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Geneticdiversityandpopulationdynamicsofdenguevectors*Aedesaegypti*and*Aedesalbopictus* inselectedlocalitiesinSriLanka

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*Aedesaegypti*and*Aedesalbopictus*arethetwomainvectorsofthe denguevirus. Knowledgeofvectorgeneticdiversitywouldbeusefulinvectorcontrol,asitreflectsthe evolutionarypotentialofvectors. Similarly, vectorpopulationdynamicswouldbeusefulinestimatingeffectivenessinvectorcontrolstrategies. Therefore, thisstudywasundertakentoestimatethegeneticdiversityandpopulationdynamicsamongselectedpopulationsof*Aedesaegypti*and*Aedesalbopictus*inSriLanka, usingExonPrimedIntronCrossing(EPIC) markers. Larvalsamplesofeachspecieswerecollectedfromtwodengueendemicareas,Colombo (N=32) andGalle (N=30) for*Ae*. *aegypti*andGampaha (N=20) andKalutara (N=30) for*Ae. albopictus.* DNAwasextractedandPCRamplifiedforRpS20bandRpL30amarkersfollowedby 6% PAGE. PCRampliconsweresequencedandanalyzedwithClustalWinMega 7.0.14. DnaSP 5.10 wasusedtoinferthenucleotidediversity (Piandθ), InDeldiversity (pi(i)), haplotypediversity (Hd), averagenumberofnucleotidedifferences (k) andFuandLi'sD* andF* statistics. Anaverageof 480 and 464 bpDNAfragmentswereanalyzedforthetwomarkersfor*Ae. aegypti*and*Ae. albopictus,* respectively. ThevaluesobtainedforPi, Pi(i) andkwereslightlyhigherfor*Ae. albopictus*comparedto*Ae. aegypti,*butwerenotsignificantly(P>0.05) different (Pi_{alb}:Pi_{aeg}=0.0333:0.0165; θ_{alb}:θ_{aeg}=0.0508:0.0149; $Pi(i)_{albo}$:$Pi(i)_{aeg}$=1.2733:1.049; k_{alb}:k_{aeg}=8.801:3.544). However, asignificantlyhigherHdwasobservedfor*Ae. albopictus* (0.913) incomparisonto*Ae. aegypti* (0.675). TheobtainedPivaluesforthetwospecieswerecomparablewithpreviousstudiesconductedinotherregions oftheworld,*i.e*.,*Ae. albopictus*fromIndonesia (0.03878), *Ae. aegypti*fromAustralia (0.0202) andBrazil (0.0102). Nevertheless, Pi(i)observedinthepresentstudyfor*Ae. aegypti*issignificantlyhighercomparedtothereportsfromAustralianpopulations (0.0052) (P<0.05). Further, *Ae. albopictus*populationatImbulgodashowedsignificantlynegativeFLD* (-2.558) andFLF* (-2.716) valueswithrespecttothe RpS20bmarker (P<0.05) indicatingpossiblepopulationexpansionevents. Thepopulationstestedindicateahighandcomparablelevelsofgeneticdiversityamong*Ae. aegypti*and*Ae. albopictus*foundinSriLankareflectingtheirsubstantialevolutionarypotential. Thesuggestedpopulationexpansionin*Ae. albopictus*isfurtherevidentwiththehighhaplotypediversity,andmayrequirecautionwithrespecttocontrollingdenguetransmission.

Keywords: EPIC markers, FuandLi'sD* andF*, nucleotide diversity, population expansion, vector genetics

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