*Available online at* www.ijpab.com

DOI: http://dx.doi.org/10.18782/2320-7051.2749

**ISSN: 2320 – 7051**

*Int. J. Pure App. Biosci.* **5 (2):** 1207-1214 (2017)

*Research Article*

International Journal of Pure & Applied Bioscience

OPEN ACCESS

# Genetics of Seed Colour in Sunflower (*Helianthus annuus* L.)

**Siddhesh R. Nadkarni[1*], I. Shanker Goud[2], Sheshaiah. K. C. [3], Ningaraj Dalawai[4] and Muttappa Hosamani[5]**

[1, 3, 5]Department of Genetics and Plant Breeding, College of Agriculture Raichur

[2]Director of Research, University of Agricultural Sciences Raichur

[4]Department of Plant Biotechnology, UAS, GKVK, Bengaluru

University of Agricultural Sciences, Raichur – 584 104, India

*Corresponding Author E-mail: sidd.nadkarni@gmail.com

Received: 24.03.2017 | Revised: 5.04.2017 | Accepted: 6.04.2017

## ABSTRACT

*Investigation was carried to study the inheritance of seed colour in sunflower (Three crosses for seed colour direct and reciprocal). $F_1$ selfed seeds of six crosses were raised during kharif 2013 season at Main Agricultural Research Station, Raichur (Karnataka). For the seed colour inheritance a set of three crosses were raised in the first cross both direct and reciprocal crosses exhibited a ratio (CMS 17A x 104B) and (CMS104A x 17B) of black seed to the brown seed plants approximated 9:3:3:1 a typical dihybrid segregation in $F_2$ population with different phenotypic expressions indicating the gene interaction effects. In the second set of cross involving direct and reciprocal revealed (DWSNB x 104B) and (CMS 104B x DWSNB) a ratio of dull white seed to the black seed plants approximated 12:3:1 in $F_2$ indicate a masking gene action with different phenotypic expressions showed the gene interaction effects while in the third set of cross (DWSNB x 17B) and (CMS17A x DWSNB) with direct and reciprocal crosses showed a ratio 9:7 a complementary gene action with different phenotypic expressions of dull white seed to brown seed plants indicating the gene interaction effects.*

***Key words:*** *Seed colour, Inheritance, Chi-square Test*

## INTRODUCTION

Inheritance studies are important both from theoretical and applied point of view. They are coupled with the study of inter-relationship of genes or linkage. Yield levels can be stepped up by eliminating the undesirable genes and incorporating the desirable genes. There is a lot of scope for improvement of yields through gene manipulation. This is possible only when the genetic architecture of the plant is properly understood. Inheritance studies greatly help in simplifying the planning and execution of breeding strategies. Further the knowledge of inheritance of various characters of qualitative and quantitative nature is paramount importance to achieve success in plant breeding in general and sunflower breeding in particular.

**Cite this article:** Nadkarni, S.R., Goud, I.S., Sheshaiah, K.C., Dalawai, N. and Hosamani, M., Genetics of Seed Colour in Sunflower (*Helianthus annuus* L.), *Int. J. Pure App. Biosci.* **5(2):** 1207-1214 (2017). doi: http://dx.doi.org/10.18782/2320-7051.2749

The knowledge of inter relationship of character like seed colour with economically important character like oil content, hull content, hull thickness etc would be valuable information to breeders in selecting superior genotypes for desirable traits and their relationship with other desirable linked characters help in this regard. The white seeded varieties having the lowest oil content, followed by the striped and black varieties respectively. Sunflower varieties with thin seed coats are usually higher in oil content than those with thick coats and are preferred for crushing because they cause less damage to the screw presses. Usually dark coloured seed tend to be higher in oil content than light coloured seeds[1].

## MATERIALS AND METHODS

The plant material used in the present study comprising of $F_1$ selfed seeds of six crosses *viz,*. CMS17A x 104B, CMS104A x 17B, DWSNB x 104B, CMS104A x DWSNB, DWSNB x 17B, CMS17A x DWSNB were sown in separate plots during *kharif* season. Sufficient plant population was maintained by sowing all the available selfed $F_1$ seeds to raise the $F_2$ segregating population for the study of inheritance of seed colour and other observations. Plant populations in each plot were ranged from 417 to 2542. A spacing of 60 cm between rows and 30 cm between plants. The recommended dose of fertilizer was applied at the rate of 60:75:60 NPK kg per ha. Half of the recommended dose of nitrogen along with the entire dose of phosphorus and potassium was applied at the time of sowing in the furrows. The remaining 50 per cent of nitrogen was top dressed at 30 days after sowing, crop was grown under irrigated condition and all the recommended package of practices was followed to raise the crop.

