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Genetic differentiation in the phlebotomidae species of Indian sand fly (Diptera)

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Abstract: The Old World sandflies consist of three genera;*Phlebotomus, Sergentomyia,* and *Chinius*, whichare found in the Palaearctic, Afrotropical, Malagasy, Oriental, and Australian regions.Genus *Phlebotomus*(Rondani and Berté, 1840) includes 13 subgenera: *Adlerius*(Nitzulescu, 1931), *Anaphlebotomus*(Theodor, 1948),*Australophlebotomus*(Theodor, 1948), *Euphlebotomus*(Theodor, 1948), *Idiophlebotomus*(*Quate* & *Fairchild*, 1961), *Kasaulius*(Lewis, 1982), *Larroussius*(Theodor, 1948), *Madaphlebotomus*(Depaquit and Leger, 2015), *Paraphlebotomus*(Theodor, 1948), *Phlebotomus*(Rondani and Berté, 1840), *Spelaeophlebotomus* (Theodor, 1948), *Synphlebotomus*(Theodor, 1948), and *Transphlebotomus* (Artemiev, 1984). This genus includes many human blood feeders and some endophilic species.This paper includes information on Genetic differentiation on Indian elements.

Key words : Genetic differentiation sandfly

Introduction: The incidence of Visceral Leishmaniasis and Cutaneous Leishmaniasis is in agreement with the population dynamics of *P. argentipes*, *P. papatasi*, *P. salehi*and *P. sergenti. P. argentipes* is a vector for Anthropogenetic Visceral Leishamniasis and *P. papatasi*&*P. salehi*serve as the vectors of Zoonotic Cutaneous Leishmaniasis while *P. sergenti* is established as a vector for Anthropogentic Cutaneous Leishmaniasis. We have seen during the last few years that the incidence of VL cases have been decreased in India due to several reasons yet the establishment of new foci of VL has been a major concern in recent years. Therefore, it is essential to work out on the Genetic differentiation of this vector fly.

GENETIC DIFFERENTIATION:

The divergence was calculated in between the different populations. The average number of nucleotide differences, average number of nucleotide substitution per site and number of net nucleotide substitution per site between population A_1 and $A_2$was calculated as 35.833, 0.05836 and 0.05071 respectively. For population A_1 and $A_{3,}$ the average number of nucleotide differences, average number of nucleotide substitution per site and number of net nucleotide substitution per site was calculated as 85.500, 0.13925 and 0.12182 respectively. For population A_1 and $A_{4,}$ the average number of nucleotide differences, average number of nucleotide substitution per site and number of net nucleotide substitution per site was calculated as 94.389, 0.15373 and 0.13332 respectively. For population A_1 and $B_{1,}$ the average number of nucleotide differences, average number of nucleotide substitution per site and number of net nucleotide substitution per site was calculated as 108.167, 0.17617 and 0.16417 respectively. For population A_1 and $B_{2,}$ the average number of nucleotide differences, average number of nucleotide substitution per site and number of net nucleotide substitution per site was calculated as 100.083, 0.16300 and 0.15128 respectively. For population A_1 and $B_{3,}$ the average number of nucleotide differences, average number of nucleotide substitution per site and number of net nucleotide substitution per site was calculated as 105.867, 0.17242 and 0.12438 respectively.

For population A_2 and $A_{3,}$ the average number of nucleotide differences, average number of nucleotide substitution per site and number of net nucleotide substitution per site was calculated as 73.500, 0.11971 and 0.10993 respectively. For population A_2 and $A_{4,}$ the average number of nucleotide differences, average number of nucleotide substitution per site and number of net nucleotide substitution per site was calculated as 87.333, 0.14224 and 0.12948 respectively. For population A_2 and $B_{1,}$ the average number of nucleotide differences, average number of nucleotide substitution per site and number of net nucleotide substitution per site was calculated as 100.333, 0.16341 and 0.15907 respectively. For population A_2 and $B_{2,}$ the average number of nucleotide differences, average number of nucleotide substitution per site and number of net nucleotide substitution per site was calculated as 95.500, 0.15554 and 0.15147 respectively. For population A_2 and $B_{3,}$ the average number of nucleotide differences, average number of nucleotide substitution per site and number of net nucleotide substitution per site was calculated as 100.400, 0.16352 and 0.12313 respectively.

For population A_3 and $A_{4,}$ the average number of nucleotide differences, average number of nucleotide substitution per site and number of net nucleotide substitution per site was calculated as 86.667, 0.14115 and 0.11862 respectively. For population A_3 and $B_{1,}$ the average number of nucleotide differences, average number of nucleotide substitution per site and number of net nucleotide substitution per site was calculated as 101.833, 0.16585 and 0.15174 respectively. For population A_3 and $B_{2,}$ the average number of nucleotide differences, average number of nucleotide substitution per site and number of net nucleotide substitution per site was calculated as 95.250, 0.15513 and 0.14129 respectively. For population A_3 and $B_{3,}$ the average number of nucleotide differences, average number of nucleotide substitution per site and number of net nucleotide substitution per site was calculated as 92.400, 0.15049 and 0.10033 respectively. For population

A_4 and $B_{1,}$ the average number of nucleotide differences, average number of nucleotide substitution per site and number of net nucleotide substitution per site was calculated as 110.000, 0.17915 and 0.16205 respectively. For population A_4 and $B_{2,}$ the average number of nucleotide differences, average number of nucleotide substitution per site and number of net nucleotide substitution per site was calculated as 103.167, 0.16802 and 0.15119 respectively. For population A_4 and $B_{3,}$ the average number of nucleotide differences, average number of nucleotide substitution per site and number of net nucleotide substitution per site was calculated as 93.933, 0.15299 and 0.09984 respectively.

For population B_1 and $B_{2,}$ the average number of nucleotide differences, average number of nucleotide substitution per site and number of net nucleotide substitution per site was calculated as 16.500, 0.02687 and 0.01846 respectively. For population B_1 and $B_{3,}$ the average number of nucleotide differences, average number of nucleotide substitution per site and number of net nucleotide substitution per site was calculated as 91.667, 0.14929 and 0.10456 respectively. For population B_2 and $B_{3,}$ the average number of nucleotide differences, average number of nucleotide substitution per site and number of net nucleotide substitution per site was calculated as 84.900, 0.13827 and 0.09381 respectively.

The number of fixed differences in between population A_1& A_2, A_1& A_3, A_1& A_4, A_1& B_1, A_1& B_2, A_1& B_3, A_2& A_3, A_2& A_4, A_2& B_1, A_2& B_2, A_2& B_3, A_3& A_4, A_3& B_1, A_3& B_2, A_3& B_3, A_4& B_1, A_4& B_2, A_4& B_3, B_1& B_2, B_1& B_3, B_2& B_3 was calculated as 27, 73, 81, 96, 89, 51, 69, 79, 97, 93, 56, 75, 94, 89, 43, 98, 93, 44, 11, 46, 42 respectively.

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