Research Article

Vikrant Tyagi*, Satwinder Kaur Dhillon and Gurpreet Kaur Gene action for oil content and quality in diverse cytoplasmic sources in sunflower under varied moisture environments

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Abstract: Sunflower breeding aims to developing good heterotic hybrids which can be achieved by tapping combining ability of hybrids belongs to diverse parents. Nine diversified CMS lines along with one maintainer lines were hybridized with four male lines in a line \times tester manner thereby, developing a total 40 hybrids. The experimental material was grown over two environments i.e. recommended irrigation and other moisture stress environments continuously for two years 2011 and 2012 in randomized complete block design with three replications at Punjab Agricultural University, Ludhiana, Punjab, India. The experiment was design to estimate combining ability of parental lines, gene effects and effect of divers CMS sources on oil content and quality traits. It was observed that the nonadditive component of genetic variance played major role in inheritance of these traits as recommended by analysis of variance of combining abilities and analysis of genetic variance components. Further supporting this conclusion was the fact that the GCA/SCA ratio for oil content and quality traits observed in F_1 generation was less than one under both the environments. These results indicated the preponderance of dominant gene action and the feasibility of hybrid sunflower development. GCA estimates revealed that CMS analogues CMS-XA (Unknown), ARG-2A (H. argophyllus) and PRUN-29A (H. praecox spp. runyonic) were very good combiner for oil content under both the environments. The pollen parents RCR-8297 and P69R were observed as very good combiners for oil content and stearic acid under moisture stress condition. The male parent P100R was recorded very good combiner for oil content under normal environment while, RCR-8297

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and P100R were very good combiners for oleic acid under both the environments. A total seven crosses were identified for oil content and eight crosses for oleic acid as having high SCA effects under both the water regimes.

Keywords: additive and non-additive genes; combining ability; CMS sources; F_1 hybrids; sunflower and water stress.

Introduction

Sunflower is one of the four most important oilseed crops in the world, and the nutritional quality of its edible oil ranks among the best vegetable oils in cultivation. It can easily be adjusted in existing crop rotations of wheat, cotton, rice and sugarcane and therefore sufficient area for sunflower could be made available in India without disturbing major crops. Sunflower oil is naturally rich in both unsaturated fatty acids and numerous minor components. Typically, major amount of fatty acids in conventional sunflower oil are unsaturated, namely oleic (C18:1, 16–19%) and linoleic (C18:2, 68–72%) fatty acids. Palmitic (C16:0, 6%), stearic (C18:0, 5%) and minor amounts of myristic (C14:0), myristoleic (C14:1), palmitoleic (C16:1), arachidic (C20:0), behenic (C22:0) and other fatty acids account for the only 10% of the total amount (Skorić [et al. 2008\)](#page-15-0). Sunflower oil with high oleic acid content is in great demand due to its nutritional as well as industrial benefits. Sunflower hybrids having higher genetic potential for achene yield and oil contents are required to fulfill the gap between supply and demand of vegetable oil all over the world. Like other cross pollinated crops sunflower hybrids are preferred over open pollinated varieties due to high yield and uniformity. Foremost prerequisite of hybrid development is the manifestation of heterosis ([Hladni et al. 2007; Hilli et al. 2020; Skoric](#page-14-0) [et al. 2000](#page-14-0)). Heterosis is exploited to increase seed yield and oil contents. Heterosis ranging from 33-73% for seed weight, 7–16% for oil content, 20–77% for seeds per head and 30–73% for seed produce has been reported in various studies [\(Yilmaz and](#page-15-1) [Emiroglu 1995](#page-15-1)). It is vital to find out the best parents with good combining abilities for hybridization and superior combinations among them [\(Gangappa et al. 1997\)](#page-14-1). Higher general combining ability (GCA) effects show additive gene effects whereas higher specific combining ability (SCA) effects indicate dominance gene effects. Epistatic effect may also be found due to the non-significant of GCA and SCA effects [\(Fehr 1993\)](#page-14-2). Water is fundamental for crop generation, and best utilization of accessible water must be made for effective harvest creation and more significant returns. Water shortfall influences crop development, depending upon the phase of development and the intensity of water stress ([Clavel et al. 2005](#page-14-3)). To some extent, sunflower is considered to be tolerant of water deficit. Supplementary irrigation can improve crop productivity in areas of low rainfall. Seed yield and sunflower oil content were the main sensitive parameters to water deficit during flowering and reproduction stages ([Kazemeini et al. 2009](#page-14-4)). Diversification of cytoplasmic male sterility in sunflower is the urgent need for development high yield and quality hybrids having diversified cytoplasm which can provide tolerance to biotic and abiotic stress cause due to uniformity of cytoplasm. Diversified CMS sources in sunflower were developed at Punjab Agricultural University, Ludhiana and evaluated for their performance under normal irrigated environment ([Tyagi et al. 2013;](#page-15-2) [Tyagi et al. 2015; Tyagi et al. 2020](#page-15-2)) as well as under moisture-stress conditions [\(Tyagi](#page-15-3) [and Dhillon 2016a; Tyagi and Dhillon 2016b\)](#page-15-3) at PAU, Ludhiana. These sources were used to develop sunflower hybrids and estimate the combining ability for agronomic and yield traits under different irrigation environments [\(Dhillon and Tyagi 2016;](#page-14-5) [Tyagi et al. 2015\)](#page-14-5). The objectives of present research to study the combining ability effects and role of additive and non-additive genes under different water conditions so as to help breeders for designing efficient breeding strategies to improve oil and quality traits and diversification of CMS sources for oil and quality traits.

