1944). Based on my observations and results, I conclude that temperature plays a crucial role in the development of *Drosophila* and may affect the development of other insects, in general. Future experiments using natural and laboratory populations will be employed to test the adaptability and genetic factors on development time and aging.

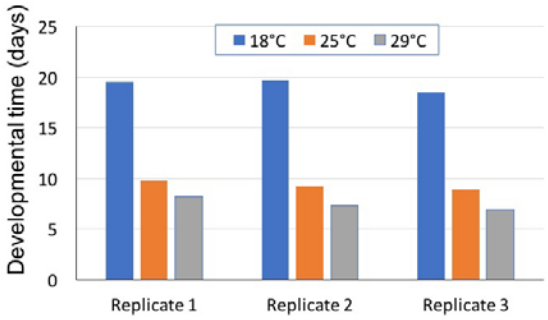

Figure 1.

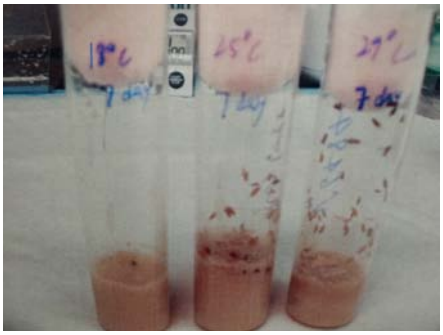

Figure 2.

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Inferring the evolutionary significance of chromosomal inversion polymorphism: insight from *Drosophila* model.

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Abstract

Inversions play a major role in shaping evolutionary processes like speciation and adaptation, by suppressing recombination between advantageous genes spanning inversion breakpoints. Chromosome inversion polymorphism is mostly found to be associated with disease pathogenesis in human beings; however, due to various study limitations, the molecular mechanism behind the appearance of this mutational change is poorly understood. A wealth of information was generated especially on frequency and distribution of chromosomal inversions in species populations using various *in vivo* systems. In addition, their evolutionary significance has been established by gaining knowledge from various cytogenetics and behavioral studies conducted using these model systems. To this respect, *Drosophila* is considered to be one of the popular model organisms as it carries polytene chromosomes in one of its larval stages. Also it shares 75% of genome homology with humans and the basic cellular and biological processes are found to be conserved amongst both of them, thus clearly showing the significance of the study outcome of this model in

understanding human disease biology and evolution. In the present article, we have reviewed and compiled the research outcome of chromosomal inversion polymorphism studies carried out in different *Drosophila* species to determine the significant role played by inversions at organismal level. This article aims to provide an insight in understanding the genotype and phenotype architectural changes occurring through inversion polymorphism and their evolutionary consequences in humans as well as other organisms. Keywords: Mutation**,** Chromosome inversion polymorphism, *Drosophila*, Life history traits, Adaptation, Speciation

Introduction

The genome of an organism is susceptible to changes that may occur due to different biological, physical, or biochemical processes. Mutation can be defined as any random change in the gene sequence of an organism that may or may not affect the normal functioning of the body (Ohta, 1992; Kimura *et al*., 1994; Alberts *et al*., 2000). Mutations can occur due to exposure to some environmental mutagens, which may alter the functioning of any gene, leading to a diseased condition. Inversion is a kind of mutation in which two breaks occur in one chromosome and the region between the breaks rotates 180 degrees before rejoining with the two end fragments. Inversions fall into two classes: pericentric inversions include a centromere, while paracentric inversions do not include a centromere. Pericentric inversions may reduce fertility by producing unbalanced gametes that carry insertions, deletions, and chromosomes with either zero or two centromeres (Kirkpatrick, 2010).

