

## Inversion polymorphism and extra bristles in Indian natural populations of *Drosophila ananassae*: joint variation

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Five Indian natural populations of *Drosophila ananassae* were analysed for chromosome inversions and the presence of individuals with extra scutellar bristles in the  $F_1$  progeny of isofemale lines initiated from naturally impregnated females. Three commonly occurring inversions were found in these populations with varying frequencies as was the number of individuals with extra bristles (e.b.). Female individuals were more often found to carry extra scutellar bristles than were males. This result reveals that polygenic loci responsible for the determination of e.b. are widespread in Indian natural populations of *D. ananassae*. A significant positive correlation between the inversion frequency and the number of individuals with e.b. was detected in the isofemale lines of all the five populations. The 2L inversion, alpha, was found to be closely associated with individuals with the e.b. phenotype. The observed results are compared with earlier results obtained for *D. melanogaster*. The association of the alpha inversion with the e.b. phenotype is discussed in relation to chromosomal evolution in the *melanogaster* species group.

**Keywords:** *Drosophila ananassae*, extra scutellar bristles, inversion polymorphism, sex difference.

### Introduction

Inversion polymorphism is clearly a part of the adaptive machinery in natural populations of *Drosophila*. Several species of *Drosophila* have been screened worldwide for this phenomenon and different situations have been found to exist. In India, two cosmopolitan species of *Drosophila*, *D. melanogaster* and *D. ananassae*, have been widely investigated for chromosome inversion polymorphism (Das, 1994 for a review). Although a considerable amount of genotypic variation is generally detected in natural populations, few differences in phenotypic characters are usually observed. It has been suggested that the genetic basis of phenotypic changes is fundamental for understanding the mechanism of evolution in natural and experimental populations (Lande, 1983) and the study of quantitative characters in wild populations could prove to be interesting for evolutionary studies (David *et al.*, 1977).

In *D. melanogaster*, it has been found that the scutellar phenotype is strongly canalized at four macrochaetae (bristles) and that the canalization is regulated by the scute locus (Rendel *et al.*, 1965). Also, it has been determined that the normal number of four scutellar bristles in *D. melanogaster* is often so tightly controlled developmentally that a change in visible phenotype occurs only after a considerable amount of gene substitution (Rendel *et al.*, 1965; Das & Singh, 1992). It also has been estimated that to alter the chaeta number from four to three or five takes about eight times as many genetic changes as to alter the number from three to one (Lee & Parsons, 1968). In natural populations of this species genetic variation for extra scutellar bristle phenotypes has been reported in India (Singh & Das, 1991), Spain (García-Vazquez *et al.*, 1989) and Austria (Izquierdo *et al.*, 1991). In all these studies, chromosome inversions, especially In(3R)C, are found to be positively correlated with the extra bristle phenotypes.

*Drosophila ananassae* is a cosmopolitan and domestic species which occurs throughout the tropical regions of the world and is found in abundance in the Indian subcontinent. Studies on the population genetics of

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# Drosophila Inversion Polymorphism

**Mariangela Bonizzoni, Lino Ometto**



## **Drosophila Inversion Polymorphism:**

**Drosophila Inversion Polymorphism** Costas B. Krimbas, Jeffrey R. Powell, 1992-08-21 Inversion polymorphism in *Drosophila* has long served as a research subject for a variety of evolutionary studies and continues to be extremely important in understanding evolutionary principles today. Until now no single volume has ever been assembled as a summary of this work. *Drosophila Inversion Polymorphism* provides background information, explores new and rigorous approaches to reconstructing phylogenetic relationships from inversion variation, and discusses inversion polymorphism in the six most studied species groups. Some chapters examine general principles and conclusions, some present detailed data sets, many of which have never before been published, and others offer detailed chromosome maps for identification. The book is a one-of-a-kind source of summary discussions and data ripe for analysis. Geneticists, evolutionary biologists, biologists, and all investigators researching inversion polymorphisms should consider *Drosophila Inversion Polymorphism* a must-have volume.

