is a very versatile crop as it is eaten either raw or cooked, and it is a common ingredient in various cuisines. The history of spinach, both from a domestication and a breeding history perspective, is arguably little known and not many references are available on this topic. For this reason, this study intends to be a review of what is known about spinach and what are the current trends on the breeding of this vegetable.

Keywords: Genetics, Spinach

I. INTRODUCTION

Spinacia oleracea Linn. is annual plant having medicinal property. It is native to central and southwestern Asia. It is cultivated for the sake of its succulent leaves and was introduced in Europe in the 15th century. It is the favorite food among Indians in winter season. The *Spinacia oleracea* is commonly known as Spinach (English). This paper addresses the genetic history of spinach as a comprehensive review of these crop aspects is currently unavailable.



Wild relatives:

Currently, 11 species from the genus *Blitum* and two species from the genus *Spinacia* are considered to be part of the gene pool of cultivated spinach (Vincent et al. 2013). While the *Blitum* species are classified in the tertiary gene pool, *Spinacia tetrandra* Steven ex M. Bieb and *Spinacia turkestanica* Iljin are assigned to the primary gene pool of cultivated spinach. Interestingly, Fujito et al. (2015) found that hybrids of *S. oleracea* × *S. tetrandra* and *S. tetrandra* × *S. oleracea* showed a highly diminished pollen fertility, which might question the primary gene pool position of *S. tetrandra*. Additionally, recent studies (Fujito et al. 2015; Xu et al. 2017) indicated that *S. oleracea* is phylogenetically closer to *S. turkestanica* than to *S. tetrandra*, suggesting that *S. turkestanica* is the wild ancestor of cultivated spinach.

Geographical spread

Spread of spinach followed two separate directions, one to Southern and Eastern Asia and another one to Africa, the Mediterranean and Northern Europe, from which it was later introduced in the Americas. A distinction is often made between two main groups of spinach cultivars, namely Asian-type and Western-type cultivars (Simoons 1990; Van der Vossen 2004). Recent phylogenetic studies have shown an association between genetic relationship and geographical

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origin of spinach accessions, with consistent differences between Asian and Western cultivars (Shi et al. 2017; Xu et al. 2017). At the morphological level, Asian cultivars preserved the narrow, hastate and smooth leaf shape and the long petioles of wild spinach, whereas Western cultivars changed the hastate leaf shape to a round form, while leaves were enlarged and the savoy leaf texture appeared (Van der Vossen 2004).

Early breeding history

Studying how spinach looked like in previous times and how new cultivars arose is difficult due to scarce documentation. During the 1950s, Sneep collected evidence regarding the domestication and breeding history of spinach. Since the end of the 19th century, Dutch breeders have played a leading role in spinach breeding (Sneep 1983). In particular, the role of Sluis & Groot (currently part of Syngenta) and Rijk Zwaan has been significant in the breeding history of spinach.

The chemical composition of spinach has been shown to differ significantly between cultivars, including oxalic acid, nitrate, vitamin C, lutein, carotenoid and phenolic content (Murphy and Morelock 2000; Murphy 2001; Howard et al. 2002; Pandjaitan et al. 2005; Solberg et al. 2015; Wang et al. 2018b). Although nutritional composition is known to be influenced by factors such as cultivation method and storage procedures (Lester et al. 2010; Koh et al. 2012), the large variation observed among cultivars indicates a genetic basis, suggesting that nutritional quality can be improved by plant breeding (Howard et al. 2002; Morelock and Correll 2008; Wang et al. 2018b)

Crop breeding

In 2017, an assembly of the spinach genome was published (Xu et al. 2017), which is available from Spinach Base (<http://www.spinachbase.org>). The spinach genome has an estimated size of ~1000 Mb, containing 74.4% of repetitive sequences and an approximate number of 25,500 protein-coding genes. Previous research revealed a total of 93 genomic regions associated with wild species introgressions that are potentially related with spinach domestication and breeding (Xu et al. 2017)

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