According to the demographic theory proposed by Mettler *et al*. (1977), inversions are categorised into four types: i) common cosmopolitans are those that occur in many populations at a frequency greater than 5%; ii) rare cosmopolitans, too, are those that are present in many populations, but at frequency usually less than 5%; iii) recurrent endemics are those that occur in only a few individuals in the same or adjacent populations; iv) unique endemics are those that are recorded only once. Inversions can either occur as homozygous wherein the sequence is inverted on both chromosomes (Inv/Inv) or there is standard sequence on both chromosomes (ST/ST), or they can be heterozygous (ST/Inv) wherein there is inverted sequence in one chromosome only (Singh and Mohanty, 1990). Heterozygous inversions are easily identifiable as they lead to formation of an inversion loop while pairing, and the same has been thoroughly studied in certain Dipterans using their polytene chromosomes. The recombination in case of heterozygous inversions may result in the formation of non-viable gametes and as a consequence, the probability of recombination decreases. In this situation, the genes located within the inversion loop undergo no or fewer changes, thus escaping them from the effect of environmental change. It has been proved experimentally in *Drosophila* (Singh and Mohanty, 1990) that inversion heterozygosity present in one chromosome enhances the crossing-over rate in other chromosomes, whereas decreases crossing-over not only within the inverted loop, but also in its adjacent region. Moreover, a correlation has been established between the crossing-over frequency and the DNA fragments involved within the inversion breakpoints (Singh and Mohanty, 1991). Unlike deletions and duplications, inversions do not change the overall amount of the genetic material, thus organisms carrying inversions are found to be viable without showing any particular abnormalities at the phenotypic level (Griffiths *et al*., 2000). In some cases, when one of the chromosomes breaks within a functional gene then that inversion breakpoint is considered to be a lethal gene mutation.

Inversions occur as a normal phenomenon in natural populations of different species, and inversion polymorphisms are known to have important phenotypic and evolutionary consequences in humans (Caceres *et al*., 2015). Frequency of inversion polymorphism has been studied in species populations of different geographical origins and is found to be species–specific. In an attempt to study the evolutionary forces leading to primate evolution, Feus *et al*. (2005) compared the inversions present in the genome of chimpanzees and humans and could trace the role of inversion in the process. Nine pericentric inversions are identified to be the potential candidates in the speciation events of hominids and chimpanzees and occurred approximately five-six million years ago (Kehrer *et al*., 2005). Breakpoint analysis of those inversions strongly evidenced that specific high copy repetitive elements play a major role in bringing changes in the genome architecture during hominoid evolution (Kehrer *et al*., 2005; Guillen and Ruiz, 2012).

Several inversions in the human population have been identified playing a role in disease etiology, for instance, a 48 kb inversion was found to be linked to the Emery-Dreifuss muscular dystrophy (Broman *et al*.,

2003), 17q21 to neurodegenerative disorder (Skipper *et al*., 2004; Stefansson *et al*., 2005; Webb *et al*., 2008), and 16p11 to asthma and obesity (Gonzalez *et al*., 2014). Another common paracentric inversion polymorphism 8p was found to have substantial clinical impact (Giglio *et al*., 2001; Broman *et al*., 2003). Equally important, an inversion on chromosome 17 is thought to affect fertility and is noted to be positively selected in European populations (Stefansson *et al*., 2005). Inversions on chromosome four and eight are found to be involved in translocations, and such rearrangements in the chromosome drastically affect the expression of some important genes spanning the inversion breakpoints (Giglio *et al*., 2001; Broman *et al*., 2003). On chromosome 19, a 415 kb human polymorphic inversion (HsInv0379) was studied by Puig *et al*. (2015), which disrupts and inactivates a transcription factor gene. As an outcome, a new transcript of that gene is created and the manifestation of this change has been observed at the phenotypic level. However, the molecular mechanism behind the occurrence of these inversions and their role in disease pathogenesis is poorly understood. Therefore, research efforts are being continuously made on various model and non-model organisms to explore more in this field.

The genus *Drosophila* has been extensively researched in various fields including genetics, evolution, and medical biotechnology, which makes it an ideal model system. It is one of those model organisms whose genome has been completely sequenced in twelve species. The species of this genus, like other Dipterans, harbours polytene chromosomes in their salivary gland of third instar larvae, gut cells, ovary nurse cells, follicle cells surrounding ooctyes, and fat body cells (Zhimulev and Koryakov, 2009). However, most of the cytogenetic studies have been carried out using the salivary gland cells.

