

The *Drosophila bipectinata* species complex: phylogenetic relationships among different members

The *Drosophila bipectinata* species complex is an interesting model for population genetic, behavioural and evolutionary studies. It is more valuable for evolutionary studies, with particular interest to the mechanism of speciation. This complex belongs to the *ananassae* subgroup of the *melanogaster* species of genus *Drosophila*. There are four species in this complex which are closely related and partly sympatric having wide geographical distribution: *D. bipectinata*, *D. parabipectinata*, *D. malerkotliana* and *D. pseudoananassae*. Except *D. parabipectinata*, rest three species have subspecies^{1,2}. They remain reproductively isolated by means of pre-mating and post-mating reproductive isolating mechanisms. However, in the laboratory, all the four species hybridize and produce fertile females and sterile males³. Further, sterility and dystrophied ovaries have been observed in hybrid females of certain crosses⁴. Only one case of natural hybridization between *D. bipectinata* and *D. malerkotliana* has been reported by Gupta⁵.

This complex has been extensively utilized by a large number of researchers for various kinds of studies. These include chromosomal polymorphism, intra- and interspecific chromosomal variations, protein polymorphism, sexual isolation, pattern of mating preference and direction of evolution, sexual behaviour, female remating and sperm displacement, morphology of sex combs, hybridization, degree of crossability, character displacement, nucleotide diversity, fluctuating asymmetry (FA), hybrid sterility and chromosome interactions, genetic basis of hybrid sterility and non-sexual behaviour^{3,6–30}. Results of a number of studies have been used to discuss the phylogenetic relationships among these four species. Fluctuating asymmetry demonstrating developmental instability remains more or less similar in the four species which shows that evolutionary divergence has not affected developmental precision in these four species²³. Further, no significant differences were noted in the FA level in the hybrids when compared with parental species²⁴. The results of studies on remating behaviour in these species indi-

cated that *D. pseudoananassae* and *D. bipectinata* lie at opposite extremes, whereas the other two species are in intermediate position²⁶. Phylogenetic relationships have been discussed mainly on the basis of degree of crossability, pattern of sexual isolation, intra- and interspecific chromosomal variations, and nucleotide diversity among the species. The degree of crossability varied significantly in different crosses^{3,19}. It was maximum between *D. bipectinata* and *D. parabipectinata*, and least between *D. malerkotliana* and *D. pseudoananassae*. The pattern of sexual isolation was also used to discuss the phylogenetic relationship among these species^{10,21}. The pattern of mating showed that *D. bipectinata*, *D. parabipectinata* and *D. malerkotliana* are closely related, but *D. pseudoananassae* is distantly related to these three species. It was also postulated that *D. bipectinata* and *D. malerkotliana* share a common ancestor, whereas *D. bipectinata* has given rise to *D. parabipectinata*²¹. Kopp and Barmina¹⁶ and Kopp *et al.*¹⁷ utilized nucleotide diversity to discuss their phylogenetic relationships. They observed that nucleotide diversity is very low in *D. bipectinata*, *D. parabipectinata* and *D. malerkotliana*, and suggested that in the evolutionary timescale they have diverged not very long ago. Mishra and Singh^{18–20} studied the genetic basis of hybrid sterility in this complex using markers, making backcrosses, and observing the morphology of testis and seminal vesicles. They have suggested that: (i) *D. parabipectinata*, *D. bipectinata* and *D. malerkotliana* show close phylogenetic relationship while *D. pseudoananassae* is distantly related to them, and (ii) the X-Y and X-autosome interactions cause hybrid sterility. Bock⁶ was the first to study the intra- and interspecific inversions in this complex. He found inversion and synapsis of chromosomes in F1 larvae were good when *D. bipectinata*, *D. parabipectinata* and *D. malerkotliana* were used. However, synapsis of chromosomes in F1 larvae was poor when *D. pseudoananassae* was used for making crosses. Based on these observations, Bock⁶ suggested the phylogenetic relationships among these species: '*D. malerkotliana*, *D. pseudoananassae*

and a population ancestral to *D. bipectinata* and *D. parabipectinata* were said to be derived from a common ancestral population'. Tomimura *et al.*¹⁵ also observed high degree of inversion polymorphism in these species and their hybrids. According to them¹⁵: '*D. pseudoananassae* derives directly from *D. malerkotliana*, from which *D. bipectinata* and *D. parabipectinata* have also been derived'. Based on intra- and interspecific chromosomal variations, Banerjee and Singh²⁵ suggested that '*D. pseudoananassae* must have diverged long back in the evolutionary history from the same common ancestor that gave rise to *D. bipectinata* and *D. malerkotliana*, and there is ancestral-derived relationship between *D. bipectinata* and *D. parabipectinata*'.

