

Analyses of the Genetic Parameters (Variability, Heritability, Genetic Advance, Relationship of Yield and Yield Contributing Characters) for some Plant Traits among *Brassica* Cultivars under Phosphorus Starved Environmental Cues

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The potential of a crop to favorably respond to breeding/selection and bioengineering programs depends upon the nature and magnitude of genetic variability. For effective selection, information on nature and magnitude of variation in population, association of character with dry matter yield and among themselves and the extent of environmental influence on the expression of these characters are necessary. The estimates of genetic parameters help in understanding the role of various plant traits in establishing the growth behavior of cultivars under a given set of environmental conditions. Genetic analysis leads us to a clear understanding of different morphological, physiological and genetic characters and also the type and extent of their contribution to dry matter yield. Six *Brassica* cultivars were grown in a P-deficient sandy loam soil for 49 days after sowing. Significant variations were observed for all the characters in all the cultivars used in the experiment. All the characters showed high heritability coupled with high genetic advance. Heritability (h^2) is an approximate measure of the expression of a character. The highest estimates of broad sense heritability ($h^2 = 0.90$) and relative expected genetic advance (85.72 %) were noted for root dry matter (RDM), while the estimate of expected genetic advance at 10% selection intensity was quite high ($\Delta G = 85.30 \text{ cm}^2$) for leaf area per plant. The estimates of coheritability were positive and relatively higher for root-shoot ratio (RSR) in combination with shoot dry matter (SDM) ($\text{coh}^2 = 2.002$) and phosphorus use efficiency (PUE) ($\text{coh}^2 = 1.875$), whereas coheritability estimates were negative between leaf area per plant and RSR ($\text{coh}^2 = -0.2010$) indicating lack of association between these traits. High heritability with high genetic advance was exhibited by all the studied plant traits of cultivars evidencing that the traits could be further improved through individual plant selection. The innate variations within the *Brassica* gene-pool impel to drive a concentrated effort to understand the basis of adaptability. Access to the relevant genetic traits and information will provide necessary tools to select the optimal combinations of alleles adapted to local and changing growing environments especially nutrient stress conditions such as phosphorus (P) starvation.

Key words: *Brassica*, Coheritability, Genetic advance, Genetic variability, P-starvation, Selection intensity

1 INTRODUCTION

Brassica's importance in edible oil and bio-diesel production cannot be overemphasized, but it has low per ha yield due to slow phosphorus (P) diffusion (10^{-12} to $10^{-15} \text{ m}^2 \text{ Sec}^{-1}$; Rausch and Bucher, 2002), imbalanced and inadequate P-fertilizer application, low use efficiency, organic and inorganic fixation coupled with day in/ day out increasing prices of P-fertilizers in many resource poor environments. Yield in *Brassica* like other crops, is a complex and multiplicative character and many morphological, physiological and genetic characters constitute it. These yield contributing characters are related

between themselves in addition to complex chain with their relationship with yield. Quantitative characters which are of economic value, highly influenced by environmental conditions, progress of breeding and bioengineering in such characters are primarily conditioned by the magnitude and nature of variation, and interrelationship among them. Success in crop selection, breeding and bioengineering is also depending on the isolation of genetically superior genotypes based on the amount of variability present in the material. Therefore, information on genetic variability existed in a group of populations of *Brassica* are of prime importance and priority area of research.

Estimation of genetic parameters in the context of trait characterization is an essential component of future targeted crop improvement. *Brassica* species and cultivars are characterized by extensive morphological diversity and the ability to adapt to a wide range of habitats and

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growing environments. There appear to be several primary and secondary centers of diversity, with crop domestication involving further selection of adaptations from northern temperate to tropical regions. Understanding the basis of particular crop morphotypes in the context of the wider range of genetic, biochemical and metabolic variation present within the species will make it possible for breeders, plant physiologists and soil scientists of a given crop to utilize beneficial characters found in other crop types or wild germplasm in an informed and efficient manner.