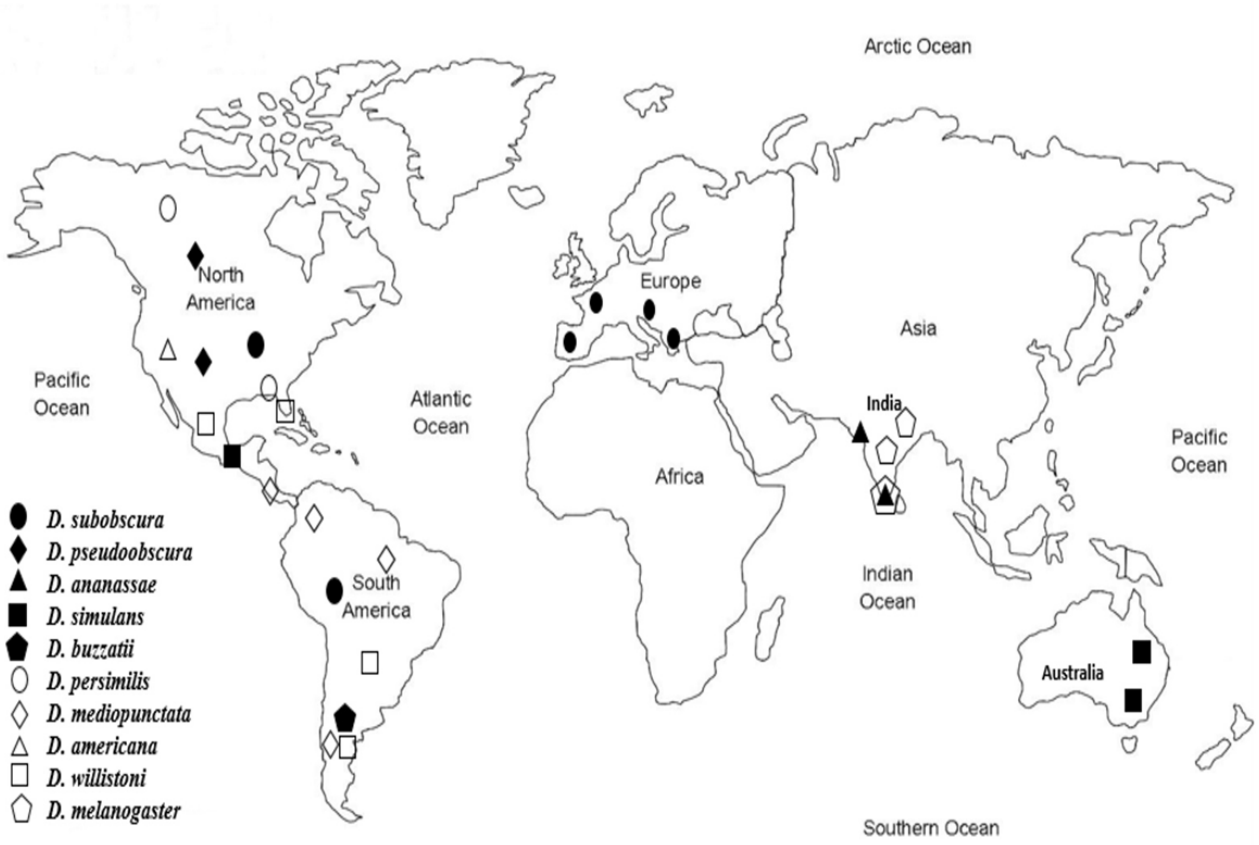

Figure 1. Shows the *Drosophila* species used in inversion polymorphism studies worldwide.

