

rare and endemic species, out of which 3 species are cosmopolitan and a remaining 18 species are endemic to South Asia. Most of the species collected have revealed to belong to subgenus *Sophophora* and *Drosophila*. Among the *Sophophoran* subgenus all the species belong to *melanogaster* species group. This is on par with the conclusion of Bock and Wheeler (1972) that the *melanogaster* species group must have originated from the South Asian or Indian subcontinent. This result may provide further insights into the evolutionary origin and diversification of *melanogaster* species group. Further the diversity of the *Drosophila* subgenus has also proved to be interesting with the Indian species of *D. daruma* reported for the first time from South India (Srinath and Shivanna, 2012). *Z. bogoriensis* belonging to subgenus *Anaprionus* is also a rare species, which was reported by Yassin and David (2010) from Bangalore, India; they also discussed its morphological characters.

Gupta and Raychaudri (1970) described *D. latifshahi* for the first time from Chakia forest in North India. They categorized this species under subgenus *Scaptodrosophila*. The *Polychaeta* species group is characterised with 3 pairs of dorsocentral bristles and surstylus with more or less pubescent flap (Toda and Peng, 1989). Later Toda and Peng (1989) reported this species for the first time from Guangdong province, China. They reclassified the taxonomic status of this species and categorized it under *Polychaeta* species group of the subgenus *Drosophila*. The species collected from Dharwad district in North Karnataka of South India has the similar characteristic feature of *Polychaeta* species group. It is one of the rare species which was not reported by earlier workers from South India.

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**References:** Bachli, G., 2014, Taxodros: The database on taxonomy of Drosophilidae. URL: <http://www.taxodros.unizh.ch>; Bock, I.R., and M.R. Wheeler 1972, Univ. Texas. Pub. 7213: 1-102; Fartyal, R.S., and B.K. Singh 2001, Dros. Inf. Serv. 84: 30-38; Gupta, J.P., and S.P. Raychaudhuri 1970, Proc. R. Entomol. Soc. (B) Taxonomy 39(5-6): 57-72; Gowda, S.L., and N.B. Krishnamurthy 1972, Dros. Inf. Serv. 48: 38; Hegde, S.N., and N.B. Krishnamurthy 1980, Dros. Inf. Serv. 55: 60-61; Hegde, S.N., V. Vasudev, and M.S. Krishna 2001, In: *Trends in Wildlife Biodiversity Conservation and Management* (Hosetti, B.B., and M. Venkateswarulu, eds.). Daya Publishers, New Delhi, pp. 55-68; Markow, T.A., and P.M. O'Grady 2006, *Drosophila, A Guide to Species Identification and Use*. Academic Press, London. 247 pp.; Mateus, R.P., M.L.T. Buschini, and F.M. Sene 2006, Braz. J. Biol. 66(2B): 719-729; Nagaraj, H.J., and N.B. Krishnamurthy 1980, Dros. Inf. Serv. 55: 114; Okada, T., 1956, *Systematic Study of Drosophilidae and Allied Families of Japan*. Gihodo Co. Ltd., Tokyo, Japan. 183 pp.; Prakash, A., and N.B. Ramachandra 2008, Dros. Inf. Serv. 91: 82-87; Prakash, H.S., and G.S. Reddy 1978, Entomon. 3(1): 85-90; Prakash, H.S., and G.S. Reddy 1979, Proc. Indian Acad. Sci. 88(1): 65-72; Ranganath, H.A., and N.B. Krishnamurthy 1972, Dros. Inf. Serv. 48: 132; Reddy, G.S., and N.B. Krishnamurthy 1974, J. Univ. Mysore 26(B): 54-64; Shivanna, N., G.S. Siddalingamurthy, and S.R. Ramesh 1996, Genome 39: 105-111; Srinath, B.S., and N. Shivanna 2012, Biosystematica 6(1): 39-42; Toda, M.J., and T.X. Peng 1989, Zool. Science 6(1): 155-166; Vasudev, V., H.J. Nagaraj, Nagabhushana, and S.N. Hegde 2001, Entomon 26(special issue): 326-331; Yassin, A., and J.R. David 2010, Zookeys 51: 33-72.