Materials and methods

The present investigation was conceded in the research fields of the oilseeds section, Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana, India. Nine CMS analogues from different cytoplasmic sources viz; CMS-XA (Unknown), E002-91, PKU-2 (Helianthus annuus), ARG-2, ARG-3, ARG-6 (H. argophyllus), DV-10A (H. debilis spp. vestitus), PHIR-27 (H. praecox ssp. Hirtus) and PRUN-29A (H. praecox spp. runyonic) were developed using a common maintainer NC-41B (H. petiolaris) and four common perfect restorers from PET-1 source for these CMS sources were identified. All CMS analogues along with NC-41B (common maintainer) were crossed in a line \times tester fashion with four common restorer lines, thus 40 F_1 hybrids developed and study the effect of different cytoplasmic sources on performance of hybrids. Also the efforts were made to identify some good combining CMS analogues and heterotic combinations for high oil content and good quality. The material was raised in paired rows of 4.5 m length with 60 and 30 cm inter and intra row spacing respectively, in the randomized block design with three replications during the years 2011 and 2012 under two water environments normal irrigated and water stress. Water stress induced by withholding irrigation after anthesis. All the agronomic practices recommended for the region were followed to raise a good crop. The oil content was estimated using a benchtop pulsed nuclear magnetic resonance (NMR)–MQC-5 analyser (Oxford, London). The gas liquid chromatography (GLC) was used for fatty acid estimation. The data were analyzed for determining the differences among genotypes, parents, crosses, parents vs. crosses according to Gomez [\(Gomez and Gomez 1984\)](#page-14-6), combing ability analysis from lines \times tester interactions according to statistical procedures developed by Kempthore [\(Kempthorne 1957](#page-14-7)) and estimation of components of genetic varation for both the environments separately.

Results and discussion

Analysis of variance: The analysis of variance pooled over the years for oil content and quality traits studied in a line \times tester design were highly significant differences for different parameters for all the traits under both normal and stress environment [Table 1](#page-4-0). The differences among the parents, parents vs crosses and crosses were observed to be highly significant for all the traits that's indicating the existence of wider genetic differences among parents and crosses. The mean squares due to lines (female), tester (male) and their interactions (female \times male) were found to be highly significant for all the traits in both the treatments. Significant interaction effects were observed in lines \times testers \times locations for all the characters studied, indicates the SCA effects of hybrids interacted with the environments for all the characters studied which are contradictory with the earlier reports ([Binodh et al. 2008; Sharma et al. 2003](#page-14-8)).

Genetic components of variances: The higher values of SCA variances over the GCA variances and the ratio of σ^2 GCA/ σ^2 SCA being lower and degree of dominance ($σ²$ GCA/ $σ²$ SCA) less than unity ([Table 1\)](#page-4-0) under both normal and stress environment confirmed the major role of dominant effects for all the traits and suggested the feasibility for exploitation of non-additive genetic variation for such traits through hybrid breeding programmes. Non-additive gene action have reported for oil yield while additive gene action for oil content [\(Binodh et al. 2008\)](#page-14-8) however, additive gene action for the inheritance of oil content and other physiological and agronomic characters in sunflower [\(Salem and Ali 2012](#page-15-4)). A non additive gene effect for oil content has also been reported [\(Memon et al. 2015; Parameswari et al. 2004\)](#page-14-9).