Small number of chromosomes and presence of polytene chromosomes in its salivary gland cells make this model instrumental in cytogenetic studies. A number of experiments involving inversion frequencies, their association and co-existence have been carried out in various *Drosophila* species worldwide such as *D.*

ananassae, D. willistoni, D. robusta, D. pseudoobscura, etc. (Figure 1) in order to understand their consequences and role in different evolutionary processes like adaptation and speciation (Dobzhansky, 1970; Rieseberg *et al*., 1999; Noor *et al*., 2001; Kirkpatrick and Barton, 2005). Chromosomal inversion polymorphism has been extensively studied in one of the cosmopolitan species, *D. ananassae*, and a total number of 70 paracentric inversions were reported. This species shows unusual mutational properties due to presence of pericentric inversions and translocations and carry three of the most common cosmopolitan inversions (subterminal or alpha in 2L, terminal or delta in 3L, basal or eta in 3R) in its worldwide populations (Kaufman, 1936; Singh, 1970). Singh (1989) studied inversion polymorphism in 12 Indian natural populations of *D. ananassae* and concluded that chromosomal polymorphism is adaptively important and populations undergo genetic divergence as a consequence of their adaptation to varying environments. The populations of this species are known to show high population sub structure across the whole distribution range. Inversion frequency is known to vary along with geographical, latitudinal distribution of different population of *Drosophila* species as found by Dobzhansky and co- workers in a species known as *D. willistoni* (Dobzhansky, 1947). Their findings suggest that chromosomal polymorphism is more prevalent amongst populations at the centre of geographical distribution rather than in marginal populations (Hoffmann and Rieseberg, 2012). The same pattern of adaptation of polymorphism was also reported by Carson (1949) in *D. robusta*. They hypothesised the prevalence of homoselection owing to low levels of inversion polymorphism and thus higher adaptability amongst the marginal population, whereas in the central population the level of inversion polymorphism is high and heteroselection is favored resulting in higher adaptation (Singh, 2001). Similar kinds of studies performed in *D. pseudoobscura* infer that inversion polymorphism is adaptive and balanced due to higher Darwin fitness of inversion heterozygotes. Studies were also done to find the association of inversion polymorphism heterozygosity with the genes located within and also in the vicinity of the inversion. A linkage study was done in Japanese populations of *D. melanogaster* between the *Adh* locus and 2L inversion and both of them were found to be positively correlated (Watanabe and Watanabe, 1977). The sequence specificity at the inversion breakpoints was also studied by some workers after advanced molecular biology techniques had been introduced (Kehrer *et al*., 2005).

The overall studies on occurrence and maintenance of inversion polymorphism in natural populations of *Drosophila* are found to be associated with an organism's fitness and adaptation to different ecological niches. The present review is a compilation of advantageous role played by different inversion polymorphisms in affecting both phenotype and genotype of an organism.

Effect of Inversion on Life History Traits

It is evidenced that inversion polymorphism affects various life history traits in different organisms including *Drosophila, Anopheles,* and *Neurospora*. The traits affected by inversion polymorphism have been enlisted in Table 1. Inversion polymorphisms in *Drosophila* have been found to be associated with several life-history traits, *e.g*., body size, shape, pigmentation, and bristle number. (Bertran *et al*., 1998; Rodriguez *et al*., 1999; Dahlgaard *et al*., 2001). Body size and bristle number again are found to be linked with several factors like reproductive success and longevity of an organism (Robertson, 1957; Santos *et al*., 1988; Das *et al*., 1994; Norry and Loeschcke, 2002; Iriarte *et al*., 2003). The correlation between body pigmentation and chromosomal inversion was studied by Hatadani *et al*. (2004) in *D. mediopunctata*. This species possesses three dark spots in its abdomen and this color pattern is genetically determined mainly by the second chromosome, which is highly polymorphic for inversions. Body color was also studied in *D. americana* and similar results were observed suggesting that body color is an adaptive trait (Wittkopp *et al*., 2011). Experiments carried out in *D. mediopunctata* and *D. buzzati* populations suggest that inversion polymorphism affects the wing size and body shape (Iriarte *et al*., 2003; Hatadani *et al*., 2004). There are research reports showing inversion polymorphism affecting different developmental traits such as larva and pupa developmental time period (Norry *et al*., 1995; Iriarte and Hasson, 2000; Singh, 2008). A link between the frequency of inversion polymorphism (2L: alpha inversion) and presence of extra scutellar bristles has also been found by Das *et al*. (1994) among five Indian natural population of *D. ananassae* belong to different eco-geographic regions.

Table 1. Literature showing examples of chromosomal inversion polymorphism affecting different traits of *Drosophila* species.