Tolerance to P-stress based on accumulation of shoot dry matter (SDM) is regarded as the product of plant mechanisms involving plant traits (acquisition, translocation, assimilation, utilization and redistribution) of P (Blume, 1988; Akhtar et al., 2006ab). Plant traits such as nutrient uptake and utilization are found to be under genetic influence (Sattelmacher et al., 1994; Vance et al., 2003; Hammond et al., 2004; Raghothama, 2005), improvement in these traits through breeding and bioengineering techniques may lead to the development of crop cultivars better adaptable to conditions of low soil P. In this scenario, genetic analyses of data provide important information for designing appropriate techniques for identifying/developing crop cultivars that can better utilize specified environments such as nutrient deficient areas.

Crop improvement is a key route to ensuring that continued benefits arise from these food and plant products. The presence of genetic variation in the breeding material at hand determines the success or failure of any breeding or bio-engineering program. The measurement of genetic variation and understanding of mode of inheritance of quantitative traits, therefore, are essential steps in any crop improvement program. Heritability estimates provide authentic information about the faithfulness with which a particular genetic attribute will be transmitted to the successive generation. The higher the heritability, the simpler the selection process and greater the response to selection. A broad-sense heritability estimate provides information on the relative magnitude of genetic and environmental variation in the population (Dudley and Moll, 1969; Marwede et al., 2004; Rafi and Nath, 2004).

The heritability (h^2) is an approximate measure of the expression of a character. The estimates of heritability alone give no indication of the associating genetic progress that would result from selecting the best plants. The heritability along with phenotypic variance and the selection intensity, however, promise the estimation of genetic advance or response to selection which is more useful in the selection of promising lines (Johnson et al., 1955; Iqbal et al., 2003; Rohman et al., 2003). Genetic coefficient of variation together with the h^2 estimates are generally thought to give the best estimates of the magnitude of response to be expected from selection. Similarly, a coheritability estimate in genetic sense is an index of transmissibility of two traits together to the next generation. The advantage of this genetic parameter over genetic correlation coefficient is quite obvious as the latter throws light only on the

magnitude of relationship between the two traits in the existing generation and not their coinheritance (Makan and Saini, 1982; Kumar and Dubey, 2001).

For effective crop-based studies it is also essential to be able to navigate between trait and genetic character, and thus integrate information from multidisciplinary (e.g. physiology, soil science, agronomy, breeding, genetics and genomics) approaches. With similar considerations in view, the present study was undertaken by growing six *Brassica* cultivars under P-deficiency stress. The objectives of this study were i) to determine genetic variability among these cultivars and to obtain the estimates of genetic and environmental variances and covariances for various plant traits; ii) to calculate broad-sense heritabilities and response to selection for these traits, and iii) to obtain coheritability estimates for all pairs of traits. This will provide a functional understanding of relevant systems to underpin future crop and product development within a sustainable framework.

2 MATERIALS AND METHODS

2.1 Experimental Protocol

Six *Brassica* cultivars tested were Brown Raya, Con-1, Peela Raya, Rainbow, Toria Selection and Sultan Raya. Pot experiment was conducted using a P-deficient (NaHCO_3 -extractable P= 3.9 mg kg^{-1}) sandy loam soil with EC_e 1.4 dS m^{-1} . Experiment was conducted in a glasshouse in winter and the temperature during growth period varied from a minimum of 5°C to a maximum of 25°C. The soil was air-dried and coarse-ground before filling in glazed china clay pots (30 cm deep and 22 cm diameter) at the rate of 10 kg per pot. To the pots, N was applied as NH_4NO_3 at the rate of 175 mg N kg^{-1} : half in liquid form before sowing and the other half after 27 days of sowing (DAS), while K was applied at the rate of 75 mg K kg^{-1} soil as K_2SO_4 , and Zn at the rate of 5 mg Zn kg^{-1} soil as ZnSO_4 at the time of sowing. A solution containing secondary and micronutrients was also added as [pot⁻¹] @ 50 mg $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$, 20 mg $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$, 200 mg $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$ and $\text{Na}_2\text{B}_4\text{O}_7 \cdot 10\text{H}_2\text{O}$. Five seeds of each of the six cultivars were sown per pot. The plants were thinned to two plants per pot after one week of germination. The two-factorial (two P-levels, six cultivars) experiment was laid out according to completely randomized design with three replicates.