### **Latitudinal clines of allozymes in Indian natural populations of *Drosophila ananassae*.**

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Animal species are known to live in environments that vary through time and space. In many situations, such environmental heterogeneity can act as a strong selective force causing adaptive differentiation among populations. Evolutionary biologists try to quantify the magnitude of adaptive differentiation among

populations and also to scrutinize gene loci responsible for such adaptive differentiation in different populations. A number of species of animals including *Drosophila* has been examined for their genetic differentiation between populations. Many latitudinal clines have been demonstrated for various quantitative traits in *Drosophila* species. Latitudinal clines are also reported for chromosomal polymorphism and show climatic selection over chromosomal arrangements in many species of *Drosophila*. Geneticists have also tried to demonstrate that chromosomal arrangements are not solely responsible for these clines and have proved that many quantitative traits (*viz.* body size, starvation resistance, and chill coma recovery) exhibit significant linear clines in inversion free species of *Drosophila simulans* (Arthur *et al.*, 2008). Numerous clinal studies have been performed in invertebrate species including *Drosophila* (Hoffmann and Weeks, 2007). These studies not only look into action of climatic selection but also allow genetic variation in these traits to be linked to particular genes.

Study with regard to electrophoretic variants of enzymes has also shown interesting aspects for *Drosophila* workers (Mulley *et al.*, 1979; Cavener and Clegg, 1981; Santos *et al.*, 1989; Prout and Barker, 1993; Moraes and Sene, 2002). Oakeshott *et al.* (1982) selected four gene loci, *Adh*,  $\alpha$ -*Gpdh*, *Est-6* and *Pgm* in *D. melanogaster* and found them to be polymorphic. They could observe latitudinal clines for three enzyme loci except for *Pgm*. The results obtained helped them to conclude that selection operates on the *Adh* and  $\alpha$ -*Gpdh* loci due to the advantage of heterozygotes. Mulley *et al.* (1979) found association between allozyme and environmental variables in the Australian populations of *D. buzzatii*. They detected significant association between genotypes and environment for five of the six loci studied. Bubliy *et al.* (1994, 1999) analysed several natural populations of *D. melanogaster* coming from different parts of the world for *Adh*,  $\alpha$ -*Gpdh*, *Est-6*, *Odh*, *G6pd*, and *Pgd* enzyme polymorphism. Their study clearly indicated the clinal variation with respect to allelic frequency of respective enzyme and geographical locations. Based on the results they concluded that allozyme polymorphisms are maintained by climatic selection. Negative correlation with latitude were found for *Adh-S* and  $\alpha$ -*Gpdh-F* allele frequencies by Land *et al.* (2000) in natural populations of *D. melanogaster* collected from central and South America. Umina *et al.* (2005) reported geographical clines in genetic polymorphism, which was evidence for climatic selection and which was expected to shift with climate changes. They showed that the classic latitudinal cline in the *Adh* polymorphism of *D. melanogaster* shifted over 20 years in eastern coastal Australia. Moraes and Sene (2002) studied temporal and spatial intra-population allozyme variation in two natural populations of cactophilic species of *Drosophila*: *D. antonietae* and *D. gouveai*. Their results suggested that environmental variation influences temporal variation in allozyme polymorphism. They could not find cyclical variation in allozyme polymorphisms but detected an association between genetic distance and rain precipitation.

*Drosophila ananassae*, which was initially described from Indonesia by Doleschall in 1858, is a cosmopolitan and domestic species. It belongs to the *ananassae* species complex of the *ananassae* subgroup in the *melanogaster* species group (Bock and Wheeler, 1972). It occupies a unique status in the genus *Drosophila* due to certain peculiarities in its genetic behavior (Singh, 2010). Chromosomal polymorphism has been extensively studied in natural and laboratory populations of this species (Singh, 2010). This species has also been involved to see allozyme polymorphism in different Indian natural populations (Parkash *et al.*, 1994; Kumar and Singh, 2012, 2013, 2014; Krishnamoorti and Singh, 2013; Singh *et al.*, 2013). In the present study we wish to report that some of the enzyme loci in *D. ananassae* show graded variation in the frequency of their alleles when compared with populations derived from different geographical locations (varying latitude).

*D. ananassae* flies were collected from fifteen different eco-geographical regions of India by using net sweeping method from fruits and vegetable markets. Place of collection and their latitudinal position are given in Table 1. After bringing the flies to laboratory, naturally impregnated females were cultured in separate vials to establish isofemale lines. The isofemale lines were maintained on simple yeast-agar culture medium at 24±1°C with 12 hour cycle of dark-light period. Individual flies from isofemale lines were used to analyze allozyme polymorphism. For allozyme analysis, a single fly was homogenized in 50 µl 20 mM Tris buffer (pH 7.4) sample buffer and the homogenate was centrifuged at 12000 rpm at 4°C for 10 minutes (Kumar and Singh, 2013). Supernatant was separated into two aliquots and subjected to 8% native polyacrylamide gel electrophoresis in 25 mM Tris and 250 mM Glycine electrode buffer (pH 8.2) at 200V for 4 hour at 4°C. In-gel staining for enzymes was performed according to Shaw and Prasad (1970) and Ayala *et al.* (1972). The

locus and allele designations were done following the standardized genetic nomenclature for enzyme coding loci (Lakovaara and Saura, 1971).

