RESEARCH NOTE

Genetics of early growth vigour in lentil (*Lens culinaris* Medik.)

JITENDRA KUMAR*, EKATA SRIVASTVA and MRATUNJAY SINGH

Division of Crop Improvement, Indian Institute of Pulses Research, Kalyanpur, Kanpur 208 024, India

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Introduction

Genetics of early growth vigour was studied in two crosses of lentil (*Lens culinaris* ssp. *culinaris*) involving ILL6002 and ILL7663 as rapid early growth vigour parents and DPL15 as slow early growth vigour parent. The early growth vigour was measured on the basis of seedling length and data was recorded on 114 and 834 individual F_2 plants derived from DPL15 × ILL6002 and DPL15 × ILL7663 crosses, respectively. Frequency distribution of F_2 plants appeared to be normal for seedling length, but it was skewed towards slow early growth vigour. Hence, analysis of early growth vigour as a qualitative trait in F_2 and F_3 revealed that slow early growth vigour was dominant over rapid early growth vigour and a single recessive gene controlled the rapid early growth vigour in lentil. However, occurrence of transgressive segregants for seedling length indicated that some minor genes also interacted with one major gene for early growth vigour. Therefore, QTL analysis for early growth vigour can help to identify major and minor gene(s), for making genetic improvement in lentil by the use of marker assisted selection.

Lentil is an important cool season food legume crop of rainfed agriculture and it is one of important pulse crops for diversifying cereal-based cropping systems worldwide. Presently, it occupies 3.74 million ha area producing 3.40 million tons grains in the world with an average yield of 915 kg/ha (Erskine *et al.* 2011). The major geographical regions of lentil production are South Asia and China (44.3%), northern great plains in North America (41%), west Asia and north Africa (6.7%), sub-Saharan Africa (3.5%) and Australia (2.5%) (FAOSTAT 2010). Among countries, India accounts for the largest global area under lentil with 1.48 million ha area and 1.01 million ton production (AICRP 2010–2011). The present productivity of lentil in India is very low as it is mostly grown as post-rainy season crop under receding soil moisture conditions during the winter season. As a result, the crop invariably encounters terminal moisture stress, thus, leading to forced maturity and lower yield. In environments with typical Mediterranean type climates also, lentil crop often experiences terminal as well as intermittent droughts throughout the growing season (Silim *et al.* 1993). Hence, drought has become an important major yield constraint in production of lentil (Fouad *et al.* 2011).

Earlier studies suggest that shoot and root attributes at an early growth stage of plants are related to drought tolerance through dehydration avoidance, a mechanism that allows a crop plant to thrive in water-limited environments (Sarker *et al.* 2005). Early growth vigour and subsequent rapid ground coverage has been shown to be associated with drought tolerance (Passioura 1982). This trait is necessary to optimize the utilization of the production environment by reducing surface soil evaporation. Genetic variation in early growth vigour has been reported in many grain legumes (Onim 1983; Silim *et al.* 1993), which indicates the feasibility of manipulating this trait through classical breeding techniques. In lentil, genetic variation for faster growth rate was observed and a positive association has been observed between stem length and taproot length as well as number of lateral roots (Sarker *et al.* 2005). These workers have also identified a breeding line (ILL 6002), which exhibited a faster growth rate and formed a large number of laterals at early stage of seedling establishment (Sarker *et al.* 2005). These studies showed that genetic variability of rapid early growth vigour is present among the lentil germplasm. To utilize this genetic variability in lentil breeding programme, it is essential to investigate the genetic control of early growth vigour. Knowledge of genetics of a trait helps to effectively choose the parents and construct an appropriate breeding scheme (Sarker *et al.* 1999). Previously genetics of quantitative traits such days to flowering and resistance to ascochyta blight have been shown to be inherited in Mendelian fashion in lentil (Ford *et al.* 1999; Sarker *et al.* 1999). Besides, inheritance studies of several other traits such seed colour, rust resistance, wilt resistance etc. have also been studied in lentil (Haddad *et al.* 1978; Emami and Sharma 2000; Shrama

*For correspondence. E-mail: jitendra73@gmail.com.