Plants were harvested 49 DAS, and separated into shoots (leaves + stem) and roots. Roots were extracted from soils manually by gently washing away the soil. Leaves of each plant were placed on a leaf area meter for measuring leaf area per plant. Dry matter of roots and shoots were recorded after drying in a forced air oven at 70°C for 48 hours, using an analytical balance. The ratio of dried roots and shoots were obtained by using the formula given by Nour and Weibal (1978). Uniform plant samples were digested in di-acid mixture of nitric acid (HNO_3) and perchloric acids (HClO_4) (3:1) (Miller, 1998)

after grinding in a Wiley Mill and passing through 0.42 mm screen (40-mesh sieve). Tissue-P concentration was determined from digested material using vanadate-molybdate yellow colour method (Chapman and Pratt, 1961). Total-P uptake was calculated by summing up the products of P-concentrations of root, leaf stem and their respective dry matters.

P-uptake (mg plant^{-1}) = P concentration (mg g^{-1}) X dry matter (g plant^{-1})

Phosphorus-use efficiency (PUE) was determined as the reciprocal of P concentration times SDM (Siddiqi and Glass, 1981).

$$\text{PUE} (\text{g}^2 \text{SDM mg}^{-1} \text{shoot-P}) = \frac{\text{SDM} (\text{g plant}^{-1})}{\text{Shoot P concentration} (\text{mg g}^{-1})}$$

2.2 Statistical Background

Separate analyses of variance and covariance for all plant traits and pairs of traits selected for this study were carried out by following the procedures described by Steel and Torrie (1980). The genetic components of variance and covariance were computed using mean squares and expected mean products, respectively. The genetic components of variance and covariance were calculated as outlined by Robinson et al., (1951) by using following formulae:

$$\sigma_g^2 = (MS_2 - MS_1)/r$$

$$\sigma_p^2 = MS_2/r$$

$$\sigma_g = (MP_2 - MP_1)/r$$

$$\sigma_p = MP_2/r$$

Where

σ_g^2 = the estimates of genetic variance,

σ_p^2 = the estimates of phenotypic variance,

σ_g = the estimates of genetic covariance,

σ_p = the estimates of phenotypic covariance,

MS_2, MS_1 = the estimates of cultivar mean squares and error mean squares, respectively,

$MP_2 - MP_1$ = the estimates of cultivar and error mean cross products, and

r = the number of repeats.

The estimates of genetic correlation coefficients were calculated for all pairs of traits by using the formula:

$$r_{gxy} = \frac{\sigma_{gxy}}{\text{SQRT}(\sigma_{gx}^2 \times \sigma_{gy}^2)}$$

Where

σ_{gxy} = genetic covariance between traits 'x' and 'y',

σ_{gx}^2 = genetic variance for trait 'x', and

σ_{gy}^2 = genetic variance for trait 'y'.

The phenotypic correlation coefficients were similarly calculated using phenotypic variance and covariance estimates. The estimates of standard error of genetic correlation coefficients were computed after Reeve (1955) and Robertson (1959) as follows:

$$\text{SE}(r_g) = \frac{1-r_g^2}{\text{SQRT}(2)} \times \text{SQRT} \frac{[(\text{SQRT}(h^2x) \times \text{SQRT}(h^2y))]}{h^2x \cdot h^2y}$$

Where

$\text{SE}(r_g)$ = the standard error of genetic correlation

r_g = the genetic correlation coefficient

h^2x, h^2y = the broad sense heritability estimates in fraction of trait 'x' and 'y', respectively.

Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) were estimated (dividing the square root of the genotypic and phenotypic variances by the population mean and multiplying by 100) by the formula suggested by Burton (1952) and Dudley and Moll (1969), while genetic advance (GA) as percent means and relative expected genetic advance (REGA %) was estimated by the formula given by Lush (1949), Johnson et al. (1955) and Singh and Chaudhry (1979).

The estimates of broad-sense heritability were calculated for each trait using the formula:

$$H^2_{(BS)} = \sigma_g^2 / \sigma_p^2$$

Where σ_g^2 and σ_p^2 are the estimates of genetic and phenotypic variances, respectively.