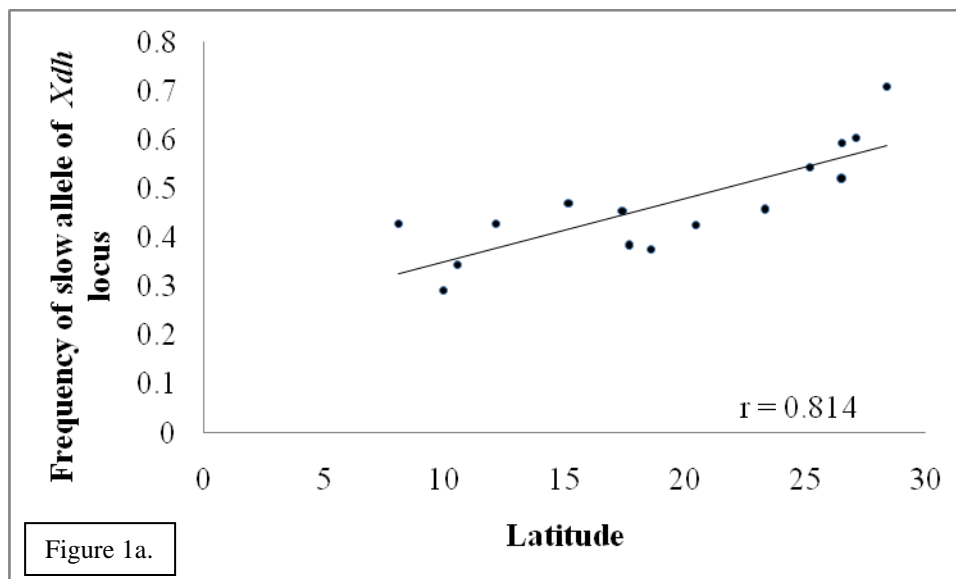
Table 1. Geographical localities, their abbreviation and latitude of natural populations of *D. ananassae*.

S. No.	Populations	Abbreviation	Latitude
1	Kanniyakumari	KKR	8.08
2	Madurai	MDR	9.93
3	Thrissur	TSR	10.52
4	Dharmapuri	DMP	12.13
5	Bellary	BLY	15.15
6	Hyderabad	HYD	17.38
7	Solapur	SLP	17.68
8	Washi	WSI	18.58
9	Akola	AKL	20.44
10	Ranchi	RNC	23.35
11	Varanasi	VNS	25.2
12	Lucknow	LKO	26.51
13	Jaipur	JPR	26.55
14	Agra	AGR	27.11
15	Delhi	DLH	28.4

Table 2. Correlation coefficient ( $r$ ) for slow allele of 12 enzyme loci and latitude of 15 natural populations of *D. ananassae*.

