BREEDING POTENTIAL OF *VIGNA SUBLOBATA* (ROXB.) BABU & SHARMA IN THE IMPROVEMENT OF MUNG BEAN

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ABSTRACT

Population differentiation, protein content and seed weight of eight natural populations of *Vigna sublobata*—the wild progenitor of mung bean—inhabiting Palney Hills (Tamil Nadu, India) have been investigated. The two enzyme loci—acid phosphatases and esterases—investigated by polyacrylamide gel electrophoresis demonstrate that there is a substantial genetic variability and that the populations are well-differentiated. The genetic base for seed protein content is broad and it offers a breeding potential for the development of high protein lines of mung bean. One of the populations is a perennial offering further scope for breeding. The range of variation in the 100-seed weight is narrow; the relationship between seed weight and protein content is negative and the *r* value is statistically highly significant at $P < 0.05$.

INTRODUCTION

THE wild progenitors constitute additional resources for the genetic upgrading of crop plants[1–4]. Attempts have been made to utilize the gene pools of wild and domesticated tepary beans for the development of drought tolerant, heat and disease resistant common beans (*Phaseolus vulgaris* Linn.)[5,6].

Vigna sublobata is the putative progenitor of *V. mungo*—one of the major Asian pulse-yielding legumes. It is widely distributed in the hilly tracts of Peninsular India and is composed of local, regional and geographical races[7,8].

The genetic differentiation, protein content and seed weight of natural populations inhabiting Palney Hills (Tamil Nadu, India) are reported in this paper.

MATERIALS AND METHODS

Eight natural populations of *V. sublobata* (designated as $P_1 \ldots P_8$) were sampled from different ecozones of Palney Hills—an eastward offshoot of Western Ghats of Tamil Nadu (India). Seeds of these populations were collected and these were used for experimentation.

Polyacrylamide gel electrophoresis was used to investigate the enzyme polymorphism in seed esterases and acid phosphatases, following Davis[9] and Ornstein[10]. The staining methodology outlined by Scandalios[11] was followed to detect bands of both the enzymes. The similarity index between pairs of populations based on isoenzyme profiles was determined according to Vaughan[12].

The seed protein content was determined by microkjeldahl method and was expressed as PNU (N per cent × 6.25) at a constant moisture content of 10.25 %. The weight of 100 air-dried ripe seeds (selected at random from the seed lot) was determined. The relationship between protein content and seed weight was determined by Pearson product-moment Correlation Coefficient.

RESULTS AND DISCUSSION

Figure 1 illustrates the banding patterns of acid phosphatases and esterases. For acid phosphatases, altogether 18 bands were resolved on the gels, of which only I was monomorphic and the rest were polymorphic. For esterases 7 bands were detected, of which 2 were monomorphic, and the remaining ones were polymorphic. These results suggest that the loci controlling the isoenzymes of acid phosphatases and esterases are highly heterozygous and the populations differ in the frequencies of different alleles. Consequently, the populations are genetically well-differentiated in relation to spatio-temporal environments prevalent in the area surveyed. Similar observations have been made in the land races of barley[13], different geographical populations of tea[14] and populations of *Eucalyptus*[5,15].

The similarity index values between pairs of populations based on isoenzyme patterns of both the enzymatic systems substantiate the population differentiation (table 1). P_5 is distantly related to all other populations. P_7 is a perennial, a feature not found in any one of the pulse-yielding species of *Vigna*, and it is also less closely related to all other populations except