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2009). Therefore, the present study aimed to determine the inheritance of early growth vigour in lentil.

Material and methods

In the present study, inheritance of early growth vigour was studied in two crosses involving ILL6002 and ILL7663 as rapid early growth vigour (REGV) parents and DPL15 as slow early growth vigour (SEGV) parent (table 1). To differentiate the REGV from SEGV, data was recorded on seedling length (cm) after 47 days of sowing. The cross between DPL15 and ILL6602 was made in 2008–2009 while between DPL15 and ILL7663 in 2009–2010 and their F_1, and F_2 were raised during 2009–2010 to 2010–2011, respectively. To confirm the inheritance for early growth vigour, F_3 progenies derived from above crosses were sown in separate experiments in single row plots (3.0 × 0.3 m) at IIPR in 2011–12 (DPL 15 × ILL6002) and in 2012–13 (DPL15 × ILL7663). Segregating and nonsegregating F_3 progenies derived from each F_2 plant were differentiated visually on the basis of seedling length, while 10 plants were recorded for seedling length from each nonsegregating progeny.

For studying the genetics of early growth vigour, plants having seedling length >22 cm (22–36 cm) were accounted as REGV while plants with <22 cm (9–21 cm) seedling length were accounted as SEGV in first cross (DPL15 × ILL6002). Likewise, in second cross (DPL15 × ILL7663), REGV plants were accounted with >13 cm (13–21 cm) seedling length and SEGV plants were accounted <13 cm (4–12 cm) seedling length. Thus, range of seedling length within each group was accounted not less than the differences in mean seedling length of parents involved in each cross. The frequency of F_2 plants was calculated in each group and χ^2 test was applied to test goodness fit to the expected segregating ratio.

Results

In the present investigation, we studied the inheritance of gene(s) controlling the early growth vigour (EGV) in two crosses [DPL15 (SEGV) × ILL6002 (REGV) and DPL15 (SEGV) × ILL7663 (REGV)] on the basis of variation observed in seedling length after 47 days of sowing as explained in material and methods. In F_1, average seedling

Table 1. Pedigree, type of material, source, origin and characteristics of genotypes used in present study.

Genotype	Pedigree	Type of material	Source/origin	Characteristics
DPL15	PL406 × L4076	Cultivar	IIPR, Kanpur, India	High yield, slow early growth vigour
ILL7663	Cross between two locals	Exotic line	ICARDA, Syria	Rapid early growth vigour, 60–65 days to flowering, early maturing
ILL6002	ILL4349 × ILL4605 (Precoz)	Exotic line	ICARDA, Syria	Rapid early growth vigour, 70–75 days to flowering