Species	Inversion Reported	Chromosome Arm	Role of inversion	Reference
D. ananassae (India)	4 Cosmopolitan Paracentric inversions	2L, 2R; 3L; 3R	Population genetics; Positive correlation between inversion and extra bristles	Das *et al.* 1994;Singh 1998; Singh & Singh 2008
D. mediopunctata	2 Paracentric inversions	2nd	Role in color polymorphism, Wing size and shape	Hatadani *et al*. 2004
D. melanogaster (India)	23 Paracentric inversion	2L; 2R; 3L; 3R	Inversion frequency varies with latitudes; Epistatic interaction between unlinked inversions	Das & Singh 1991a; Singh & Das 1991b
D. melanogaster (Europe)	Five Cosmopolitan Paracentric inversion	2L; 2R; 3L; 3R; 3R	Change in inversion frequency with respect to seasonal fluctuations suggesting a role in adaptation	Gonzalez & Mensua 1987 ;Refusta & Rubio1990
D. melanogaster (Japan)	27 Paracentric One pericentric	2L; 2R; 3L; 3R; X, 3L	Comparison of changes and similarities between the inversion frequencies: Studying the evolutionary forces	Inoue & Watanabe 1979
D. pallidosa	One Paracentric inversion	2R	Species divergence from *D. ananassae*	Singh *et al.* 2012
D. persimilis	Three inversions	XL; XR; 2nd	Species divergence from *D pseudoobscura*.	McGaugh & Noor 2012
D. subobscura (Europe)	Eight inversions	2 in autosomes, 1 in sex chromosome	Genetic uniformity maintained across wide latitudinal gradient	Simo *et al*. 2012
Drosophila (Other *Drosophila* species)	Both paracentric and pericentric	Both on autosomes and X-chromosome	Body size, Wing shape, Resistance to heat and cold stress, Development time, Reproductive success	Hoffmann & Rieseberg 2008

Role of Inversion Polymorphism In Adaptation

Inversion polymorphism is known to play an important role in thermal adaptation. Several studies on *Drosophila* show a correlation among changes in inversion frequencies to the recent climate changes. Those studies infer that widespread species may adapt in response to the 0.2ºC increase in temperature per decade in the past 30 years (IPCC, 2007). There is also literature evidence showing a strong correlation between change in temperature and *Drosophila* species distribution. A clinal pattern exhibited by the *In (3R)P* inversion has been detected in *D. melanogaster* along the eastern coast of Australia over more than 20 years (Anderson *et al*., 2005; Umina *et al*., 2005). This inversion increases sharply from a low frequency in the temperate south of Australia to be close to fixation in tropical populations. Inversions are also known to harbor many heat shock response genes of Hsp family (Molto *et al*., 1992; Rego *et al*., 2010). Similar studies have been conducted in *D. subobscura,* which harbors a large number of inversion polymorphisms in its five large acrocentric chromosomes (Rezende, 2010). In *D. subobscura*, the chromosome O, which is homologous to the third and second chromosome of *D. melanogaster* and *D. pseudoobscura*, respectively, is the longest and most polymorphic chromosome, carrying about 40 natural chromosomal arrangements and maximum number of overlapping and non-overlapping inversions (Krimbas and Loukas, 1980; Krimbas, 1993). In a study done on

South and North American population of *D. subobscura*, it was observed that behavioral thermoregulation and heat tolerance are "coadapted" (Dolgova *et al*., 2010). The different arrangements on chromosome O determine thermal preference of adults as observed in a laboratory temperature gradient study. The cold climate *Drosophila* flies with standard arrangement on 'O' chromosome (O_{st}) with respect to inversion polymorphism prefer lower temperature than their warm-climate counterparts carrying different inversion polymorphisms (O_{3+4} and O_{3+4+8}) (Dolgova *et al*., 2010). Thus, it is concluded that in *D. subobscura* thermal preference/ heat tolerance and chromosomal inversion polymorphism maintain parallel latitudinal clines throughout worldwide populations.