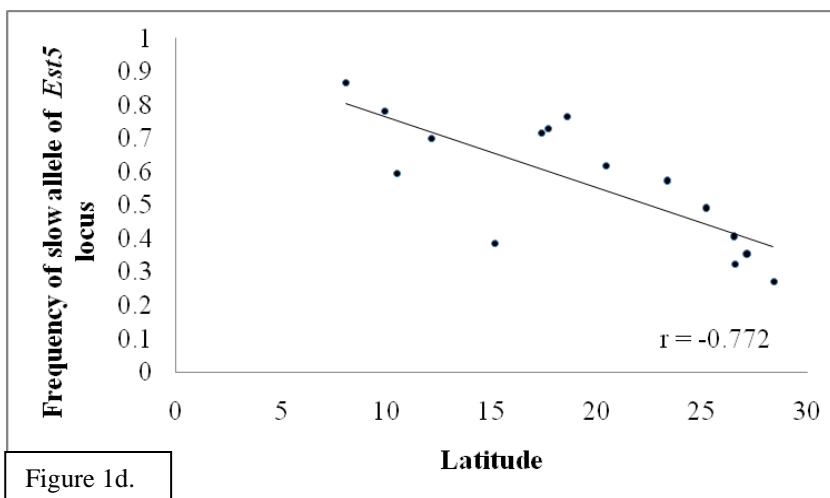
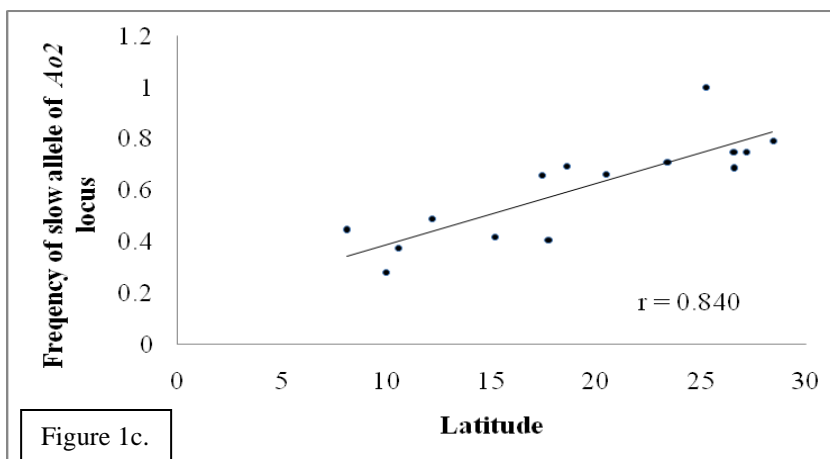
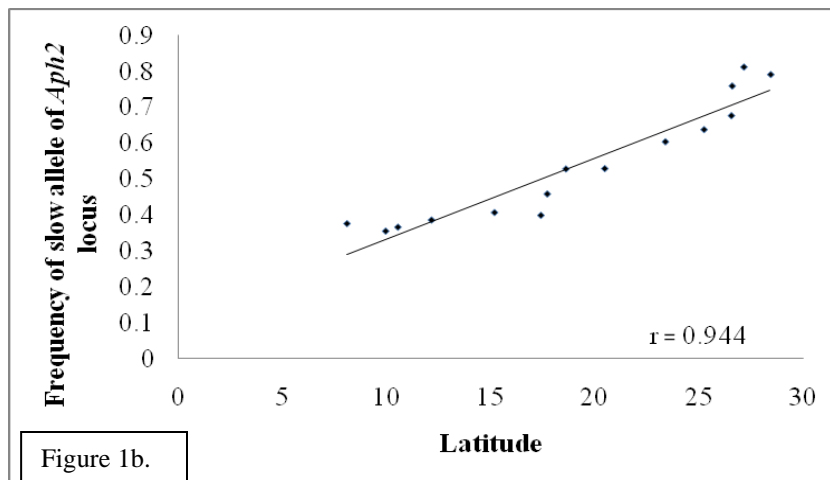
S. No.	Locus	Correlation coefficient ( $r$ )
1	<i>Acph1</i>	-0.256
2	<i>Acph2</i>	0.366
3	<i>Xdh</i>	0.814
4	<i>Aph2</i>	0.944
5	<i>Aph3</i>	0.007
6	<i>Ao1</i>	0.009
7	<i>Ao2</i>	0.840
8	<i>Est2</i>	-0.37
9	<i>Est3</i>	-0.151
10	<i>Est5</i>	-0.772
11	<i>Mdh</i>	0.861
12	<i>Me</i>	-0.177

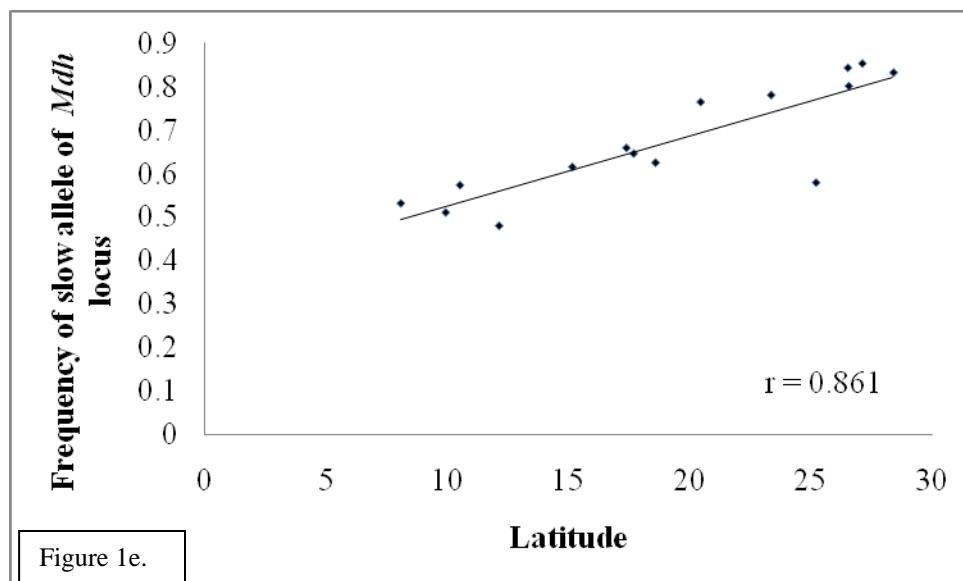
Figure 1. Graphs (1a to 1e) showing clinal variation between latitude and frequency of slow allele of five enzyme loci.



