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Abstract. Supra-genera Classification within family Tachinidae was unclear in the most studies before Herting's catalogue (1984) that achieved depending on cladistic analysis. However, the taxonomic position of the upper-taxa still fuzzy till recently, once were used the molecular information with biological process analysis for inferring the relationships of the parasitoid family, several placements and relationships of upper taxa were resolved.

Key words: Markers, monophyly, Tachinidae.

Introduction:

In the past the analyses on tachinds proposed monophyly of some clusters (Tschornig, 1985; Wood, 1987); John Henry O'Hara (2013) divided Polideini into 9 tribes in 2 subfamilies. analyses used morphological and molecular analyses to clarify relationships of the major clades of family Tachinidae (Stireman, 2002; Tachi and Shima, 2002, 2008, 2010; Cerretti *et al.*, 2010, 2012, Davis, 2012; Zhao, *et al.*, 2013; 2014; Winkler *et al.*, 2015; Pohjoismäki, *et al.*, 2016; Blaschke *et al.*, 2018), and just one study has used molecular information to research inclusive cladistic relationships of taxa that constituent the family (Stirman *et al.*, 2019). Our review targets are: (1) Survey of some molecular cladistics of Tachinidae which will play an honest role in the future works to know the evolutionary relationships among Tachinidae and might use this information to boost tachinid classification. (2) Show of the position of Tachinidae among its taxonomic groups.

Results and Disscussion:

The family Tachinidae as parasitoids, characterized by developed labrum of the mouthparts in the first larval instars, and bulge subscutellum in adult, confirmed tachinid cluster as monophyletic (Pape, 1992). However, classification position within the family are little varied among many authors who dealt with family (John Henry O'Hara, 2009, 2016).

Herting (1984) studied and commenced some stability with him morphological and molecular analyses recently projected schemes with polyparaphyletic clusters (Blaschke *et al.*, 2018). In the Palaearctic Region Herting classified four subfamilies in 1984. The classification position of the tribes in family Tachinidae are varied over time and it still failed to reach agreement thereon globally (O'Hara, 2013). Despite many tribes with high homogeneity and additional characteristic, continuing, of debatable tribes as monophyletic, embody immensely diverse forms which will overlap in look with alternative groups. There are progresses in understanding of constituents and relationships of some taxa (O'Hara, 2002). Known studies by Herting (1957) and Karl Waldemar Ziegler (1998) on feminine, male genital organs, larvae, puparia and eggs, severally were informative. However, recent molecular analyses has the good ability to resolve complicated debatable and ambiguous taxa within family Tachinidae (Stirman *et al.*, 2019).

Stireman's (2002) discussed Exoristinae relationships in Nearctic region employing molecular information (28S rDNA and EF-1 α) building some tribes. This study supported family Tachinidae and Exoristinae as monophyletic clusters; although, subfamilies Tachininae and Phasiinae were para-phyletic or polyphyletic.

After that, Tachi and Shima (2010) analyzed Palaearctic Exoristinae using 18S, 16S, white, and 28S, so resolved the foremost tribes, wherever enclosed Goniini. However, in these analyses, rest subfamilies (Tachininae, Dexiinae and Phasiinae) poorly pictured. In 2014 Cerretti *et al.* used the morphological information as a primary inclusive study to research the family together with nearly five hundreds species. These cladistc studies established relationships among the foremost clades, supposed monophyly of some groups and bestowed many new relationships composed of:

(1) A non-monophyletic Tachininae with one grade (Myiophasiini + Palpostomatini) as sister to the remaining of family Tachinidae, (2) Dexiinae + Phasiinae as sister to Exoristinae + (most) Tachininae, (3) Phasiinae originating from among Dexiinae taxa and (4) Exoristinae erecting within Tachininae. Relationships within the Exoristinae and Tachininae were poorly resolved and sensitive to model assumptions. Employing various genes (18s, 28s, COI, EF α , TPI, CAD, LGL, MCS, MAC), Winkler *et al.* (2015) processed the relationships of the subfamilies, greatly declarative the hypotheses Cerretti *et al.* (2014) and placed the Polleniinae (Calliphoridae) as a sister to family Tachinidae (Cerretti *et al.*, 2017). Despite, this study used solely twenty two genera/tribes, inferred relationships among tribes for them. Blaschke *et al.* in 2018 distributed a deep analysis of Phasiinae using molecular genes (CAD, LGL, MCS, and MAC) and enclosed one hundred and twenty eight taxa within eighty genera.

This is often sturdy molecular cladistic examination of family Tachinidae, robustly beginning the structure of the subfamily and its tribes and hypothesizing Dexiinae and Phasiinae as sister groups.

Stireman *et al.* (2019), this is often the foremost sturdy molecular cladistic of tachinid cluster thus far. The foremost groups were discussed, the exemplars enclosed more than five hundreds terminal species in fifty four tribes. They got molecular genes (CAD, 28S, MCS and MAC). As in former investigations (Winkler *et al.*, 2015; Stireman, *et al.*, 2019), they in agreement powerfully with Cerretti *et al.* (2014) that Polleniidae and Tachinidae are sister clusters. Despite an absence of obvious morphological connections between these clades, the consistency of this result across completely different markers and analyses suggests that the relationship was strong.

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УДК 504.75:339.138:338.439 ПРИМЕНЕНИЕ БИОТЕХНОЛОГИЧЕСКИХ МЕТОДОВ ОЗДОРОВЛЕНИЯ КАРТОФЕЛЯ В УСЛОВИЯХ КХ Н.С.КОЛЕСНИКОВА

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Аннотация. Разработана система первичного семеноводства картофеля высоких репродукций. Семеноводческое хозяйство Колесникова H.C. полностью обеспечивает себя и другие хозяйства, занимающиеся производством товарного картофеля, высокими репродукциями собственного производства.

Ключевые слова: картофель, клубни, фунгициды, урожайность, меристема.