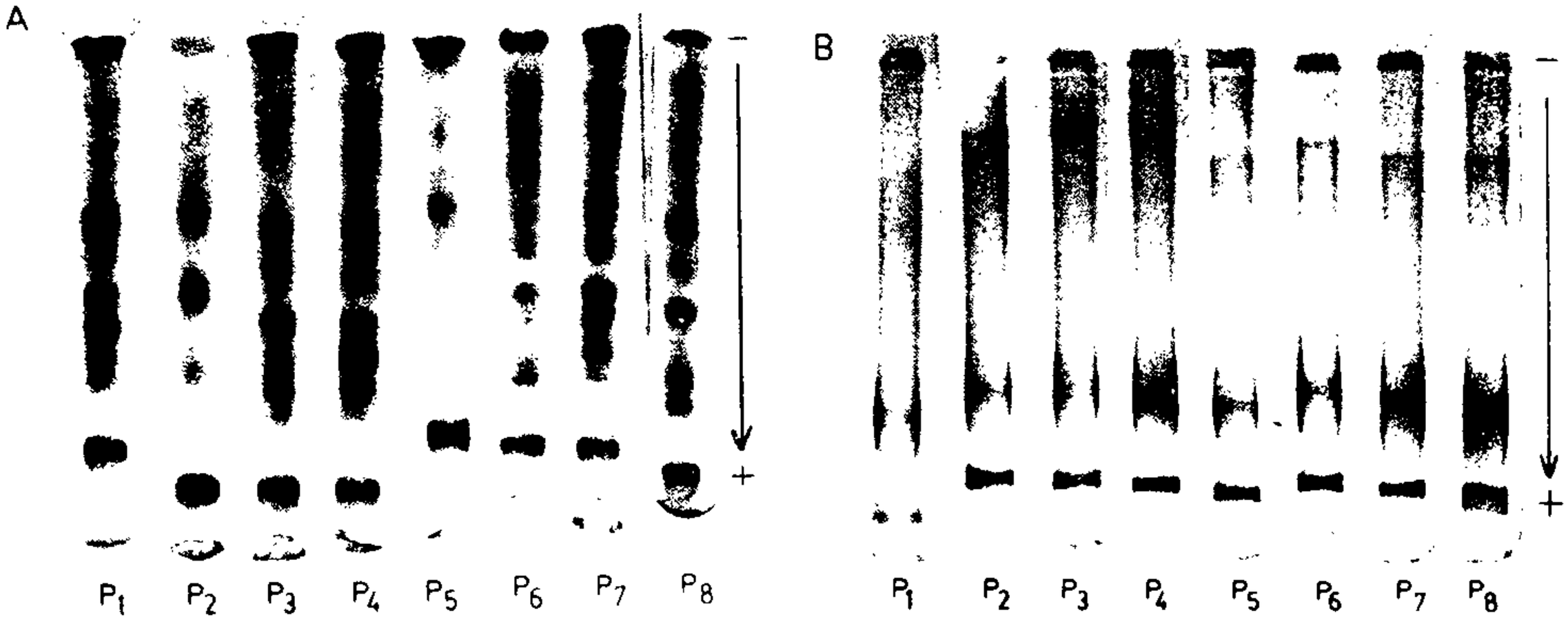

Figure 1A & B. Electrophoretic variation in two enzyme loci. **A.** Acid phosphatases, **B.** Esterases.

Table 1 *Similarity index values between pairs of populations based on isoenzymes of acid phosphatases and esterases.*

Population	P_1	P_2	P_3	P_4	P_5	P_6	P_7	P_8
P_1	—	27.0	50.0	25.0	42.0	54.0	25.0	43.0
P_2		—	28.0	40.0	20.0	24.0	40.0	24.0
P_3			—	33.0	24.0	60.0	33.0	50.0
P_4				—	19.0	47.0	83.0	69.0
P_5					—	36.0	22.0	19.0
P_6						—	57.0	68.0
P_7							—	57.0
P_8								—

P_4. Consequently it is of immense value in breeding perennial varieties of mung bean.

Data on protein content and 100-seed weight of different populations are provided in table 2. The range of variation in the protein content is wide (16.4% to 25.6%), suggesting a broad genetic base. The protein content of P_5 is much higher than that of *V. mungo*. Similar results have been obtained in wild and domesticated tepary beans[16]. The range of seed weight is narrow; the relationship between protein content and seed weight is negative, and the *r* value is statistically significant at $P < 0.05$. The negative relationship between yield component and protein content is perhaps associated with sink-source relationships. Similar explanation has been offered by Leleji[17] for *Phaseolus vulgaris*.

Table 2 *Percent protein, 100-seed weight and their correlation in Vigna sublobata*

Population	Percentage protein	100-seed weight (g)
P_1	24.8*	0.87*
P_2	18.9*	0.94*
P_3	24.9*	0.86*
P_4	23.9*	0.89*
P_5	25.6*	0.86*
P_6	16.4*	0.94*
P_7	19.7*	0.95*
P_8	21.4*	0.92*

* Mean values based on two replicates.

The findings presented in this paper demonstrate that: (i) the natural populations of *V. sublobata* are genetically well-differentiated; (ii) they possess substantial genetic variability; (iii) the broad genetic base in seed protein content can be utilized in breeding high protein lines of mung bean; (iv) P_7 and P_5 populations may be used as potential breeding material for the

development of perennial and high protein varieties of mung bean.

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NEWS

INDUSTRIAL EFFLUENTS, SERIOUS HEALTH HAZARD

Heavy metal pollution from industrial effluents is causing serious health and environmental hazards in the country.

According to Dr B. N. Gupta and Dr A. K. Mathur of the Industrial Toxicology Research Centre, Lucknow, out of 92 natural and 14 synthetic elements about 20 metals – including arsenic, antimony, cobalt, chromium, cadmium, lead, manganese, mercury, molybdenum, nickel and tin – have been found to produce serious health problems to man and environment.

Reporting the findings of their study in the *Indian Journal of Medical Science*, the scientists say that industrial smoke containing arsenic, antimony, copper, manganese and nickel is an important source of environmental pollution. Burning of domestic fuels and vehicle exhausts also constitute a significant source of atmospheric pollution.

The scientists found that tetraethyl lead, added to petrol as an anti-knock compound, ultimately came out of the motor exhaust and contaminated the air with a significant amount of lead.

Lead compounds were found in the surface soil along highways in Ahmadabad, according to the study.

In the manufacture of caustic soda by mercury cell process, significant amounts of mercury were discharged into the atmosphere.

Such effluents are a major source of metal pollution of water. Toxic elements often end up in the food chain of the marine ecosystems, ultimately affecting the birds and mammals, dependent on sea for food. (*ISI Bulletin*, Vol. 36, March 1984, p. 95.)