3 RESULTS AND DISCUSSION

The area of the world's arable land is decreasing, whilst the human population continues to grow. There is increasing pressure to grow arable and other crops on land with marginal nutrition or water availability. There is considerable scope for increasing the added value from *Brassica*-based production. For oil-based products these include high-value lubricants, bio-fuels, plastics and composites, as well as fiber-based products. Sustainable yields are dependent upon efficient use of macro- and micro-nutrients. Nitrogen and phosphate limit yield potential, but there is considerable genetic variation for their efficient uptake and utilization within *Brassica*. Understanding, conserving, accessing and harnessing genetic diversity is a pressing requirement for considerable progress in the genetic analysis of agronomic and related plant traits.

*Brassic*as are primarily adapted to temperate climates, and due to inherent phenotypic plasticity, are well adapted to a range of intensive or low input cultivation techniques. Higher plants have complex adaptive systems with overlapping and interacting mechanisms for modulating their own development in response to environmental cues. They are characterized by a highly developed secondary metabolism, and multilayered regulatory networks, reflected in complex and diverse genome organization. Crop domestication, selection and targeted breeding have enabled human civilization to develop. This continues into the modern age, with increasingly sophisticated technologies available for the interchange and selection of genetic pool meeting the needs of different markets and growing environments.

Table 1. Mean, range and coefficients of variation for various plant traits of *Brassica* cultivars.

| Plant trait | Mean | Range | Coefficient of variation (%) | |
|---|--------|----------------|------------------------------|------------|
| | | | Genetic | Phenotypic |
| SDM (g plant ⁻¹) | 2.94 | 1.65 – 4.98 | 32.72 | 39.51 |
| RDM (g plant ⁻¹) | 2.14 | 1.38 – 3.07 | 53.09 | 57.01 |
| LA (cm ²) | 163.69 | 42.01 – 343.12 | 34.71 | 40.13 |
| RSR | 0.67 | 31.12 – 167.15 | 20.19 | 27.47 |
| PUE (g ² SDM mg ⁻¹ P) | 2.46 | 1.36 – 4.09 | 32.16 | 43.99 |
| TPU (mg plant ⁻¹) | 5.93 | 2.47 – 10.11 | 41.75 | 45.04 |
| TCaU (mg plant ⁻¹) | 95.89 | 32.89 – 151.36 | 39.17 | 43.65 |

SDM = Shoot dry matter; RDM = Root dry matter; LA = Leaf area per plant; RSR = Root-shoot ratio; PUE = P-use efficiency; TCaU = Total-Ca uptake, TPU = Total-P uptake.

Crop improvement is based both on understanding which genes are involved in a phenotype, as well as the degree of environmental variation. Thus the ability to understand the genetic basis and heritability of traits (phenotype) selected in breeding programmes provides the opportunity to deploy novel allelic combinations.

3.1 Genetical Parameters

Understanding plant adaptations to changes in the environment (e.g. P-stress environment), and the availability of robust genetic variation will be essential to underpinning relevant crop improvement. The basic objective of any breeding and bio-engineering program is the improvement of crop yield and quality. The measurement and evaluation of variability are essential steps in drawing meaningful conclusions from a given set of observations (Mehdi and Khan, 1994; Marwede et al., 2004)). The genetic variability of a metric trait can be

studied through the use of various statistical parameters like mean, range, variance components and coefficients of variation.

Mean, range, genotypic coefficients of variation (GCV %) and phenotypic coefficients of variation (PCV %) among *Brassica* cultivars revealed the presence of genetic variation for all plant traits studied in this experiment (Table 1). The estimates of phenotypic coefficients of variation, nevertheless, were greater than their respective genotypic coefficients. The variation among cultivars for all the traits showed promise for their improvement through breeding. Mean squares from the analyses of variance for various plant traits also indicated highly significant differences among cultivars for leaf area per plant, shoot dry matter (SDM), root dry matter (RDM), and total P and total Ca-uptake.

