Chapter 8

Chloroplast and Mitochondrial Genome, Small RNA, and DNA Methylation of Canola Plant

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ABSTRACT

The canola plant (Brassica napus L.) is a major oilseed crop globally providing high-quality oil and protein feed for livestock. However, there is limited understanding of the genetic and molecular processes that govern the plant's growth, development

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and response to stress. This project seeks to investigate the genetic makeup of canola with a specific focus on the chloroplast and mitochondrial genomes, as well as the regulation of gene expression through small RNA and DNA methylation. It is with this in mind that we strive to elucidate the complex interaction between these components to explain the underlying mechanisms that impinge on canola productivity and its adaptability. This research shall stand as one of the major steps toward generation of high-yielding stress-tolerant and climate-resilient canola varieties, thereby further supporting the enhancement of global food security as well as sustainable agriculture.

1. INTRODUCTION

Canola belonging to the family of Brassicaceae, thrives in temperate climates, serving food and industrial purposes (McVetty & Scarth, 2012). Its oil is used in cooking, food processing, and non-food applications such as biodiesel production, while its by-products, such as canola meal, are a valuable protein source for livestock (O'Brien, 2016). The crop is also used in crop rotation systems, contributing to soil health by breaking pest cycles and enhancing nutrient availability for subsequent crops.

B. napus (rapeseed), initially resulted from natural hybridization between the two diploid species - *Brassica rapa* ($2n = 2x = 20$) and *Brassica oleracea* ($2n = 2x = 18$) (Nagaharu & Nagaharu, 1935), later led to the development of canola by selective breeding. Globally, the largest producer of canola is Canada accounting for 23% of the global production followed by China and India with 18% and 14% respectively ("USDA Foreign Agricultural Service," 2024). In India, canola is usually referred to as rapeseed and its yield can significantly vary based on various factors such as region, soil type and quality, climate and agricultural practices. Traditional rapeseed, while useful in industrial applications, was unsuitable for human consumption due to high levels of erucic acid and glucosinolates, compounds linked to potential health risks. Prolonged consumption of higher levels of erucic acid leads to the accumulation of lipids in the heart muscle fibres eventually weakening the muscle function (Galanty et al., 2023). Understanding its classical genetics provides essential insights into the traits that contribute to its agricultural value, including yield, disease resistance, and adaptability.

Traditional breeding methods primarily involve selection and crossbreeding which generally span over several generations. Plants with desirable traits such as improved oil content, disease resistance and yield are identified and are exposed to controlled pollination to develop hybrids. This meticulous process often requires multiple generations (F_1, F_2, F_3, etc.) to stabilize desired traits before commercialization. Additionally, mutation breeding has been utilized to introduce genetic variability

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