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The Study of the Relationship Between Seed Yield and Yield Components on *Nigella sativa* Genotypes

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ABSTRACT

In order to study the relationships among seed yield and its components in *Nigella sativa*, path coefficient and factor analysis was done using some agro- morphological traits of 21 different genotypes. Genotypes were evaluated using a completely randomized design with four replications in Ardestan University Research Farms. There was a high and positive correlation between seed yield and biological yield, seed number in follicle, number of stem branches, bush height and harvest index. Stepwise regression analysis for seed yield showed that biological yield, seed number per follicle, number of stem branches and harvest index were entered in the model, respectively, and justified 45 percent of total variation of seed yield. Based on path analysis, biological yield and number of seed in follicle had the highest direct effect on seed yield. Factor analysis revealed 3 hidden factors which totally accounted for 94.12% of variations among traits. These factors were named as efficiency factor (seed yield and biological yield), yield components factor (number of stem branches and follicle number per plant) and follicle trail factor (follicle weight and number of seeds in follicle), respectively. Therefore, the research suggested that biological yield, seed number per follicle and number of stem branches had the most relative effects on seed yield and can be consider as suitable selection criteria for improving seed yield per plant in *Nigella sativa.*

Keywords: *Nigella sativa*, Seed yield, Path analysis, Factor analysis

INTRODUCTION

Nigella sativa, is a bisect medical annual, grassy plant which belongs to ranunculus family (Bassim, 2003). *Nigella sativa* is seen as a self growing plant from southern Europe to Middle

East and Indian subcontinent (D'Antuono *et al.*, 2002). This plan is seen in some parts of Iran like Kermanshah and Arak as a self growing plant and in some other parts like Isfahan and Khorasan. It is grown as an agricultural plant (Kabiri *et al.*, 2012 and Mordi and Rashed-Mohassel, 1997) and has vast usages in food and medical industries of the country. Seeds of this plant have some characteristics such as anti- epileptic, anti- bacterial, anti- tumor, painkiller and reducer of blood sugar (Bath *et al.,* 2005 ؛ Mohammad Ismail, 2009). In plant improvement programs, selection is based on some agricultural characteristics among which there may be some positive and negative correlations. So statistical analysis methods which reduce the number of effective traits in yield are valuable for plant breeders. In this regard using correlations among traits is especially common. Seed yield is a polygenic trait, and direct selection for its improvement is not so effective and therefor can be improved throught its components. Most of the correlations do not show cause and effect relationship among traits, because these relationships are due to some unknown factors (Johnson and Wichern, 1988). Efficiency and multiple regression is of doubt because of parallel relationship among trait and limitations in the statement of cause and effect relationships (Lakha *et al.*, 1992؛ Solanaki and Paliwal, 1979). Therefore, in order to solve such problems factor analysis method is used (Lakha *et al.*, 1992). Factor analysis is a powerful multi parameter statistical method which is used for guessing component parts, of recognition biologic relationship among traits, reducing a great number of correlated traits to a few numbers of factors and explanation of correlations among parameters (Dewy and Lu, 1959). In a study on genotypes of *Nigella sativa* and *Plantago ovata*, Bannayan *et al.*, (2008) found that seed number in follicle and biological yield can be useful indices for selection in limited irrigation conditions. Zahoor *et al.*, (2009) studied *Nigella* genotypes in Pakistan and reported that biologic yield has the most direct effect on seed yield and diversity of seed yield among genotypes is mostly related to 1000 seed number diversity and stem branches. Faravani *et al.*, (2006) studied anatomic and agronomic characters of 28 groups of *Nigella sativa* in different parts of Khorasan and suggested that among investigated characters, biological yield, harvest index and 1000 seed weight justified seed yield variations.

The purpose of this study was to study the effects of seed yield components which have the most role in determining *Nigella* seed yield.