Table 2. Estimates of components of variance, heritability and genetic advance for various plant traits in *Brassica* cultivars.

| Plant trait | Genetic variance (σ_g^2) | Phenotypic variance (σ_p^2) | Environmental (σ_e^2) | Heritability (h^2) | Genetic advance (ΔG) [†] | Relative expected genetic advance (REGA %) |
|---|-----------------------------------|--------------------------------------|--------------------------------|------------------------|---|--|
| SDM (g plant ⁻¹) | 6.15 | 7.93 | 1.78 | 0.78 | 3.43 | 87.12 |
| RDM (g plant ⁻¹) | 6.05 | 6.71 | 0.66 | 0.90 | 1.83 | 85.72 |
| LA (cm ²) | 3339.1 | 4532.5 | 1193.5 | 0.77 | 85.30 | 52.12 |
| RSR | 0.025 | 0.05 | 0.025 | 0.50 | 0.103 | 15.32 |
| PUE (g ² SDM mg ⁻¹ P) | 1.13 | 1.30 | 0.17 | 0.87 | 1.97 | 80.43 |
| TPU (mg plant ⁻¹) | 3.94 | 4.58 | 0.64 | 0.86 | 4.11 | 69.32 |
| TCaU (mg plant ⁻¹) | 1185.6 | 150.32 | 317.6 | 0.78 | 57.84 | 60.32 |

SDM = Shoot dry matter; RDM = Root dry matter; LA = Leaf area per plant; RSR = Root-shoot ratio; PUE = P-use efficiency; TCaU = Total-Ca uptake, TPU = Total-P uptake.

[†]Calculated at 10% selection intensity.

3.2 Components of Variance and Covariance

The estimates of genetic variance revealed that differences existed among selection for all traits recorded in this study. In general, the estimates of genetic variance were smaller than their respective phenotypic variances and greater than their respective environmental variances (Table 2). These results are consistent with the findings of Walters et al. (1991) and Raffi and Nath (2004). In general, the estimates of genetic covariance for various pairs of traits were smaller in magnitude than their respective estimates of phenotypic covariances (Table 3). Root-shoot ratio (RSR)

in combination with SDM and P-use efficiency (PUE) was, however, exceptions in this respect. The value of genetic covariance was found negative between RSR and leaf area per plant, indicating negative associations between these traits.

3.3 Heritability and Coheritability

Maximum estimates of broad sense heritability were noted for SDM, RDM, PUE, total-P uptake, and total-Ca uptake (Table 2). These high estimates of heritability suggested the feasibility of selection for these traits under phosphorus-deficiency stress. Very low estimates of

broad-sense heritability were noted for RSR, which indicated that this trait could not be considered as basis for selection.

The information about the coheritability for all possible pairs of plant traits is given in Table 3. An examination of this table reveals that coheritability between leaf area per plant and characters like SDM, RDM, total-P uptake and PUE was positive and high, while with total-Ca uptake, it was positive and moderate. The coheritability of leaf area per plant with RSR was negative and moderate showing marginally negative association between these traits for associative transmission to next generations.

Coheritability of SDM with RDM and total-P uptake was high and positive, which indicates better chances of their coinheritance. The value of coheritability of SDM with total-Ca uptake was positive and moderately high, while with PUE, it was positive and moderate. High and positive coheritability values of RDM in combination with RSR, PUE, total-P uptake and total-Ca uptake indicated that these traits would likely be transmitted in combinations to the next generations. Coheritability of RSR with SDM and PUE was extremely high and positive, which reflects that chances of their coinheritance are very high. Coheritability of RSR with total-P uptake and total-Ca uptake was also high and positive, indicating likelihood for these characters entering next generation together.

Coheritability of PUE with total-P uptake was high and positive. The magnitude of coheritability of PUE with total-Ca uptake was moderately high and positive. Coheritability of total-P uptake in combination with total-Ca uptake was high and positive. This reflects that both these characters could be transmitted together to the next generation. Makan and Saini (1982) considered coheritability as better genetic parameter to which selection is applied. The foregoing discussion suggests that RSR would coinherit with SDM

and PUE, and hence might be utilized in future breeding and bio-engineering programs.

