



Pattern of nodulation and biological nitrogen fixation in grasspea (*Lathyrus sativus* L.) genotypes

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As in other grain legumes, grass pea (*Lathyrus sativus* L.) fixes atmospheric N₂ at root nodules in association with rhizobium and thereby enriches soil fertility. In this context the study on nodulation and biological nitrogen fixation in grass pea assumes a practical significance. Two genotypes of grasspea namely Nirmal evolved in West Bengal and P-24 at IARI, New Delhi were grown without any fertilizer at the farm of Bidhan Chandra Krishi Viswavidyalaya, Kalyani, which represents alluvial soil having pH 6.3 and NPK of 0.09%, 0.4% and 0.29% respectively. Samples of four plants were collected without causing any damage to the roots at 30 days, 55 days (flowering started) and at 80 days after sowing when pods were fully developed. Nodule counts were done from primary and lateral roots of 5 cm of root length as also beyond 5 cm. From these two root zones nodules were analysed for their nitrogenase activity through acetylene reduction method as suggested by Hardy *et al.* [1].

At 30 days of plant growth more number of nodules were formed in primary root in both the genotypes at both the root zones (Table 1). At flowering after 55 days of sowing more nodules started appearing in lateral roots. Thereafter there was a decline in nodulation at fully developed pod stage. A general trend appeared in the pattern of nodulation. Irrespective of genotypes, nodulation gradually increased from preflowering, reached its peak at flowering and then went down at the fully developed pod stage. Similar, pattern of nodulation was also recorded in mungbean [2] and groundnut [3]. However, a genotypic difference in nodule formation was observed. At 5 cm of root length during preflowering, P-24 recorded distinctly more number of nodules both in primary and lateral roots. On the other hand, Nirmal displayed relatively more number of nodules during flowering and developed pod stage at a root length beyond 5 cm indicating a root zonewise differential nodulation between genotypes. Within the genotype also there was a tendency of differential nodule formation with respect to root zone. This became

evident at three stages of plant growth (Table 1). Nitrogenase activity also reflected a conspicuous trend where in both the genotypes at two different root zones nitrogenase activity progressively increased from preflowering stage and displayed its maximum activity

Table 1. Average numbers of nodules at different root zones and their nitrogenase activity (n.mol.C₂H₄g⁻¹ h⁻¹)** during different stages of plant growth in grasspea genotypes

Geno- type	Root zone	Root	Growth stages*			
			30 DAS	55 DAS	80 DAS	
Nirmal	5 cm	Primary	2.7	5.5	1.5	
		Lateral	2.7	2.5	2.5	
		Total	5.4 (98.2)	8.0 (989.2)	4.0 (1.65)	
	Beyond 5 cm	Primary	1.7	5.0	7.0	
		Lateral	1.7	6.0	1.2	
		Total	3.4 (18.1)	11.0 (197.8)	8.2 (7.20)	
	Grand		8.8	19.0	12.2	
	Total					
	P-24	5 cm	Primary	6.0	5.5	3.3
			Lateral	2.5	4.5	2.0
Total			8.5 (117.1)	10.0 (756.2)	5.3 (9.74)	
Beyond 5 cm		Primary	3.3	5.2	3.0	
		Lateral	1.5	2.5	2.0	
		Total	4.8 (11.7)	7.7 (447.1)	5.0 (1.83)	
Grand		13.3	17.7	10.3		
Total						

*I = 30 DAS; II = 55 DAS; III = 80 DAS; DAS = days after sowing

at flowering followed by abrupt decline at fully developed pod stage which corroborates the findings of Misra [3] in groundnut. Here again genotypic difference was very much pronounced. At flowering Nirmal recorded higher nitrogenase activity at both the root zones than P-24. However, P-24 maintained higher nitrogenase activity at 5 cm of root length where it was higher in Nirmal beyond 5 cm during fully pod developed stage. Thus root zonewise genotypic differences can be demonstrated. It became apparent that nodules at later

stage of development (developed pod stage) were not as efficient as in early stage of growth. In fact, both the genotypes produced more or less comparable number of nodules both at flowering and fully developed stage but they recorded miserably low nitrogenase activity at advanced stage of plant growth i.e. fully developed pod stage. Hence the study demonstrates a conspicuous nodulation pattern root zonewise and also nitrogenase activity during different stages of plant growth in grass pea genotypes. These findings however, have to be considered in the light of competitive native soil microbes as the experimentation was done under natural environmental condition.

References

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