The Maintenance of Inversion Polymorphism in *Drosophila Melanogaster* Colin A.M. Semple, 1994     *The Maintenance of Inversion Polymorphism in *Drosophila Melanogaster** Colin A. M. Semple, 1994     Chromosomal Inversion Polymorphism in *Drosophila* Kin San Tam, 1984     Inversion Polymorphism in *Drosophila* from South East Asia Adrienne Kristina Pope, 1985     Evolutionary Genetics R. S. Singh, Costas B. Krimbas, 2000-03-28 This book brings out the central role of evolutionary genetics in all aspects of its connection to evolutionary biology     *Insect Genomics* Mariangela Bonizzoni, Lino Ometto, 2025-08-19 This collection explores advances in genome sequencing and analysis tools for the understanding of insect genomes and hence their biology. Beginning with obtaining a high quality genome assembly using the latest sequencing data, the book continues with the identification of genome variability including single nucleotide polymorphisms and genomic inversions, and the annotation of insect genomes through genes, transposable elements, and piRNA clusters. Notably, chapters also delve into downstream analyses such as the evolution of gene families and phylogenetics, molecular biology protocols pertinent to the study of insects, as well as CRISPR-era genome editing tools to manipulate non-model insects. Written for the highly successful *Methods in Molecular Biology* series, chapters include the kind of detailed implementation advice to ensure success in the laboratory. *Insect Genomics: Methods and Protocols* serves as an ideal source for state-of-the-art methods and comprehensive reviews to help researchers design and implement their own studies.     Environmental Stress, Adaptation and Evolution K. Bijlsma, Volker Loeschcke, 2013-03-08 Most organisms and populations have to cope with hostile environments threatening their existence. Their ability to respond phenotypically and genetically to these challenges, and to evolve adaptive mechanisms, is therefore crucial. The contributions to this book aim at understanding from an evolutionary perspective the impact of stress on biological systems. Scientists applying different approaches spanning from the molecular and the protein level to individuals, populations, and ecosystems explore how organisms adapt to extreme environments, how stress changes genetic structure, and affects life histories, how

organisms cope with thermal stress through acclimation and how environmental and genetic stress induce fluctuating asymmetry shape selection pressure and cause extinction of populations Finally it discusses the role of stress in evolutionary change from stress induced mutations and selection to speciation and evolution at the geological time scale The book contains reviews and novel scientific results on the subject It will be of interest to both researchers and graduate students and may serve as a text for graduate courses

*Chromosomal Inversion Polymorphism in Drosophila from Phuket, Thailand* Rosanne Elena Casu,1987

*Microevolution Rate, Pattern, Process* Andrew P. Hendry,Michael T. Kinnison,2012-12-06

From guppies to Galapagos finches and from adaptive landscapes to haldanes this compilation of contributed works provides reviews perspectives theoretical models statistical developments and empirical demonstrations exploring the tempo and mode of microevolution on contemporary to geological time scales New developments and reviews of classic and novel empirical systems demonstrate the strength and diversity of evolutionary processes producing biodiversity within species Perspectives and theoretical insights expand these empirical observations to explore patterns and mechanisms of microevolution methods for its quantification and implications for the evolution of biodiversity on other scales This diverse assemblage of manuscripts is aimed at professionals graduate students and advanced undergraduates who desire a timely synthesis of current knowledge an illustration of exciting new directions and a springboard for future investigations in the study of microevolution in the wild

**Evolutionary Population Genetics of *Drosophila ananassae*** Pranveer Singh,2015-10-16

This book introduces readers to classical population genetics and the ways in which it can be applied to practical problems including testing for natural selection genetic drift genetic differentiation population structuring gene flow and linkage disequilibrium It provides a comprehensive monograph on the topic addressing the theory applications and evolutionary deductions which are clearly explained using experimental results It also offers separate chapters on origin establishment and spread of chromosomal aberrations in populations along with details of culturing maintaining and using *Drosophila ananassae* genetically unique and the most commonly used species along with *D melanogaster* for genetic research Encompassing topics like genetics evolution *Drosophila* genetics population genetics population structuring natural selection and genetic drift in considerable detail it provides a valuable resource to undergraduate and postgraduate students as well as researchers at all level This book explores some fundamental questions concerning the role of natural selection and genetic drift on the degree of inversion polymorphism India with its wide diversity in geo climatic conditions provides an excellent platform to conduct such studies The book showcases sampling records of inversion frequencies in natural Indian populations of *D ananassae* that cover more than two decades It highlights case studies in which sampling data on inversion frequencies was combined with that from earlier surveys generating a time series that allows the evolutionary dynamics of inversion polymorphism to be explored Such long time series are rare but nonetheless crucial for studying the evolutionary dynamics of inversion polymorphism The population genetic analysis discussed is unprecedented in terms of its temporal two

decades and spatial most regions of India covered scale and investigates the patterns of polymorphic system in *D. ananassae* to see if there is any temporal divergence. It endeavors to present a holistic picture of inversion polymorphism across the country India. Chromosomal aberrations particularly paracentric inversions are used as a tool for discussing population genetic studies helping human geneticists, gynecologists and other medical professionals understand why some aberrations are fatal in humans with affected embryos often not surviving the first trimester of pregnancy while similar aberrations in *Drosophila* flies aid in their adaptation to the environmental heterogeneity across the globe.