3.4 Genetic Advance (ΔG) and Relative Expected Genetic Advance (REGA %)

The expected genetic advance is a gain or a change produced by selection and is of main interest to the plant breeder since it changes the population mean. Estimation of progress from selection has been one of the most important contributions of quantitative genetics to plant breeding (Zubair, 1993; Raffi and Nath, 2004). The estimates of expected genetic advance for plant traits like leaf area per plant and total-Ca uptake were quite high followed by total-P uptake, SDM, PUE, RDM, and RSR, respectively when calculated at 10% selection intensity. However, the relative expected genetic advance at the same selection intensity was high for SDM, RDM, PUE, total-P uptake and total-Ca uptake followed by leaf area per plant (moderate value), while low for RSR. Higher values of expected genetic advance for various plant traits revealed effectiveness of the selection for these traits and these parameters were under the control of additive genes. This study suggested that through selection, SDM of *Brassica* cultivars can be increased from 2.94 g plant⁻¹ to 6.37 g plant⁻¹, with RDM of 3.97 g plant⁻¹, RSR of 0.77, and a gain of 10.04 mg plant⁻¹ for total-P uptake.

Within different growing regions and crop types there are priorities vary for research focused on agronomic traits. Dependent upon availability of natural or managed resource, the genetic variation within *Brassica* can be utilized to provide information and solutions to improve nutrient use efficiency (e.g. PUE), water use efficiency, germination, seedling establishment and vigour, yield components and the basis of genotype x environment interactions. The harvest index (harvestable yield as a

Table 3. Estimates of genetic (top figures), phenotypic (middle figures) covariances, and coheritability (bottom figures) for various plant traits.

| | SDM | RDM | RSR | PUE | TPU | TCaU |
|-----|-------|--------|---------|--------|--------|---------|
| LA | 33.45 | 21.44 | -0.4531 | 23.43 | 105.93 | 1829.72 |
| | 46.55 | 24.64 | 1.9160 | 34.62 | 121.73 | 2327.92 |
| | 0.832 | 0.984 | -0.2010 | 0.898 | 0.989 | 0.786 |
| SDM | | 0.4101 | 0.0461 | 0.3844 | 2.381 | 23.09 |
| | | 0.4643 | 0.0331 | 0.5289 | 2.5983 | 29.69 |
| | | 0.9641 | 2.002 | 0.767 | 0.973 | 0.789 |
| RDM | | | 0.0558 | 0.4229 | 1.1104 | 19.163 |
| | | | 0.0653 | 0.6119 | 1.2529 | 22.363 |
| | | | 0.8333 | 0.989 | 0.997 | 0.972 |
| RSR | | | | 0.0406 | 0.1032 | 1.973 |
| | | | | 0.0303 | 0.2279 | 1.883 |
| | | | | 1.875 | 0.985 | 0.9613 |
| PUE | | | | | 1.2026 | 18.653 |
| | | | | | 1.3042 | 24.023 |
| | | | | | 0.9243 | 0.725 |
| TPU | | | | | | 73.803 |
| | | | | | | 85.925 |
| | | | | | | 0.982 |

SDM = Shoot dry matter; RDM = Root dry matter; LA = Leaf area per plant; RSR = Root-shoot ratio; PUE = P-use efficiency; TCaU = Total-Ca uptake. TPU = Total-P uptake.