All the data obtained were statistically analysed by using chi square test proposed by Karl Pearson to test the goodness of fit. Karl Pearson[8] developed $\chi^2$ (Chi-square) test and it is defined as "The sum of square of the deviations from observed to expected frequencies divided by expected frequencies". The general formula for $\chi^2$ is as follows:

$$\chi^2 = \sum \frac{(O - E)^2}{E} \quad \text{with (n-1) d.f.}$$

Where,

O = Observed frequencies

E = Expected frequencies

n = Number of classes

d.f. = Degrees of freedom

$\sum$ = Summation

Thus, application of $\chi^2$ requires observed and expected frequencies. The expected frequencies can be calculated from the observed frequencies assuming a particular hypothetical segregation ratio. Each deviation (O-E) is squared and each squared deviation is then added together to give a single value of $\chi^2$. This value is tested against table $\chi^2$ at five per cent for (n-1) d. f., where 'n' is the number of segregation classes. The degrees of freedom are '1' for two-class segregation (3:1) and it is '3' for four class segregation (9:3:3:1) and each class of data should have at least about 50 observations.

## RESULTS AND DISCUSSION

In the first set of direct cross Out of 2542 $F_2$ plants raised from the cross CMS17A (Brown seed ) x 104B (Black seed), 1438 plants exhibited black with striped seeds, 476 plants exhibited black seeds, 472 plants exhibited brown with light striped seeds and remaining 156 had light grey coloured seeds and in reciprocal cross of out of 1903 $F_2$ plants from the cross CMS104A (Black seed) x 17B (Brown seed), 1072 plants exhibited black with striped seeds, 354 plants exhibited black seeds, 359 plants exhibited brown with light striped seeds and remaining 118 Plants had light grey coloured seeds. The ratios of brown seed to the black seed and vice versa plants approximated 9:3:3:1 typical dihybrid segregation with different phenotypic expressions indicating the gene interaction effects (Table 1 & Plate 1 (a) (b). This type of segregation in the pattern 9:3:3:1 dihybrid gene interaction for the inheritance of seed

colour was earlier reported by Meena *et al*[7]., in chickpea and Gupta and Gudu[5] in *Amaranthus.* The ratios of brown seed to the black seed plants approximated 9:3:3:1 typical dihybrid segregation with different phenotypic expressions indicating the gene interaction effects. When the data was subjected to $\chi^2$ analysis, the calculated $\chi^2$ value is 0.143 and 0.045 which lies in the probability value of 98 to 99 per cent, indicating that the deviation observed are due to chance factors and the segregation is valid and the ratios obtained for the different phenotypic classes of seed colour observed was due to interaction effects of genes governing the characters.

In the second set of direct cross Out of 417 $F_2$ plants raised from the cross DWSNB (Dull white seed) x 104B (Black seed), 313 plants exhibited blackish dull white seeds, 77 plants exhibited black seeds and remaining 27 had black with striped seeds and in reciprocal cross out of 439 $F_2$ plants from the cross CMS 104A (Black seed) x DWSNB (Dull white seed), 332 plants exhibited blackish dull white seeds, 81 plants exhibited black seeds and remaining 26 had black with striped seeds. The ratios of dull white seed to the black seed and vice versa plants approximated 12:3:1 a masking gene action with different phenotypic expressions indicating the gene interaction effects (Table 2 & Plate 2 (a) (b). This type of segregation in the pattern 12:3:1 masking gene interaction for the inheritance of seed colour was earlier reported by Schwetka[14] in turnip (*Brassica campestris* L.). The ratios of dull white seed to the black seed plants approximated 12:3:1 a masking gene action with different phenotypic expressions indicating the gene interaction effects. When the data was subjected to $\chi^2$ analysis, the calculated $\chi^2$ value is 0.051 and 0.119 which lies in the probability value of 95-98 per cent, indicating that the deviation observed are due to chance factors and the segregation is valid and the ratios obtained for different phenotypic classes of seed colour observed was due to interaction effects of genes governing the characters.