MATERIALS AND METHODS

In this study 21 genotype of *Nigella sativa* collected from six provinces of Isfahan (Isfahan, Ardestan , Najafabad, Fereydan, Mobarakeh, zavareh), kerman (kerman, Rafsanjan), Fars (shiraz, Sepidan, Marvdasht, Abadeh), Khuzestan (Ahvaz, Msijed soleyman, Mahshar), Chahar – Mahal Bakhtiyari (Borujen, Shahre – kord, Lordegan , Farsan) and Sistan- Baluchestan (Zobol, Iranshahr) were used. The seeds used in this study were collected from Iranian Research Centers and Isfahan Pakan Bazr Company. These genotypes were planted in 20 cm diameter clower pots in Ardestan Azad University in a completely randomized plan with four replication. Experiment site based on Kupen classification has a very arid climate with hot and arid summers (Karimi, 1987). Mean annual precipitation and temperature are 140 mm and 14^0C, respectively and the soil physical gravity is 4.05 g/cm^3 (Kabiri *et al.*, 2012). Seeds were planted in pots (in each pot 9.5 kg soil) at the mid February. After the bushes grew, in some intervals, they were thinned as it is usual for medical plants and protectoral operations including irrigation, fertilizing and weeding were done regularly. Ultimately in each pot 7 bushes were kept. The first irrigation was done exactly after planting and subsequent irrigations were done once in every 3-5 day. Harvest started in July 2009 after the leaves got yellow and complete maturation and drying started. Morphological characteristics including bush height above the ground to the highest follicles in 5 random bushes in each replication was measured. Stem branch numbers, follicle number in each bush, seed number in each follicle, seed yield and biological yield were also determined in 5 harvested bushes from each replication. Follicle weight and 1000 seed weight were also determined for each replication. The means of 5 measured bushes were used in statistical analyses.

Genotypic and phenotypic correlation coefficients among traits were calculate (Farshadfar, 2001; Zahoor *et al*., 2009). Using stepwise regression method for seed yield as an independent variable and other traits as dependant variables, traits which had the highest importance in seed yield change justification were determined (Rezaei and Soltani, 1999).

For better understanding of the relationship among traits and recognizing traits which have the highest effect on seed yield, path analyses based on genetic correlation coefficients was used (Sepahi, 1996). Also, factor analysis with varimax rotation was used to understand the relationships between traits and recognizing the hidden factors (Johnson and Wichern, 1988). Statistical analysis was done using SPSS and SAS softwares.

RESULTS AND DISCUSSION

Genetipic and phenotypic correlations (Table 1) showed that seed yield per bush had positive and significant correlations with biologic yield, seed number per follicle, stem branch number, bush height and harvest index which are in agreement with the results of Faravani *et al*., (2006) and D'Antuono *et al*. (2002). Based on correlation coefficients, important seed yield components in *Nigella sativa* were biological yield, seed number in follicle and bush height, respectively So improving these yield components results in improving of seed yield. The highest correlation coefficient was observed for seed yield with biologic yield. This relation provides seed yield increase for medical usage and biologic yield for livestock usage.

It was also revealed that follicle number per bush with 1000 seed weight had a negative and significant relations with harvest index. Therefore, increase in follicle number in bush results in l000 seed weight and seed number reduction of follicle and ultimately reduction in seed yield. In this regard, Faravani *et al*. (2006) reported similar results. Stem brunch number had a positive and significant relation with biologic yield, follicle number in bush and bush height (Table 3). Our results revealed that while there is a good agreement between phenotypic and genetipic correlations, and traits with significant and positive genetipic correlations are controlled by similar genes (pleiotropic effect). D'Antuono *et al*. (2002) also reported higher genetic correlation compared with phenotype correlations.

Stepwise regression analysis for seed yield of (Table 2) showed that biological yield was the first trait that entered the model and determined 84% of the seed yield variations. After biological yield, seed number in follicle, stem branch number and harvest index enteral the model and justified 95% of the seed yield variations through harvest index. These results were in agreement with correlation coefficients (Table 1). In a study on 28 *Nigella sativa* bulks, Faravani *et al*. (2006) reported that biologic yield, harvest index and 1000 seed weight totally determined 97% of seed yield variations. Path analysis method was used to determine the importance of effective traits on seed yield. This method shows the nature of simple correlations and determines the direct and indirect effects of dependant variables (Dewy and Lu, 1959). Path analysis on all genotypes under study (Table 3) showed that biologic yield had positive and high direct effect of 0.64 on seed yield and after that seed number in follicle and stem branch number with path coefficient of 0.52 and 0.24, respectively had intermediate and low effects on seed yield. Indirect effects of biological yield through seed number in follicle were positive and medium (0.25) and through stem branch number and harvest index were positive and low. After biological yield, seed number in follicle showed high direct effect on seed yield and its indirect effects through stem brunch numbers and biological yield were positive and medium (0.23 and 0.21), respectively and through harvest index was negative and low. Indirected effect of stem brunch number through biologic yield was positive and high and through seed number was slight. Harvest index had high and positive indirect effect through seed number in follicle and indirect and positive effects through biological yield and stem branch number on seed yield.