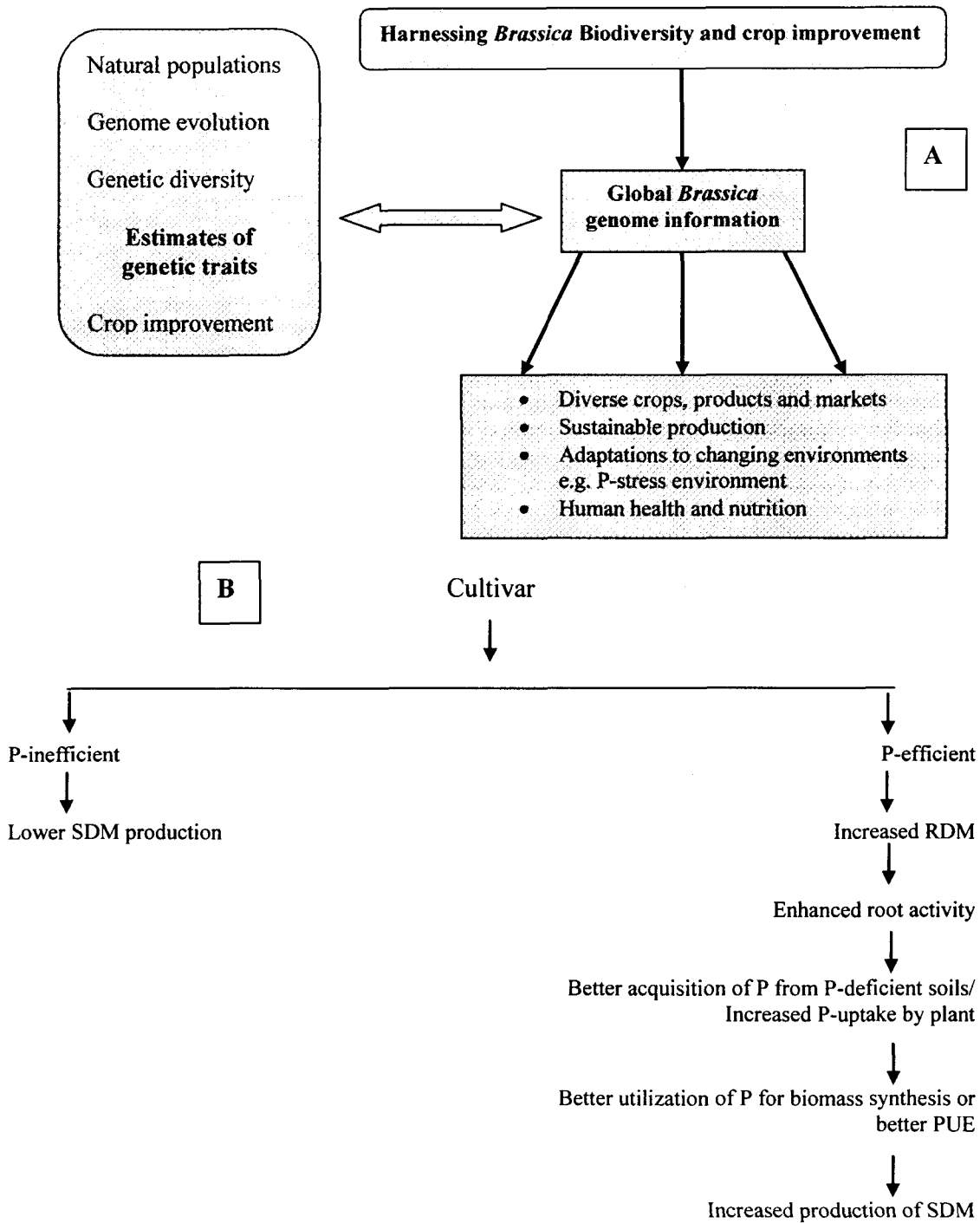


Fig. 1. (a) “Global information, local implementation” path cladogram. (b) Schematic diagram of possible pathway adopted by a P-efficient *Brassica* cultivar under P- stress environment.

proportion of total biomass) of *Brassica* is low compared with other arable crops such as cereals. There is considerable scope for improving the harvest index to increase overall yields and lower the level of fossil-fuel and other inputs for a more sustainable production. Developing a systems approach to understanding the genetic and

genomic basis of yield components requires a multidisciplinary international research environment with access to relevant genomic and trait information.

Brassica crops are derived from wild species which still exist in nature, and which they are able to be inter-crossed. There are concerns that in some crop types there

has been progressive genetic erosion and reduction in genetic diversity within the crop gene-pool. The wild relatives thus have the potential to provide access to a much wider range of allelic variation. *In situ* genetic variation exists for the diploid *Brassica* species, in the centers of diversity. Estimates of genetic parameters of plant traits under P-starvation will guide us to exploit intra-specific variations among *Brassica* to achieve maximal yield under P-stress conditions. *Brassica* crops appear to have been under different selection pressures reflecting the period over which they have been domesticated. For leafy vegetable crops, there is a wide genetic diversity and eco-geographic distribution. More specialized leafy, root or floral organ based vegetables have been progressively selected and refined as mutations have accumulated through domestication, and hence may have more restricted eco-geographic centers of diversity. The *B. napus* oil crops appear to be relatively recent crop types that have been selected since stable hybridization between domesticated diploid progenitors. A further restriction of the gene-pool is likely to have taken place following development of oil-extraction technologies and more recent selection of varieties possessing low glucosinolate and low erucic acid content (double lows).

