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Systematic identification and characterization of Tyrosine kinase linked receptor gene family from *Anopheles gambiae* genome

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Anopheles gambiae is the major vector of human malaria. In numerous African countries, millions of people die of the malaria parasite, *Plasmodium spp.*, transmitted by this mosquito. Enzyme linked receptors such as, tyrosine kinase, relay the signals from cell surface to the nucleus by a protein cascade mechanism mediated through phosphorylation. In the current study, Receptor Tyrosine Kinase (RTKs) of *A. gambiae* is identified and characterized by high throughput mining of *A. gambiae* genome with bioinformatic tools, to study the organization of RTKs, the patterns of RTK duplication and divergence, and evolutionary trend of RTK within the genome of *A. gambiae*. In achieving this objective, 233 tyrosine kinase associated sequences were retrieved from the *A. gambiae* genome database using well characterized RTK domain obtained from the NCBI conserved domains database and BLASTp tool. Following analyses of these sequences, using the NCBI Conserved Domain Search tool, TMHMM sever 2.0 and Singal IP, TargetP, Psort servers, revealed 26 sequences to have tyrosine kinase domains, transmembrane α-helical domains and membrane localization signals strongly suggesting them to be RTKs. There were four gene products with double pass transmembrane α- helical domains, in contrast to the single pass transmembrane α-helical domain that is usually found in RTKs. Analysis of the multiply aligned RTK domains of the latter sequences revealed insertions and deletions with little sequence conservation. Topology of the cladogram generated using 26 tyrosine kinase domain sequences revealed well defined seven subfamilies, with certain subfamilies evolving faster than the others diversifying into specialized functions. Analysis of other associated domains of RTKs in certain subfamilies indicated sharing of the same types of domains suggesting duplication may have occurred after translocation of the tyrosine kinase domain to RTKs. In conclusion, the sequence diversification and gene duplication are implicated as the determinants of the diversity observed among the paralogous of tyrosine kinase domains in the RTKs within the genome of *A. gambiae*.