In the third set of direct cross Out of 514 $F_2$ plants raised from the cross DWSNB (Dull white seed ) x 17B (Brown seed), 290 plants exhibited light brown with striped seeds and remaining 224 had light grey coloured seeds and in reciprocal cross out of 547 $F_2$ plants from the cross CMS 17A (Brown seed) x DWSNB (Dull white seed), 315 plants exhibited light brown with striped seeds and remaining 232 had light grey coloured seeds of dull white seed to the brown seed and vice versa plants approximated 9:7 a complementary gene action with different phenotypic expressions indicating the gene interaction effects (Table 3 & Plate 3 (a) (b). This type of segregation in the pattern 9:7 complementary gene interaction for the inheritance of seed colour was earlier reported Zaman[17] observed that seed colour in *B. campestris* controlled by two dominant genes. When the data was subjected to $\chi^2$ analysis, the calculated $\chi^2$ value is 0.006 and 0.397 which had probability value of 99 per cent, indicating that the deviation observed are due to chance factors and the segregation is valid and the ratios obtained for different phenotypic classes of seed colour observed was due to interaction effects of genes governing the characters.

The inheritance of seed color in a number of crops has been studied. For some crops seed color is controlled by two duplicate genes in Mustard *Brassica juncea*[12]. Rahman[11] observed that seed colour in *Brassica. rapa* is controlled by two genes. Yash Pal and Hari Singh[16] reported that seed colour in Indian mustard is controlled by two genes with incomplete dominance. Burbulis[2] in rapeseed reported that seed colour is controlled by three genes. Leclercq[6], Putt[10] and Stonescu[15] also reported that seed colour in sunflower was governed by single gene. Chen and Heneen[4] in *B. campestris* reported that seed colour is controlled by single gene. Chauhan *et al*[3]., reported that seed coat colour in yellow sarson is controlled by single dominant gene. Popescu and Marinescu[9] reported that seed colour in linseed is controlled by single gene. Saeidi and Rowland[13] also reported that seed coat colour in oilseed flax is govern by single gene.

**Table 1: The $F_2$ generation of direct and reciprocal crosses showing phenotypic segregation ratios for seed colour in sunflower**

| Crosses | Observed frequency | | | | Expected frequency | | | | Total observed frequency | Ratio | $\chi^2$ | P- value | Significant or Non-Significant |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Black with stripes (9) | Black (3) | Brown with light stripes (3) | Light grey (1) | Black with stripes (9) | Black (3) | Brown with light stripes (3) | Light grey (1) | | | | | |
| CMS17A x 104B (Direct) | 1438 | 476 | 472 | 156 | 1429.87 | 476.62 | 476.62 | 158.87 | 2542 | 9:3:3:1 | 0.143 | 0.99 -0.98 | NS |
| CMS104A x 17B (Reciprocal) | 1072 | 354 | 359 | 118 | 1070.43 | 356.81 | 356.81 | 118.93 | 1903 | 9:3:3:1 | 0.045 | 0.99 | NS |

**Table 2: The $F_2$ generation of direct and reciprocal crosses of showing phenotypic segregation ratios for seed colour in sunflower**

| Crosses | Observed frequency | | | Expected frequency | | | Total observed frequency | Ratio | $\chi^2$ | P- value | Significant or Non-Significant |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | Blackish dull white (12) | Black (3) | Black with stripes (1) | Blackish dull white (12) | Black (3) | Black with stripes (1) | | | | | |
| DWSNB x 104B (Direct) | 313 | 77 | 27 | 312.75 | 78.18 | 26.06 | 417 | 12:3:1 | 0.051 | 0.98 – 0.95 | NS |
| CMS104A x DWSNB (Reciprocal) | 332 | 81 | 26 | 329.25 | 82.31 | 27.43 | 439 | 12:3:1 | 0.119 | 0.98 – 0.95 | NS |