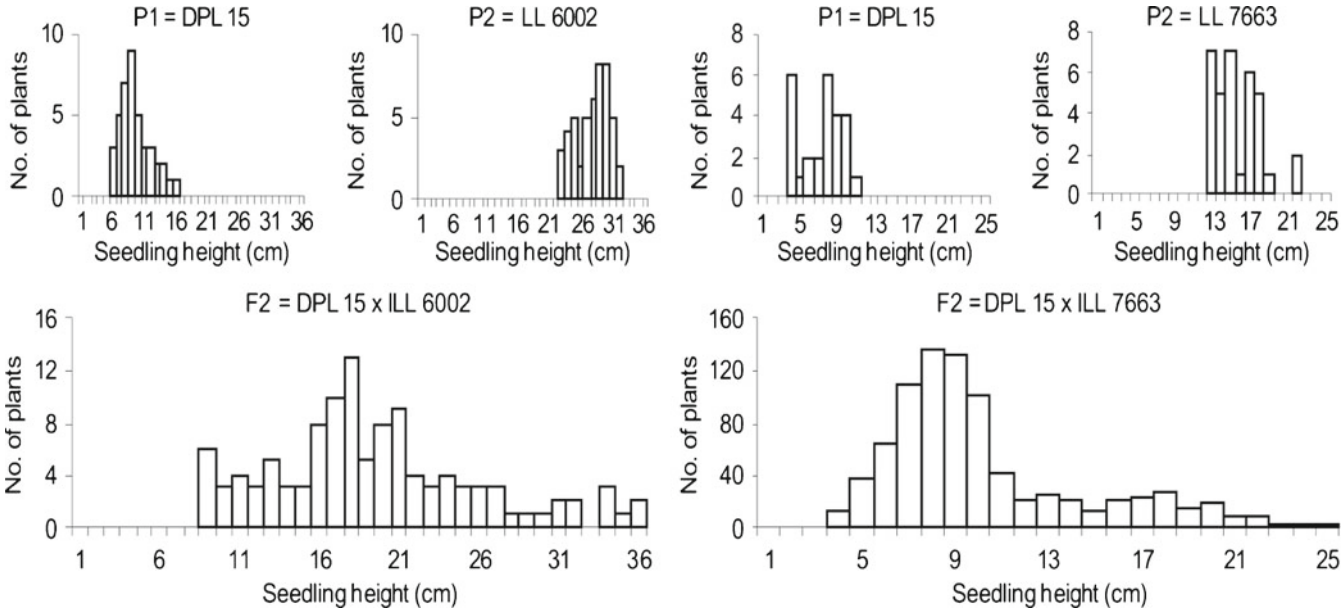

Figure 1. Frequency distributions of early growth vigour based on seedling length in parents (DPL15, ILL7663 and ILL6002) and F_2 populations derived from two crosses (DPL15 × ILL7663; DPL15 × ILL6002) in lentil.

length was shorter than the mid value of parents involved in crosses and it was almost near the average seedling length of slow early growth vigour parent. These results suggested that shorter seedling length is dominant over longer seedling length and REGV expression was under the control of recessive gene(s). In order to know the number of gene(s) underlying this trait, segregating pattern of SEGV and REGV plants was studied in F_2 populations of these crosses. Level of F_2 variance in both crosses was higher compared to their respective parents for EGV (figure 1). Although F_2 distributions seemed to be normal in these crosses, frequency of F_2 plants was skewed towards the slow early growth vigour. This suggested bimodality in F_2 as to be discontinuous. Hence, F_2 plants were classified in to two distinct classes, namely, SEGV (plants with <22 cm and <13 cm seedling length) and REGV (plants with >22 cm and >13 cm seedling length). In the first cross (DPL15 × ILL6002), the F_2 population comprising of 114 individuals segregated into 80 SEGV and 34 REGV. In the second cross (DPL15 × ILL7663), F_2 population comprising of 834 individuals segregated into 652 SEGV and 182 REGV (table 2). The χ^2 analysis was subjected to know the good fit of SEGV and REGV plants into 3:1 ratio. Results showed nonsignificant χ^2 value at 1 d.f. suggesting a good fit to a 3:1 ratio of SEGV and REGV plants in these two F_2 populations (table 2). Nonsignificance of χ^2 value for heterogeneity also suggested that these two F_2 populations fitted for 3:1 ratio. This was further confirmed in F_3 when no segregation was observed in single plant progenies of REGV group. The F_3 lines derived from F_2 plants belonging to SEGV group segregated into (one homozygous dominant SEGV plant, two segregating SEGV plants; table 3). These results suggested that a single dominant gene controlled SEGV in lentil. Since quantitative (seedling length) trait was used as criteria to record the REGV as qualitative trait, variation in seedling length was observed within the parental lines as well as within the SEGV and REGV group of plants. Besides this, transgressive segregation was also observed for seedling length in F_2 population in both crosses (figure 1).