The reason behind this latitudinal gradient may be due to correlated selection rather than genetic correlation (Dolgova *et al*., 2010; Calabria *et al*., 2012). It has been observed that flies carrying the warm-climate chromosome arrangement (O_{3+4}) have higher basal protein levels of Hsp70 than their cold-climate O_{st} counterparts and also possess more thermal tolerance, but a link between thermal tolerance and levels of Hsp70 could not be established (Molto *et al*., 1992; Calabria *et al*., 2012). Research was also being carried out to estimate the effect of April 2011 heat wave amongst the European population of *D. subobscura* (Rodrıguez *et al*., 2013). The result revealed that thermal stress affects the genetic makeup of the organism as a larger number of inversions were observed on the chromosome O of this species in warm climate in comparison colder climate. It is evidenced from these studies that evolution of chromosome inversion polymorphisms in *D. subobscura* has been found to be fast and reversible, which may be due to eco-climatic variations. In a similar study to explore more about genetic divergence at chromosome O, six candidate genes for thermal adaptation were selected and analysed for their chromosomal arrangements with respect to O_{3+4} chromosomal polymorphism in two populations of *D. subobscura* (Pegueroles *et al*.,2013). The results showed extensive gene flux outside the inverted region which supports the local adaptation hypothesis, while significant genetic differentiation was found within the inverted region. However, high levels of gene flow were detected for all six genes when comparing the same arrangement among populations, and the maintenance of these inversions in the local populations favors the '*local adaptation'* hypothesis over the '*coadapted genome'* hypothesis.

Impact of climatic changes on the genetic composition was also evidenced in a study conducted in *D. pseudoobscura* by Dobzhansky and later on in various other species, *e.g*., *D. persimilis*, *D. funebris*, *D. flavopilosa*, *D. robusta*, *D. melanica*, *D.melanogaster*, and *D. mediopunctata* (Rezende *et al*., 2010). The outcomes of all these studies show the adapting nature of chromosomal inversion polymorphism across species with respect to their geographical distribution (Rezende *et al*., 2010). Balanya *et al*. (2003) provided unambiguous evidence that selection on the chromosomal inversion polymorphism of *D. subobscura* must be strong and in that selection procedure, environmental factors associated with latitude probably play an important role. Warm-climate chromosome rearrangements are increasing in frequency in European populations of *D. subobscura* (Orengo and Prevosti, 1996; Rodriguez *et al*., 1996). The same trend has been reported in populations of South and North America, indicating warm-climate inversions are increasing in frequency at higher latitudes in all continents (Balanya *et al*., 2006). The above results suggest that variations in genetic markers including chromosomal polymorphism can be helpful to determine the impact of climatic change on the genetic makeup of populations at different locations (Rezende *et al*., 2010). The genetic uniformity of chromosomal inversions was studied by Pedro *et al*. (2012) in European population of *D. subobscura* to see the effect of latitudinal gradient on the genetic content of the inversion polymorphism of the species. Their findings were in accordance with the *local adaptation hypothesis* of Dobzhansky as very low genetic differentiation was observed amongst the flies taken from a wide geographical latitude difference suggesting that the population maintained its genetic uniformity across the wide latitude.

With increasing industrialisation the level of pollution is getting increased day by day in nature. Heavy metal pollutants affect natural population of organisms in many ways. They may cause selection pressure which may lead to genetic adaptation (Reznick and Ghalambor, 2001; Loxdale, 2010). Studies regarding the deteriorating effect of pollutants on the natural population of insects go back to the times of Dobzhansky (1971) who studied the effect of DDT a well-known pesticide, on the third chromosome of *D. persimilis* and *D. pseudoobscura.* In *D. melanogaster* of Katasunuma, Japan, stark changes in the frequency of inversions on 2nd chromosome were observed along with an increase in the frequency of lethal second chromosome. Watanabe *et al.* (1975) studied these changes and tried to establish its relation with the increased use of pesticides and the changing environmental conditions. However, any conclusive link between

these proposed reasons could be established. In a study done on *D. subobscura* the link between stress and role of inversion in adapting to the stress condition was established (Kenig *et al*., 2015). In a laboratory maintained population of *D. subobscura*, it was shown that resistance to the harmful effect of lead contamination was higher in populations originating from a more polluted locality. Also amongst the urban population the frequency of inversion polymorphism was higher due to presence of large ecological niche in such environment (Singh, 2008; Kenig *et al*., 2010). The results showed that initial difference in inversion polymorphism between populations remained in laboratory throughout experiment and in case of lead contamination has been increased significantly (Kenig *et al.,* 2015). Populations originating from a polluted environment had a higher level of inversion polymorphism and better ability to adapt and evolve. So both historical events as well as selection procedures are important for bringing evolution as both of them take part in adaptation.