**Table 3: The $F_2$ generation of direct and reciprocal crosses of showing phenotypic segregation ratios for seed colour in sunflower**

| Crosses | Observed frequency | | Expected frequency | | Total observed frequency | Ratio | $\chi^2$ | P- value | Significant or Non-significant |
|---|---|---|---|---|---|---|---|---|---|
| | Light brown with stripes (9) | Light grey (7) | Light brown with stripes (9) | Light grey (7) | | | | | |
| DWSNB x 17B (Direct) | 290 | 224 | 289.12 | 224.87 | 514 | 9:7 | 0.006 | 0.99 | NS |
| CMS17A x DWSNB (Reciprocal) | 315 | 232 | 307.68 | 239.31 | 547 | 9:7 | 0.397 | 0.90 – 0.80 | NS |

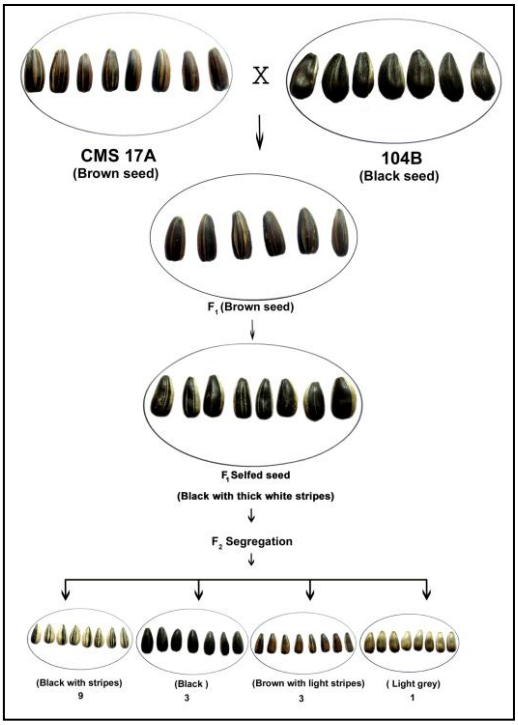


**Plate. 1 (a) CMS 17 A X 104 B**

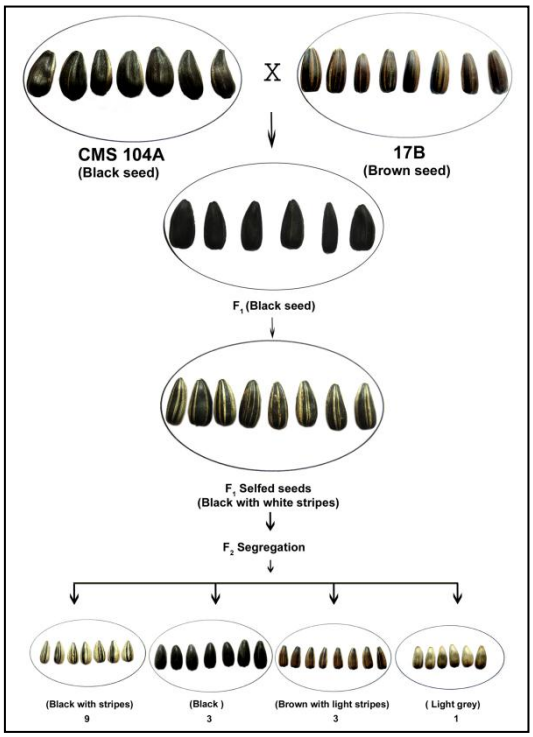


**Plate. 1 (b) CMS 104 X 17 B**

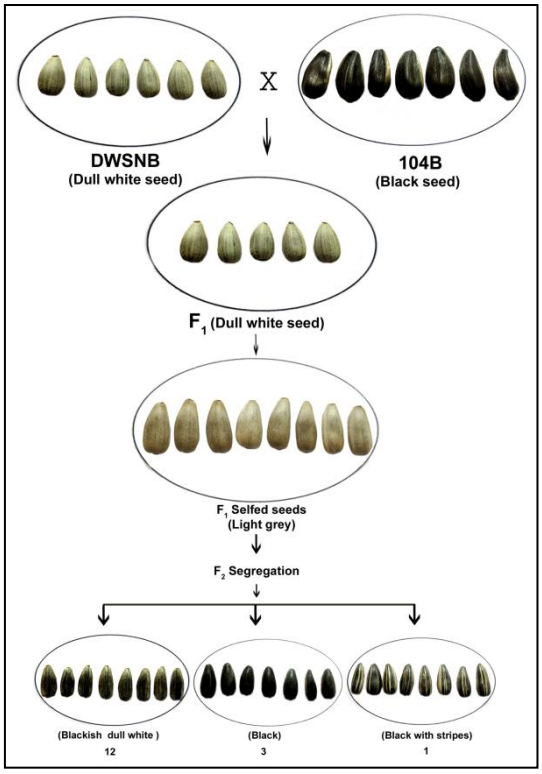


**Plate. 2 (a) DWSNB X 104 B**

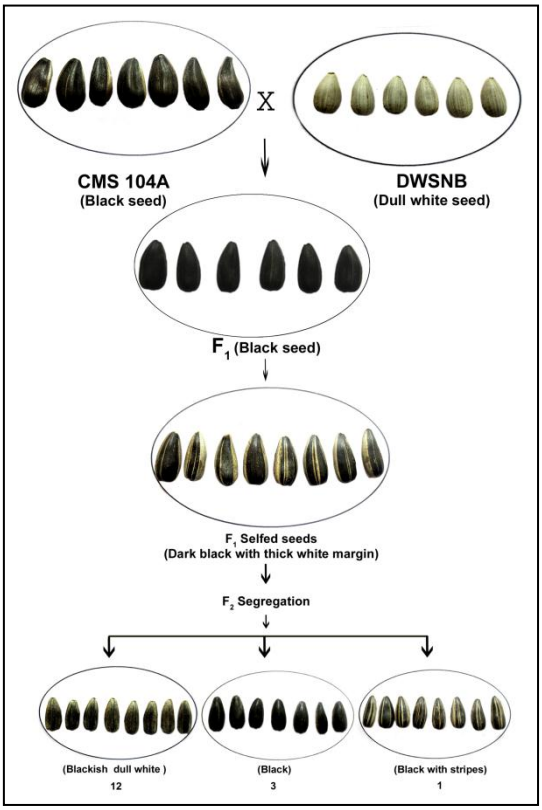


**Plate. 2 (b) CMS 104 A X DWSN**

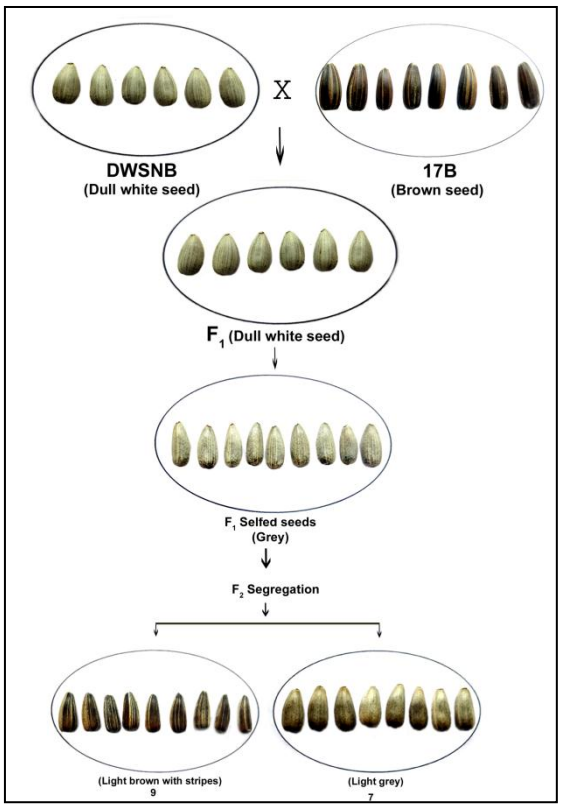


**Plate. 3 (a) DWSNB X 17 B**

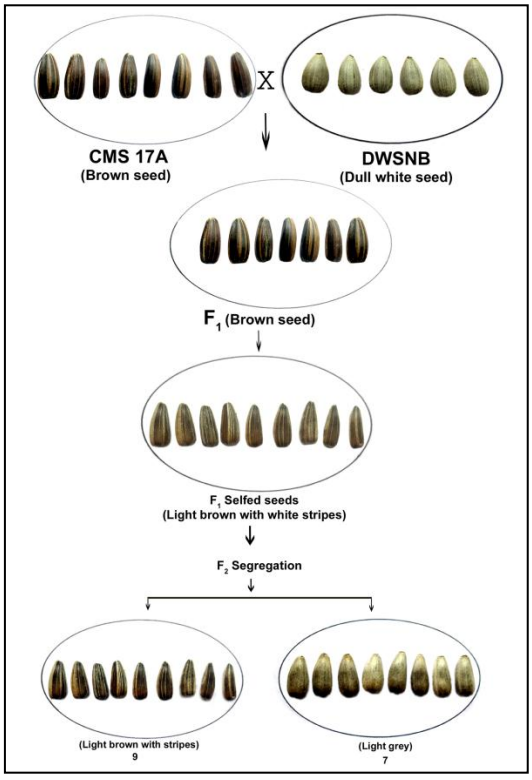


**Plate. 3 (b) CMS 17 A X DWSNB**

## REFERENCES


1. Buker, R.J., and Denton, G.W., "Sunflower Production in Uganda" A Crop Production Guide prepared for the Ministry of Agriculture; sponsored by USAID/MFAD project, Kampala, Uganda (1991).