*Inversion Polymorphism in Drosophila Paranasuta* Mahani Mansor Clyde, 1988

Chromosome Inversion Polymorphisms in *Drosophila Melanogaster* Wayne Robert Knibb, 1982

*Evolutionary Biology of Transient Unstable Populations* Antonio Fontdevila, 2012-12-06

An overview of speciation theory reveals an increasingly held view that many events leading to the origin of new species occur in transient unstable populations. A transient unstable population should be understood as a fast episodic phase in a population subjected to genetic and environmental factors that tend to disrupt its cohesive balanced genome architecture thus enhancing its probability to produce a new species. Striking the core of Darwinian thought some authors claim that these processes may be non adaptive. Among the environmental factors one may cite biotic e.g. resource availability and abiotic e.g. temperature stress conditions that break up the population stability producing random unpredictable changes in population size, population trait distribution, breeding structure, inter and/or intrapopulation hybridization etc. Genetic factors consist of those events that induce rapid changes in genetic expression and/or that determine reproductive isolation such as substitutions, insertions, deletions, duplications, transpositions, gross chromosomal rearrangements, recombination and in general any mechanism that changes the regulatory pattern of the organism or the balance of its meiotic system. Both kinds of factors are often intertwined in a complex net and may influence each other.

Mutation-Driven Evolution Masatoshi Nei, 2013-05-02

The purpose of this book is to present a new theory of mutation driven evolution which is based on recent advances in genomics and evolutionary developmental biology. This theory asserts that the driving force of evolution is mutation and natural selection is of secondary importance.

*Biotechnology, Gene Mapping in Insect and Animal Systems* Robert D. Warmbrodt, 1991

**Evolution and the Genetics of Populations, Volume 4** Sewall Wright, 1984-06-15

These volumes discuss evolutionary biology through the lens of population genetics.

*Essays in Evolution and Genetics in Honor of Theodosius Dobzhansky* Max K. Hecht, 2012-12-06

It is not often that one has the opportunity to send a public birthday greeting to a friend and colleague of many years and to congratulate him on having reached the age of reason. In fact it happens only once and comes then as a surprise. Surely it was only a few years ago that we sat together at an International Genetics Congress in Ithaca and only yesterday that we became members of the same department. The eighth floor of Schermerhorn Hall had a north end where the flies were and a south end furnished with mice and in between a seminar room and laboratory. There the distances were short and the doors open and the coffee pot busy. But it now appears that yesterday

has fallen thirty years behind and that we have grown up I find it interesting and appropriate that Dobzhansky's lifetime spans the period of maturation of the fields to which this volume is devoted. This is true in a chronological sense for his birth occurred in the same year 1900 in which modern genetics began. The rediscovery of Mendel's principles and the interpretation of the nature of heredity and variation to which this event led were necessary prerequisites to the development of evolutionary biology as presented in this collection of essays. Tempo and Mode in Evolution for the National Academy of Sciences, 1995-02-26. Since George Gaylord Simpson published *Tempo and Mode in Evolution* in 1944, discoveries in paleontology and genetics have abounded. This volume brings together the findings and insights of today's leading experts in the study of evolution, including Ayala, W. Ford Doolittle, and Stephen Jay Gould. The volume examines early cellular evolution, explores changes in the tempo of evolution between the Precambrian and Phanerozoic periods, and reconstructs the Cambrian evolutionary burst. Long neglected despite Darwin's interest in it, species extinction is discussed in detail. Although the absence of data kept Simpson from exploring human evolution in his book, the current volume covers morphological and genetic changes in human populations, contradicting the popular claim that all modern humans descend from a single woman. This book discusses the role of molecular clocks, the results of evolution in 12 populations of *Escherichia coli* propagated for 10,000 generations, a physical map of *Drosophila* chromosomes, and evidence for hitchhiking by mutations. **Coping with Climate Change: A Genomic Perspective on Thermal Adaptation** Margarida Matos, Pedro Simões, Inês Fragata, Ana Sofia Quina, Torsten Nygaard Kristensen, Mauro Santos, 2021-02-22

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