Correlation coefficient was computed between latitude and slow migrating alleles of twelve enzyme loci (Table 2). Out of twelve enzymes tested, significant correlation could be observed with five enzyme loci (Figure 1a to 1e). *Est5* locus shows significant negative correlation whereas four enzyme loci, i.e., *Xdh*, *Aph2*, *AO2* and *Mdh* showed significant positive correlation. *Aph3* and *AO1* showed very low  $r$  values (0.007 and 0.009, respectively) indicating almost no correlation in this regard. Loci encoding for enzymes *Acph1*, *Acph2*,

*Est2*, *Est3*, and *Me* did not show significant departure from zero indicating insignificant correlation between the frequency of slow allele and latitude. The present results reveal that all polymorphic enzymes may not be subject of natural selection. Therefore, only those enzyme loci that show significant correlation between the allele frequency and latitude could be considered of adaptive significance.





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**References:** Arthur, A.L., A.R. Weeks, and C.M. Sgro 2008, *J. Evol. Biol.* 21: 1470–1479; Ayala, F.J., J.R. Powell, M.L. Tracey, C.A. Mourao, and S. Perez-Salas 1972, *Genetics* 70: 113–139; Bock, I.R., and M.R. Wheeler 1972, In: *The Drosophila melanogaster species group*. Univ. Texas Pub. 7213: 1–102; Bubliy, O.A., A.G. Imasheva, and O.E. Lazebnyi 1994, *Genetika* 30: 467–477; Bubliy, O.A., B.A. Kalabushkin, and A.G. Imasheva 1999, *Hereditas* 130: 25–32; Cavener, D.R., and M.T. Clegg 1981, *Genetics* 98: 613–623; Hoffmann, A.A., and A. Weeks 2007, *Genetica* 129: 133–147; Krishnamoorti, K., and A.K. Singh 2013, *Dros. Inf. Serv.* 96: 54–55; Kumar, S., and A.K. Singh 2012, *Dros. Inf. Serv.* 95: 18–20; Kumar, S., and A.K. Singh 2013, *Dros. Inf. Serv.* 96: 52–54; Kumar, S., and A.K. Singh 2014, *Genetika* 46: 227–234; Lakovaara, S., and A. Saura 1971, *Genetics* 69: 377–384; Land, V.T., J. Van Putten, W.F.H. Villarroel, A. Kamping, and W.V. Delden 2000, *Evolution* 54: 201–209; Moraes, E.M., and F.M. Sene 2002, *J. Zool. Syst. Evol. Res.* 40: 123–128; Mulley, J.C., J.W. James, and J.S.F. Barker 1979, *Biochemical Genetics* 17: 105–126; Oakeshott, J.G., J.B. Gibson, P.R. Anderson, W.R. Knibb, D.G. Anderson, and G.K. Chambers 1982, *Evolution* 36: 86–96; Parkash, R., S. Shamina, and Neena 1994, *Gen. Sel. Evol.* 26: 485–494; Prout, T., and J.S.F. Barker 1993, *Genetics* 134: 369–375; Santos, M., A. Ruiz, and A. Fontdevila 1989, *Amer. Nat.* 133: 183–197; Shaw, C.R., and R. Prasad 1970, *Biochem. Genet.* 4: 297–320; Singh, A.K., S. Kumar, and Bhumika 2013, *J. Sci. Res.* 57: 104–108; Singh, B.N., 2010, *Ind. J. Exp. Bio.* 48: 333–345; Umina, P.A., A.R. Weeks, M.R. Kearney, S.W. McKechnie, and A.A. Hoffmann 2005, *Science* 308: 691–693.



### Cannibalism and “partial carnivorism” in *Drosophila* sp. larvae.

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The seminal observation of cannibalism in *Drosophila* sp. larvae in our laboratory is purely accidental rather than being the resultant of meticulous execution of a well-designed research plan. Initially, as post graduate students, we were in the process of conducting an experiment to separate the two mutants - one, X-linked (white), and the other, an autosomal (ebony) from a double mutant strain, (*i.e.*, white ebony). During