Contribution of lines, testers and lines \times testers interaction: The higher contribution of female parents was observed as compared to testers in the expression of all the traits indicating some degrees of maternal effect for these traits under both the environments and played very important role towards all the traits manifested significant paternal effect with non additive genes for these traits. However, interaction component (lines \times testers) had higher contributed for all the traits as compared to female and restorer lines which showed preponderance of dominant genes and predominant maternal influence for these traits under both normal and stress environment. Moreover, the importance of combining ability in a selection of parents for hybrid breeding program has been well emphasized by previous sunflower studies [\(Ghaffari et al. 2011](#page-14-10)). The higher variances of lines and testers were observed than lines \times testers for all the traits, which inferred the significance of additive gene effects on concerned traits. Significant contribution of lines, testers and lines \times testers to the overall variance, however, predominant maternal effect on the seed quality was evident due to its higher percentage ([Ghaffari et al. 2011\)](#page-14-10).

Source of variation D.F.

Mean performance of female lines and testers: The CMS analog PARUN-29A and ARG-3A had higher oil content (32.66; 30.88 and 30.48; 29.84) and oleic acid (59.01; 54.28 and 57.01; 54.09) under normal and water stress environments respectively as compared to conventional source NC-41B (27.03; 25.77 and 45.71; 45.16) under normal and water stress environment respectively while PHIR-27A (46.65 and 52.54) and NC-41B (45.88 and 45.57) recorded higher linoleic acid under both environments as compared to other which will provide oil stability for long time [Table 2](#page-6-0). ARG-3A (H. argophyllus) and PRUN-29A (H. praecox spp. runyonic) performed very well for oil content and oleic acid under both the environments, thus these CMS analogues may be utilized for further breeding programmes so as to develop new sunflower hybrids which having divers cytoplasmic background with improved oil content and quality. In the present study, among the testers P100R was observed that performing for oil content (29.49; 28.87) and oleic acid (56.23; 46.27) under normal and water stress environment [\(Table 2](#page-6-0)), their good performance was very evident for the characters under study. RCR-8297 was recorded higher linoleic acid (49.21; 50.23) under both environments which is a desirable character in sunflower for oil stability and is useful for the development of sunflower hybrids with high quality oil.

Performance of hybrids per se: The Mean values of 26 F_1 hybrids from different CMS sources were observed generally high oil content as compare to hybrids involved NC-41B sources as a female parent under normal environment whereas 41 hybrids under water stress environment [\(Table 3](#page-7-0)). The ARG-6A \times P69R had highest linoleic acid (66.29 and 62.85) under both the environments, recorded higher oil content (31.84 and 29.72) shows stability over water stress environment for oil content and quality. It is further confirmation that CMS source $(H, \text{argophyllus})$ had potential to overcome the water stress conditions and well performed under normal environment as well as under water stress environment which can be utilized to develop water use efficient sunflower hybrid for high oil content and high quality under varied moisture environments. SCA impacts are more imperative for crosspollinated plants, while CGA impacts are more imperative for self-pollinated plants [\(Kaushik 2019](#page-14-11)).

General combining ability effects: The success of any breeding programme mainly depends on selection of appropriate parental lines. Information regarding different types of gene action, relative magnitude of genetic variance and combining ability estimates are important genetic parameters for the improvement of sunflower [\(Khan et al. 2009](#page-14-12)). The importance of combining ability in selection of parents for hybridization has been emphasized by many workers in sunflower ([Putt 1966; Giriraj et al. 1987](#page-15-5)). The potentiality of any line to be used as a parent in hybridization depends on it's per se performance and the performance of F_1 hybrid derived from it and its own GCA effect. The results obtained from this study

Table 3: Mean performance of hybrids for oil and quality traits under varied moisture environment (pooled over years). Table : Mean performance of hybrids for oil and quality traits under varied moisture environment (pooled over years).

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regarding the effects of the general combining ability for lines and testers are presented in [Table 4](#page-10-0).