Discussion

Most of the cultivars released in India for rainfed areas have SEGV (up to 40–50 days after germination). However, for avoiding the terminal drought, the improved Indian cultivars should have REGV and ground coverage. Previously, genetic variability for early growth vigour has been observed in lentil and donor genotypes (ILL6002 and ILL 4605) have been identified for this trait (Sarker *et al.* 2005). Genotype ILL6002 is a derivative line of a cross involving ILL4605 as one of the parents. ILL4605 has Argentinian origin; it has early growth vigour and high biomass (Sarker *et al.* 2005). Besides, we also observed a genotype ILL7663, which is a derivative of two locals, having REGV and early maturity compared to Indian cultivars. Having knowledge of genes for controlling a trait is important to make genetic manipulation through recombination breeding and also for mapping of genes/QTL through molecular markers. In the present study, crosses made between SEGV (DPL15) and REGV (ILL6002 and ILL76663) parents indicated monogenic segregation for early growth vigour (table 2). Distribution of F_2 plants in these crosses showed bimodality, formation of two distinct classes (SEGV and REGV) suggested that seedling length behaviour in parents (ILL6002 and ILL7663) was due to a single recessive gene for REGV. However, the continuous

Table 2. Segregation for early growth vigour in the F_2 population.

Cross	Seedling length range (mean) in parents and F_1			No. of plants observed in F_2		
	P_1	P_2	F_1	SEGV	REGV	χ^2 (3:1)**
DPL15 (P_1) × ILL6002 (P_2)	6.0–16.5 (9.6)	23.0–32.0 (27.8)	8.0–19.0 (11.5)	80	34	1.42 (1)
DPL15 (P_1) × ILL7663 (P_2)	4.0–12.5 (7.4)	13–22 (15.7)	4.8–15.6 (9.6)	652	182	4.50 (1)
Total				772	216	5.92 (2)
Heterogeneity						5.55 (1)

**Nonsignificant at $P \leq 0.02$ and respective d.f. is given in parenthesis.

Table 3. Segregation for early growth vigour in F_3 derived from two crosses of lentil.

Cross	F_3 frequency			χ^2 (2:1)**
	Total progenies evaluated	Segregated	Nonsegregated	
DPL-15 (P_1)× ILL 6002 (P_2)	43 (SEGV)	32	11 (SEGV)	1.16 (1)
	34 (REGV)	0	34 (REGV)	–
DPL-15 (P_1)× ILL 7663 (P_2)	183 (SEGV)	134	49 (SEGV)	3.54 (1)
	40 (REGV)	3	37 (REGV)	–

**Nonsignificant at $P \leq 0.02$ and respective d.f. is given in parenthesis.

variation for seedling length among the F_2 segregants as well as variation within parents suggested that some other genes with minor contributions must also be involved to control early growth vigour.

One of the parent (ILL6002) exhibiting REGV is the derivative of Precoz, which is reported to have major recessive gene (*sn*) for early flowering (Sarker *et al.* 1999). Therefore, we also examined the pattern of flowering among the F_2 segregants for REGV in both crosses (data not shown). It was observed that approximately 35% segregants flowered early (<60 days after sowing) while rest of the plants were late flowering. This indicates that early growth vigour is probably not a pleiotropic effect of early flowering gene *sn*, but similar to days to flowering, both monogenic and polygenic systems are involved to control the early growth vigour in lentil (Sarker *et al.* 1999). Earlier, several quantitative traits such as disease reaction to ascochyta blight and days to flowering have been studied and analysed as Mendelian (qualitative) traits in lentil (Ford *et al.* 1999; Sarker *et al.* 1999). Subsequently, QTL analysis based on molecular markers confirmed a presence of a major QTL for resistance to foliar infection by *A. lentis* in the accession ILL5588 as identified earlier a major dominant gene (*AbR1*) through Mendelian analysis in lentil (Ford *et al.* 1999). Similarly genetic of resistance to cowpea aphid-borne mosaic virus has also been studied in cowpea (Orawu *et al.* 2013). Thus, further analysis of early growth vigour through QTL analysis will be helpful to identify the major/minor QTL controlling REGV in lentil and identified associated molecular markers with REGV could then be used through markers assisted breeding in development of early maturing high biomass genotypes in lentil.

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