Role of Inversion in Speciation

Speciation can be defined as gradual changes in the genome of an organism over a long period of time that leads to significant changes causing species divergence. Inversions are known to play a major role in speciation. The possible mechanism of inversion in speciation was explained by proposing two models (White, 1978; King, 1993). Firstly, the traditional under-dominance model which says that recombination between rearranged chromosomes generates gametes carrying chromosomal duplications or deficiencies. The gametes produced as a result of such process are in viable and cause sterility in the individual, thus creating a reproductive barrier between populations or species that differ for this rearrangement. However, this model cannot be accepted owing to the fact that heterozygotes are more fit and a rearrangement that causes a large reduction in the fitness of heterozygotes is unlikely to become established in the first place. Now the question arises that despite gene flow species do persist. So to answer the reason behind the existence of species, a second model was proposed which suggests that there is reduced rate of recombination between the inverted and non-inverted region of the chromosome by which the genes present in the inverted region remain conserved (White, 1978; King, 1993, Noor *et al*., 2001; Rieseberg, 2001). Literature proposes that chromosomal inversions partition the genome into regions protected from gene flow by reducing recombination over long stretches, which may lead to speciation (Noor *et al*., 2001; Barrientos *et al*., 2002; Navarro and Barton, 2003; Kirkpatrick and Barton, 2006).

Another mechanism by which inversions may facilitate speciation is the accumulation of alleles that contribute to reproductive isolation between populations connected by gene flow (Hoffmann *et al*., 2008). A comparative cytogenetic study using polytene chromosomes was done by Singh *et al*. (2012) in two sibling species *D. ananassae* and *D. pallidosa*. Both the species though share the same ecological niche but are reproductively isolated due to behavioral isolation. The experiment revealed the presence of inversion loops in hybrid progeny, thus suggesting a change in the order of gene arrangement which might be leading to species differentiation (Singh *et al*., 2012). Similar study was carried out on the sister species *D. pseudoobscura* and *D. persimilis*, which harbor different chromosomal arrangements with respect to inversions present on XL, XR, and 2nd chromosome, and the genes present within the inverted regions may be responsible for reproductive isolation amongst these two species (McGaugh, 2012).

Though there is absence of gene flow, the subdivided population acquires genetic variations by exposing themselves to different geographical regions, which may lead to population differentiation and species divergence. The evolutionary forces leading to speciation have also been studied by several scientists. The outcome of these studies reveal that mutations in the form of chromosomal inversions are found to be the cause of genomic divergence (Rieseberg, 2001; Faria and Navarro, 2010; Gompert *et al*., 2012; Guerrero *et al*., 2012; Feder *et al*., 2014). Similarly, rapid chromosomal evolution with respect to inversion polymorphism has been reported in *D. mojavensis*, where natural selection is found to play a major role in increasing the number of fixed inversions in a new environment (Gullean and Alfredo, 2012). However, it has been observed that favorable genes within the inversions are more favorable together in their natal habitat than they would be present individually (Nosil and Feder, 2011). The divergence pattern and the recombination rate have been studied in a pair of parapatric species *D. pseudoobscura* and *D. persimilis* and their sympatric outgroup species *D. miranda*. The results of this study revealed that within the XL and chromosome two inversions, *D.*

persimilis and *D. pseudoobscura* share a deeper ancestor than they do with *D. miranda* (Stevison, 2011; McGaugh, 2012). Though they have been diverged approximately 0.5–0.85 Ma (Aquadro *et al.*, 1991; Hey and Nielsen, 2004; Stevison, 2011), part of their genome carry a signature of more recent hybridization (Machado *et al*., 2002; Hey and Nielsen, 2004; Machado *et al*., 2007; Kulathinal *et al*., 2009; Stevison, 2011).