2. Burbulis, N., The inheritance of seed colour in spring rapeseed doubled haploid populations., *Vagos.*, **67:** 7-11 (2005).
3. Chauhan, Y.S., Kumar, K., Ram Bhajan and Maurya, K.N., Inheritance of seed coat colour and its use in determining natural cross-pollination in yellow sarson., *Cruciferae. Newslett*., **17:** 60-61 (1995).
4. Chen, B.Y. and Heneen, W.K., Inheritance of seed colour in *Brassica campestris* L. and breeding for yellow-seeded *B. napus* L., *Euphytica*, **59(2-3):** 157-163 (1992).
5. Gupta V.K. and Gundu, S., Inheritance of some morphological traits in *Amaranthus*. *Euphytica*, **46:** 79-84 (1990).
6. Leclercq, P., Inheritance of some qualitative characters in sunflower. *Ann. Amelior Plant*, **18:** 307-315 (1968).
7. Meena, H.S., Kumar, J. and Yadav, S.S., Inheritance of seed colour in chickpea (*Cicer arietinum* L.). *Indian J. Genet*., **64(2):** 151-152 (2004).
8. Pearson, K., On the criterion that a system of deviations from the probable in the case of a correlated system of variables is such that it can be reasonably suppose to have arisen from random sampling. *Phil. Mag. Ser.*, **5(50):** 157–175 (1900).