These results were in agreement with Bannayan *et al.* (2008) and Zahoor *et al*. (2009). Factor loads and cumulated explained variances for 3 factors are shown in Table 4. The first 3 factors totally explained 94.12 percent of total variance. In the first factor, seed yield and biological yield had high and positive factor loads (0.98 and 0.92, respectively). This factor can be named as the efficiency factor. In the second factor, stem branch number, and follicle number in the bush had high and positive factor loads (0.96 and 0.94, respectively) and because of the positive and significant correlation among these traits, we named this factor as the yield component factor. In the third factor, follicle weight and seed number in follicle had high and positive factor loads (0.91 and 0.89, respectively), so this factor was named as follicle trait factor. Using factor analysis in *Nigella sativa*, Filippo *et al*. (2002) recognized 3 main factors which totally explained 92% of variance. In general yield trait in *Nigella sativa*, the same as all agricultural plants, is a complex characteristics and can be more efficiently increased by considering the yield components. Based on path analysis results, stepwise regression and factor analysis, 3 traits of biological yield, seed number in follicle and stem branch number had relatively high important effects in determining seed yield.

Table 1. Phenotypic (under diameter) and genotypic (above diameter) correlation coefficients between traits

	Traits	1	2	3	4	5	6	7	8	9
1	Seed yield	1	0.97^{**}	0.37	0.81	0.27	0.62	0.45	0.62	0.56
2	Biologic yield	0.95^{**}	1	0.35	0.28	0.44	0.85	0.29	0.18	0.22
3	Follicle number	0.31^{ns}	0.32^{ns}	1	-0.31	-0.69	0.79	0.21	-0.17	-0.59
4	Seed number in follicle	0.78^{**}	0.27^{ns}	-0.29^{ns}	1	-0.78	-059	0.35	0.28	-0.18
5	l000 seed weight	0.27^{ns}	0.39^{ns}	-0.65^{*}	-0.75^{**}	1	0.37	0.26	0.19	-0.15
6	Stem branch number	0.59^{*}	0.79^{**}	0.78^{*}	-0.53^{*}	0.29^{ns}	1	0.15	0.62	0.18
7	Follicle weight	0.39^{ns}	0.25^{ns}	0.14^{ns}	0.32^{ns}	0.21^{ns}	0.14^{ns}	1	0.26	0.27
8	Bush height	0.61^{*}	0.13^{ns}	-0.16^{ns}	0.27^{ns}	0.13^{ns}	0.58^{*}	0.26^{ns}	1	0.19
9	Harvest index	0.54^{*}	0.21^{ns}	-0.51^{*}	0.75^{**}	-0.12^{ns}	0.15^{ns}	0.23^{ns}	0.16^{ns}	1

And **: significant at 5% and 1 % probability levels.

Table 2. Stepwise regression results for seed yield as a (dependant) and other traits (independent) of *Nigella sativa* genotypes

Traits	Standard regressing coefficients	Cumulative detection coefficients
Biologic yield	0.62^{**}	0.841
Seed number in follicle	0.58^{**}	0.892
Stem branch number	0.34^{**}	0.937
Harvest index	0.21^{**}	0.954

Table 3. Path analysis results for seed yield in *Nigella sativa* genotypes

Trait	Biologic yield	Seed No. in follicle	Stem branch number	Harvest index	Genetipic correlation coefficients with seed yield
Biologic yield	$\underline{0.64}$	0.25	0.05	0.03	0.97
Seed No. in follicle	0.21	$\underline{0.52}$	0.23	-0.15	0.81
Stem branch number	0.41	-0.01	$\underline{0.24}$	-0.02	0.62
Harvest index	0.06	0.47	0.07	$\underline{-0.04}$	0.56

underlined numbers, are direct effects

Table 4. Factor loads, explained variances, and cumulated explained variances for *Nigella sativa* traits

Traits	first factor	second factor	third factor
Seed yield	0.98	0.12	-0.04
Biologic yield	0.92	0.09	0.07
Follicle number	0.17	0.94	-0.26
Seed number in follicle	0.31	-0.05	0.89
l000 seed weight	-0.71	0.32	-0.17
Stem branch number	0.32	0.96	-0.18
Follicle weight	-0.01	0.14	0.19
Bush height	0.42	0.28	-0.01
Harvest index	-0.07	0.42	0.02
Explained variance (%)	45.76	29.18	19.18
Cumulated explained variance (%)	45.76	74.94	94.12

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