Ex situ genetic resources are available in the public and private sectors. The European *Brassica* database (Bras-EDB) compiles information on genetic resource accessions held in public collections. Similar information is held in the USDA/ARS Grin system. The pressure for more intensive agriculture has resulted in an overall reduction of the natural genetic diversity of crop plants, a process called 'genetic erosion' and in some cases leading to a significant loss in the adaptability and sustainability of crops, particularly in combating natural pests, diseases and nutritional stresses as P-deprivation. Traditionally, most crops were based on local selections ('landraces') developed over generations in particular farming communities and locations. Characterizing and using crop biodiversity is essential to provide the range of alternative crop varieties needed to meet the changing needs of the world. A large international effort over the past few decades has ensured (*ex situ*) conservation of many crop genetic resources. This has involved collecting traditional varieties and landraces from around the world, and in particular from centers of genetic diversity for specific crops. Modern crops contain a surprisingly narrow genetic base, despite the existence of extensive allelic variation within germplasm collections. Although breeders exploit the existing natural variation for particular target traits within crop species, there has been considerable reduction in biodiversity through canalization of alleles. A range of major challenges focus on harnessing genetic diversity through an information-led approach to crop improvement. There are a wide range of valuable traits for which genetic variation exists but where understanding is required. These include enhanced nutrient use efficiency such as PUE, improving harvest index and yields in the context of changing climate and need to reduce inputs,

estimates of genetic traits under nutrient stress environments, optimizing quality fit for purpose, and identifying scope for added value through nutritional, prophylactic health or non-food use.

Efficient *Brassica* cultivars can increase their capacity to access nutrients by altering root morphology (increasing surface area by growing long, thin roots with numerous, and long root hairs) and enhance nutrient availability and uptake. Modification in root architecture in an efficient cultivar is an important genetic adaptation to explore P from P-deficient soil environment. In the light of above discussion and work reported earlier (Akhtar et al., 2006a,b; Akhtar et al., 2007ab), a schematic diagram of possible pathway specifically adopted by a P-efficient cultivar is suggested in Fig. 1. Efficient plants show several morphological, physiological and biochemical adaptations triggered by P-starvation that enable them to scavenge P from sparingly soluble P-soil fractions. The efficient utilization of the absorbed P in biomass synthesis per unit results in better growth of a cultivar in terms of biomass accumulation. Fig. 1B elucidates the possible pathway a P-efficient *Brassica* cultivar follow to produce higher biomass under low soil P-conditions. Given the unique position of *Brassic*as with their diverse crop types and metabolites, the vision for maximizing the benefits from recent advances in genomics and genetic trait analysis can be summed up in terms of "global information, local implementation" as presented in Fig. 1A.

4 CONCLUSIONS

Conclusively, it can be stated that estimates of genetic parameters help in understanding the role of various plant traits in establishing the growth behavior of cultivars under a given set of environmental conditions. Genetic analysis leads us to a clear understanding of different morphological, physiological and genetic characters and also the type and extent of their contribution to dry matter yield. All the characters studied showed high heritability (h^2) coupled with high genetic advance indicating that these plant traits can be further improved through individual plant selection. Navigation between trait and genetic character, and integration of information from multidisciplinary approaches are the area of research priority and can lead us to understand the plant responses under different growing and changing environments such as P-stress environment. Genetic analysis of data provide information for designing appropriate techniques for identifying/developing crop cultivars better adaptable to nutrient deficiency stresses such as P-starvation and provide functional understanding of relevant systems to underpin future crop and product development within a sustainable framework. Analysis of genetic parameters helps in understanding, conserving, accessing and harnessing genetic diversity which can help us to exploit

global integration of information and resources in public domain i.e. 'Global information, local implementation'.

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