9. Popescu, F. and Marinescu, I., Y1 - a dominant gene determining yellow seed colour in linseed. *Probleme de Genetica Teoretica si Aplicata*, **28(2):** 99-106 (1996).
10. Putt, D.E., Observations on morphological characters and flowering processes in the sunflower (*Helianthus annuus* L.). *Sci. Agric*., **21:** 372-379 (1974).
11. Rahman, M.H., Inheritance of petal colour and its independent segregation from seed colour in *Brassica rapa.*, *Plant. Breed*., **120(3):** 197-200 (2001).
12. Rawat, D.S., Inheritance of seed colour in mustard. *Acta Agronomica Hungarica*., **38(1-2):** 127-130 (1989).
13. Saeidi, G. and Rowland, G.G., The inheritance of variegated seed color and palmitic acid in flax. *J. Hered*, **88(6):** 466-468 (1997).
14. Schwetka, A., Inheritance of seed colour in turnip rape (*Brassica campestris* L.), *Theoritical and Applied Genetics*, **62(2):** 161-169 (1982).
15. Stoenescu, F., Sunflower Science and Technology (Ed.). *Agronomy Monograph Am. Soc. Agron*., Madeson, W.C. No. **19:** 279-338 (1974).
16. Yash-Pal, and Hari-Singh., A note on inheritance of seed colour, size and seed shape in Indian mustard., *J. Oilseeds Res*., 7(2): 69-72 (1990).
17. Zaman, M.W., Inheritance of seed colour in *Brassica campestris*, *Sveriges-Utsadesforenings-Tidskrift.*, **99(3):** 205-207 (1989).