CMS analogues CMS-XA, ARG-2A and PRUN-29A and male P100R were recorded as very good combiner for oil content under normal environment. In stress environment all CMS analogues and male parent RCR-8297 and P69R except CMS line ARG-6A and PHIR-27A were observed as very good combiner for oil content. The CMS analogues CMS-XA, ARG-2A and PRUN-29A were recorded as very good combiner for oil content under both the environments ([Table 4](#page-10-0)). The female parents E002-91A, PKU-2A, ARG-2A and DV-10A and male parent P124R were recorded as very good combiner for palmitic acid (%) under normal environment whereas, under stress environment CMS ARG-3A and DV-10A and male P100R were recorded as very good combiner for palmitic acid and male parent P69R was recorded as very good combiner under both the environments. For stearic acid the female parents E002-91A, PKU-2A and ARG-3A and male P124R were recorded as very good combiner under both the environments. CMS analogue DV-10A and male parent RCR-8297 good combiner under normal environment and very good combiner under stress whereas, female lines AGR-2A and PRUN-29A were good combiner and very good combiner respectively for stearic acid under normal environment. The analogues CMS-XA, PKU-2A and ARG-6A were recorded very good combiners under normal environment while, under stress environment E002-91A and ARG-2A were observed as very good combiner for oleic acid and female parent NC-41B was recorded very good combiner under both the environments. The male parents RCR-8297 and P100R were recorded as very good combiner under both the environments. The male lines P69R was recorded good combiner under normal environment for oleic acid. The CMS analogues DV-10A, PHIR-27A and PHIR-29A and male parent P124R were observed very good combiner for linoleic acid under both environments. CMS E002-91A and ARG-3A was recorded very good combiner whereas, ARG-2A was good combiner for linoleic acid under normal environment. The CMS analogues CMS-XA, PKU-2A and ARG-6A and male parent P69R were recorded very good combiner for linoleic acid under stress environment [\(Table 4\)](#page-10-0). The above results were in accordance with earlier reports [\(Rather and Sandha 1998; Singh et al. 1999\)](#page-15-6).

Specific combining ability effects: Specific combining ability is very important estimate for determining the suitability of F_1 hybrid crop development. Higher SCA impacts are more significant for the development of hybrids in cross pollinated crops [\(Hallauer et al. 2010](#page-14-13)).

Twenty two hybrids under normal environment and 28 hybrids under stress environment recorded significant positive SCA effects for oil content and nine cross combinations were identified with high SCA effects for oil content under both the environments [Table 5](#page-11-0). Twenty four hybrids recorded significant positive SCA Table 4: Estimation of general combining ability effects for oil content and quality under varied moisture environment (pooled over years). Table 4: Estimation of general combining ability effects for oil content and quality under varied moisture environment (pooled over years).

*, ** - significant at 5 and 1 % level respectively. $*$, $**$ – significant at 5 and 1 % level respectively.

Table 5: Estimation of sca effects for oil content and quality under varied moisture environment (Pooled over years). Table : Estimation of sca effects for oil content and quality under varied moisture environment (Pooled over years).

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 in * σ \overline{a}

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effects under normal environment and 30 hybrids under stress environment whereas, 11 hybrids were recorded high SCA effects under both the environment for palmitic acid. Twenty four hybrids were recorded significant positive SCA effects under normal environment, 21 hybrids under stress environment and 16 hybrids under both the environment for stearic acid [Table 5](#page-11-0). A total of 29 hybrids recorded significant positive SCA effects under normal, 28 hybrids under stress and 14 hybrids under both the environments for oleic acid. Twenty five hybrids were recorded significant positive SCA effects under normal environment, 27 hybrids under stress environment and 12 hybrids both the environment for linoleic acid (%) [Table 5](#page-11-0). It is suggested that simple recurrent selection or bi parental mating followed by selection among the genotypes having desirable yield components may be effective in genetic amelioration of the characters under study. These results obtained in the study that crosses with high SCA effects for different yield related traits involve parents with low \times high or low \times low GCA are in agreement with the other studies ([Reddy and Madhavilatha 2005\)](#page-15-7).

The data revealed that, the female parent CMS-XA, ARG-2A and PRUN-29A were the best general combiner for oil content and DV-10A, PHIR-27A and PRUN-29A for linoleic acid under both the water regimes. Among the testers, RCR-8297 and P100R were best general combiner for oleic acid under both the water regimes and RCR-8297 for oil content under water stress while, P100R under normal water regime. The above results are in agreement with other studies ([Sharma et al. 2003; Tyagi and Dhillon 2017; Tyagi et al. 2018\)](#page-15-8). Similarly, significant GCA effect for seed yield and its contributing traits were reported in previous studies to identify suitable parental lines for hybrid development for potential hybrids [\(Andarkhor et al. 2012; Salem and Ali 2012;](#page-14-14) [Kaushik et al. 2017\)](#page-14-14).

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