

PDF - GENETIC DIVERSITY OF M2 MUTANTS OF SUNFLOWER (HELIANTHUS ANNUUS L INDUCED BY ETHYL- METHANESULPHONATE (EMS) - researchcub.info

CHAPTER ONE

1.0 Introduction

Cultivated sunflower (*Helianthus annuus* L.) is an annual, herbaceous ($2n=34$) and a cross pollinated crop, native to North America. It is a member of the Asteraceae family and it is regarded as the fourth most important oilseed crop grown worldwide after soya beans, palm and edible rapeseed (canola) (Moghaddasi, 2011; Sujatha et al., 2012). Sunflower is cultivated on about 18 million hectares worldwide with an annual seed production of 40 million tons (FAOSTAT, 2015). Its seeds are known for their high oil (25 – 48%) and protein (23 – 35%) content and thus used in confectionary and animal feed (Imran et al., 2015). It is used as an ornamental plant due to the attractiveness of its flower (Mayor et al., 2010). Sunflower seeds have abundant health benefits which can be attributed to the high level of polyunsaturated and monounsaturated fats, phytosterols, tocopherols, protein, copper, folates, iron, zinc, and vitamin B (Nandha et al., 2014; Roche et al., 2010). Its oil is used as raw materials in many industries due to the presence of four commercially important fatty acids namely, palmitic, stearic, oleic, and linoleic acids (Lee et al., 2010). Gene variability within a species enables the development of new improved varieties with improved characteristics. Therefore, the success of genetic improvement of sunflower depends on the magnitude of genetic variability which enables the selection of desirable genotypes for breeding purpose (Cvejic et al., 2011). In addition, realizing the need for the imperativeness of low-input agriculture being proffered for the 21st century, farmers require a suite of improved crop varieties that are genetically diverse in terms of climate change resilience, input use-efficiency, high yielding potential, resistance to biotic and abiotic stresses, enhanced nutritional and other important quality attributes (Tester and Langridge, 2010; Waines and Ehdaie, 2007). However, the envisaged genetically diverse portfolios of sunflower crop varieties are often unavailable to farmers due to its extremely narrow genetic base (Seiler and Frederick, 2011). This makes its improvement through conventional breeding method alone difficult. In view of this, the induction of genetic variability for sunflower crop, particularly in the era of increasing global food crisis and changing climatic regimes is, therefore, highly desirable.

Mutagenesis is an important tool in plant breeding for increasing genetic variability and consequently, broadening the genetic base of germplasms (Ndou et al., 2013). Spontaneous mutations occur naturally in crops but, its rate is low and cannot always be exploited for breeding, thus the need for induced mutagenesis (Jain and Suprasanna, 2011). Mutations in plants can be induced using chemical or physical mutagens and the effectiveness and efficiency of any induced mutagenesis experiment are direct results of the choice of appropriate mutagen treatments (Rupinder and Kole, 2005).

Almost all mutagens have the property of reacting with DNA and thereby bringing about changes in nucleotide sequences. However, the mode of action of each mutagen is distinct. Besides, a mutagen may effectively bring about mutations, but the accompanying undesirable effects like lethality or sterility may decrease its efficiency (Shagufta et al., 2013). Thus, in order to exploit induced mutagenesis for crop improvement, a preliminary determination of the treatment that would yield the greatest amount of desirable mutation while at the same time, producing the least density of undesirable effects is necessary (Xin et al., 2008; Mba et al., 2010). Chemical mutagens as compared with physical mutagens offer high mutation rate and predominantly, point mutations (Cvejic et al., 2011). Among chemical mutagens, ethyl methanesulfonate (EMS) is the most powerful and effective mutagen for creating mutations in plants (Cvejic et al., 2011).

Mutagenesis has become an important crop improvement tool available to breeders with no regulatory restrictions imposed as with genetically modified crops (Parry et al., 2009) with mutant varieties readily accepted by consumers. Sunflower mutants with altered agronomic traits have been created through the use of induced mutations amongst which includes; early maturing, short stature, larger head diameter, thinner husk, high oil content, cytoplasmic male sterile (CMS) lines and many more (Sabetta et al., 2011; Cvejic et al., 2015; Mostafa, 2011). Mutagenesis, in conjunction with conventional breeding methods could result in mutant varieties with desirable traits that can be used to broaden the genetic base of sunflower and to improve its various agro-morphologically important traits. There is paucity of information on the response of sunflower varieties developed by IAR, Samaru to different EMS doses, as well as, effective mutagen dose for induction of variability. The present study was focused on increasing the genetic variability within selected sunflower varieties using EMS and selecting mutants with important agro-morphological traits for further improvement. In view of these, the objectives of this study were to:

- assess the response of the sunflower varieties to different EMS doses and determine optimal EMS doses for desirable mutation
- estimate genetic variability for agronomic traits among M₂ mutants and identify some desirable mutants for oil content and other agronomic traits
- assess the degree of association among oil content, grain yield and other agronomic traits
- assess the degree of similarity among the mutants for the studied agronomic traits.

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