Literature also suggests a role of inversion at the beginning of sex chromosome evolution (Ming and Moore, 2007). This has been clearly evidenced by studying genetic variability that during the early evolution of mammalian Y a series of overlapping inversions progressively extended the size of non-recombining portions of Y (Lahn and Page, 1999). The same has been explained under sex-antagonist selection model (Kirkpatrick, 2010). Therefore, inversion helps to isolate the Y chromosome from X chromosome genetically and make Y chromosome as an asexual genetic unit. As a consequence of which Y evolves as a functional male determining chromosome in mammals and flies. Charlesworth *et al*. (2005) also suggested that chromosomal rearrangements such as inversion increase recombination suppression in sex chromosomes thus playing a role in maintaining differentiation amongst sex determining genes located on X and Y chromosomes.

Analysis of inversion breakpoints may provide an insight into the occurrence of the inversion polymorphism. Different chromosomal rearrangements including transposable elements (TE), segmental duplications(SDs), short sequence repeats, or chromosomal breakages involving single and double staggered breaks at the breakpoint region are known to play a significant role in generation of inversions (Guillen and Ruiz, 2012). Several attempts have already been made by scientists to understand this random or non-random association of specific sequences present at the breakpoint region of fixed inversions between different species. For instance, the chromosome two of *D. mojavensis* has been well studied for the breakpoint analysis of seven fixed inversions in this chromosome (Guillen and Ruiz, 2012). Similar study has also been done in *D. buzzati* and the probable reason for occurrence of these inversions has been highlighted in both the studies (Calvete *et al.*, 2012). However, the results of these studies do not provide a concurrent proof of the link between the existence of molecular markers (TE, SDs, *etc*.) at the breakpoint region and the corresponding inversion. The question as to whether the presence of these specific repetitive sequences at the inversion breakpoint has been exploited by the organisms to adapt to the changing environment by creating inversions remains unanswered and requires deeper research.

Conclusion

The overall study outcome as carried out in different parts of the world, suggest a major role of inversion polymorphism in life history trait variations, adaptation, and speciation. The species-specific nature of inversions makes them instrumental also in species identification. Although a lot of research on inversion polymorphism has been performed in world-wide populations of *Drosophila* and other arthropods, further exploration is needed to understand the basis of their occurrence, selective existence, and their role in bringing changes in gene-genome organisation of different eco-geographic species populations. With the technological advancement, genetic mapping has become less time consuming, inaccurate and provides us detailed information about mutation or changes leading to disruption or inactivation of specific genes towards a better understanding of directional selection, selective gene adaptation during speciation. The examination of inversion breakpoints has unfolded a higher level of understanding so as to gain in-depth knowledge for the reason for occurrence of repetitive sequences at the region flanking the inversions. Therefore, the cytological and the molecular studies of chromosomal mutations including inversions may altogether help in bridging the gaps between phenotype effects and genotype changes that occur in the organisms.

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Checklist of Drosophilid species so far described and recorded from the Darjeeling hill areas, West Bengal, India.

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Systematic position:

PHYLUM: ARTHROPODA
CLASS: INSECTA
SUBCLASS: PTERYGOTA
DIVISION: ENDOPTERYGOTA
ORDER: DIPTERA
SUBORDER: BRACHYCERA
SUPER FAMILY: EPHYDROIDEA
FAMILY: DROSOPHILIDAE

Subfamily Steganinae

I . Genus *Leucophenga* Mik

1. *Leucophenga rimbikiana* Singh & Gupta, 1981

II. Genus *Stegana* Meigen

2. *Stegana shirozui* Okada, 1971

Subfamily Drosophilinae

III. Genus *Dettopsomyia* Lamb

3. *Dettopsomyia argentifrons* Okada, 1956
4. *Dettopsomyia nigrovittata* Malloch, 1924

IV. Genus *Drosophila*

i. Subgenus *Dorsilopha* Sturtevant

5. *Drosophila busckii* Coquillett, 1901

ii. Subgenus Sophophora