SUMMARY

Gonadal dysgenesis, high mutability, moderate segregation distortion and spontaneous male crossing over was found in eight out of eleven populations of Indian *D. ananassae* studied in this series of experiments. Our finding that only the males of Agt, Hyd, Gar and Tik population interact with females of specific populations and not in their reciprocal crosses, the males of these populations can be compared with the P-strain of melanogaster and ca or the mutator strains of *D. ananassae*, though in this series of experiments some features of dysgenesis, viz. ovarian dysgenesis manifest in the F\(^1\), the other features viz. high mutability was observed in F\(^2\). Therefore Indian ananassae population exhibits features which are a combination of the dysgenic traits of melanogaster and ananassae. With similar analogy the Pat, Agp, Beh, Sal and a\(^k\) strains in our investigations can be compared the M strain of melanogaster and px, i.e., the absence of suppressor strain of ananassae. It was of interest to note that interacting P or mutater like strains viz. Agt and Hyd males that gave high percentage of gonadal dysgenesis when crossed to M or absence of suppressor strain females viz. Pat and Beh were all geographically far apart and within them Hyd niche represents a dry and hot ecological region. In comparison the Gar, Beh, Tik, Sal and Agp were all in the suburbs of greater Calcutta separated by not more than 30 kms and all with an apparent climatic homology, at least at the macro level with a moderate monsoon of green vegetation. Populations that are geographically close possess ample chance of a good amount of gene flow within them, at least at the periphery of the niche exploited by each population. Such a comparatively more heterogenous state of the wild population of *D. ananassae* in this subcontinent may be described as 'unstable' in comparison to the comparatively much 'stable' population of *D. melanogaster*. Our results on the ovarian dysgenesis that varied from 13.3% to 30%, may be explained on the basis of the response of the dysgenic factors and their 'modifiers' of the interacting genomes in response to each other. This is particularly pertinent for the Beh females which reacted with Hyd males most in the production of ovarian
dysgenesis (30%) and also for the pat females that had a reproducible
differential response to the males of the two strains viz. Agt and Hyd
in the series. A specific mutation cu that arose from Agt o (P or I or
mutator) with Agp or Beh o, though the males of the same populations
interacted with the females of Pat population to result only in ovarian
dysgenesis. This means that the Agt males have the combined potentia-
ality of inducing both mutations as well as ovarian dysgenesis though
only in response to a particular cytotype and/or the modifiers present
therein, which Hyd males are lacking or that the Hyd strain mutator,
that induces ovarian dysgenesis also acts as a suppressor of mutability.

An apparent correlation between ovarian dysgenesis and hyper-
mutability is lacking in this investigation. In the interacting
populations viz. a^6 q x Gar d, Beh q x Agt d and Agp q x Agt d,
where higher mutation rate was correlated with high frequencies of
male crossing over. Nonparticipation of Boy flies in the induction of
mutation, despite its higher male crossing over frequencies, is an
exception. This represents a third situation in these Indian ananassae
strains from Bombay, where it seems that only a dominant enhancer of
male crossing over works.

As transmission distortion ratio is another suggested aspect of
hybrid dysgenesis, we looked into this aspect in all the eleven
populations in the interval f-Bx for x chromosome and b-se in the
second chromosome. Our finding of a moderate distortion (k value
ranging from .71 to .83) in the b-se interval for both R and NR
classes involving both the sexes, was found to have some correlation
with enhanced male crossing over and hypermutability as is seen for
a^6, Agp and Agt populations with Boy again as an exception. Eleven
population that were randomly chosen, though displayed some relation-
ship between enhanced male crossing over and segregation distortion,
the latter represents a very minor component in the phenomenon of
hybrid dysgenesis in this species.

Analysis of our results on the distribution of isozyme do indicate
some sort of coincidence between ovarian dysgenesis and distribution of
isozyme specific electromorphs. This was most pronounced with respect
to Est III and Est IV isozymes. While Agt and Hyd individuals were
characterized by the presence of faster homozygotes (FF) and total absence of the heterozygotes (SF) in the Est III zone, the Pat and Beh flies, showed in contrast, just the reverse. Added to this was the presence of the band Est IV by all the individuals of the Hyd populations and 25% Agt individuals, while Pat and Beh populations had none of them. The Agt individuals made themselves separated further by the presence of SS homozygotes of Est III in 75% of them. Similarly the Hyd population was very much individualised by the presence of the LDH-I and LDH III isozymes, the combined presence of which was not observed in any other population. Individuals of the Agt strain, also did not tolerate heterozygosity of any of the isozymes, except ADH.

We thus observe quite a good amount genetic variation of the electromorph of different isozymes even within this small sample of eleven populations of D. ananassae. This rich heterogeneity is an obvious indication for ananassae to be a "broad-niche" species, where genetic polymorphism and heterozygosity is correlated with heterogeneity of the ecological niche it exploits. Though this heterogeneity may vary due to selection for different alleles in different times of the year or different population densities, but since gene flow is opportunistic, such variation should be considered a part of the general adaptive strategy for all the panmictic populations, which will never be knowing its polymorphic status at the time of inter-population breeding. This disharmony at the level of the genotypic frequencies of the isozymes has every chance to be reflected through the development of F<sub>1</sub> hybrids. Our results on the F<sub>1</sub> hybrid progeny of Agt ♂ x Pat ♀/Beh ♀ exemplify this.