

Abstract:

We studied biodiversity of avian trypanosomes. We used newly obtained isolates of trypanosomatids from ornitophilic bloodsucking diptera (81) and from avian hosts (145). To investigate relationships among isolates we employed RAPD method and sequence analyses of SSU rRNA, eventually gGAPDH, 5S RNA or SL RNA. Additionally we used morphological characters; cell lengths and kinetoplast widths.

All isolates obtained from biting midges belonged to monogenetic kinetoplastids. We described new species and a new genus *Sergeia podlipaevi* isolated from *Culicoides (Oecacta) festivipennis* a *C. (O.) truncorum*. We successfully infected with this species laboratory bred biting midge of different subgenus *Culicoides (Monoculicoides) nubeculosus*.

We described isolate from *Culicoides truncorum* as new species *Herpetomonas trimorpha*. Its sister species was *H. ztiplika* described previously also from biting midges.

We performed the most extensive study of biodiversity of avian trypanosomes based on comparison of wide spectrum of isolates obtained from different hosts. We confirmed that avian trypanosomes are polyphyletic and form three independent lineages within the genus *Trypanosoma*. We identified at least 11 species of avian trypanosomes. We found that ornitophilic mosquitoes belong among important vectors of avian trypanosomes as well as black flies and hippoboscids. Mosquitoes transmit at least 3 trypanosome species to raptors and songbirds.

One of newly found species of avian trypanosomes was described as *T. culicavium*. This species is transmitted by ingestion of infected mosquito by insectivorous songbird. The life-cycle and host-vector combination was further confirmed by experimental infections of laboratory bred mosquitoes (*Culex quiquiefasciatus*) and canary birds (*Serinus canaria*) by different isolates of *T. culicavium* obtained from birds and vectors.