A large number of studies have been conducted on the *D. bipectinata* complex which is a good model for evolutionary studies. Phylogenetic relationships among these species have been postulated based on the results of these studies. There is variation in the phylogeny proposed by different researchers. Bock⁶ suggested that *D. bipectinata* and *D. parabipectinata* are derived from a common ancestral population. On the other hand, according to Banerjee and Singh^{21,25}, *D. bipectinata* has given rise to *D. parabipectinata* based on chromosomal and sexual isolation studies. More extensive studies are required using four species and seven sub-species of the *D. bipectinata* complex in future by employing the techniques of molecular biology which may elucidate the mechanisms of speciation. Further, work done on nucleotide divergence is not sufficient and more emphasis should be given to such studies. In some studies, either *D. bipectinata* or *D. malerkotliana* is used as model species. However, other species should also be involved in such types of studies in future.

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Biofuel-powered electronic skin: future of healthcare

Electronic skin (e-skin) is a technological advancement over the human skin that can provide sensory facilities against temperature, and pressure measured along with extra mechanical durability and stretchability¹. Augmentation on e-skin can be done by incorporating near- or medium-range wireless communication with the help of integrated microcontroller assembly. Such e-skins are useful in smart healthcare applications².

A person wearing an e-skin assembly can transmit vital information about

his/her health to a remote system for immediate medical intervention. Bluetooth and Wi-Fi modules could be equipped with the e-skins to facilitate ultra-flexible smart healthcare services in the near future³. Existing e-skins are usually powered by near-field communication tags or in-built miniature batteries that may sometimes hinder continuous data transmission⁴. Upon discharge of the battery, e-skins tend to stop regular activities⁵.

A recent study has demonstrated the efficiency and applicability of biofuel-

powered e-skin development for better healthcare⁶. The e-skin is completely self-powered by human fluids (human sweat). Thus, a fully perspiration-powered integrated e-skin (PPES) has been devised to harness energy from lactate biofuel cell to act as a biomarker of essential human excretions like urea, NH₄⁺, glucose and pH.

PPES uses a pair of bioanodes and biocathodes to sense human vitals. It can work in continuous 20 mM lactate medium over human skin and regularly send vital information from an array of

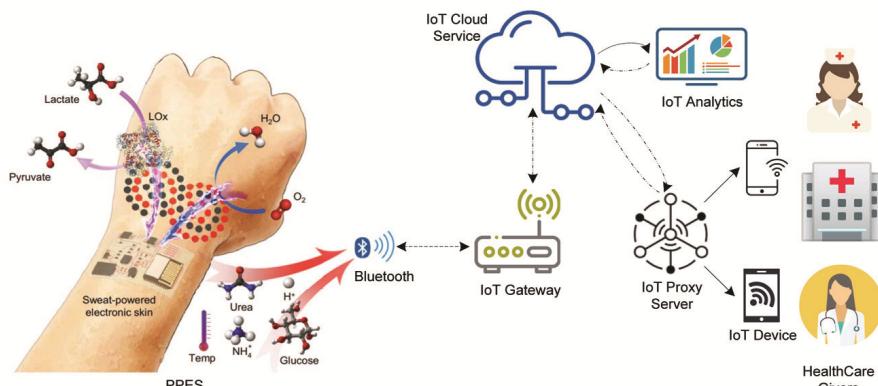


Figure 1. Perspiration-powered integrated e-skin (PPES) enabled with internet of things infrastructure from smart healthcare (PPES image courtesy Yu et al.⁶, modified by authors).