The Phylogeny of Parasitic Hemiptera Using *Multivariate Statistical Package Cluster Analysis*

Dwi Setyo Astuti*[1], Murwanto Setyo Nugroho[2]

[1]Biology Education Department, Faculty of Teacher Training and Education, Universitas Muhammadiyah Surakarta.
Jl. A. Yani Tromol Pos I, Pabelan, Kartasura, Surakarta 57162, Jawa Tengah, Indonesia
[2]Darul Arqom Junior High School, Tulung Klaten, Jawa Tengah
*Corresponding Author, E-mail address: dsa122@ums.ac.id

ABSTRACT

Hemiptera is an Insecta with the characteristic of the forewing which has been modified as a "hemelitron", namely half of the part at the base is thickened, while the rest is structured like a membrane, and the hind wing is like a thin membrane. Most of Hemiptera are parasite that attack rice plants. The purpose of this study was to determine the kinship of Hemiptera parasite species in rice fields in the Tulung area, Klaten , Central Java. The data obtained in this study is the identification of Hemiptera based on 30 morphological characters. Data analysis carried out using cluster analysis with MVSP (Multivariate Statistical Package) software. The results showed that there were 9 species of Hemiptera as parasitic species namely Gerris lacusticus, Narvesus carolinensis, Dysdercus cingulatus, Leptoglossus clypealis, Triatoma sanguisuga, Arilus cristatus, Thyanta custator, Padops cinctipes and Boisea trivittata. The most closely related species is Narvesus carolinensis and Arilus cristatus, yes, with a similarity rate of 86.9%. While the species that have the most distant kinship are Narvesus carolinensis and Gerris lacusticus that is equal to 60.4%. The high degree of similarity indicates a close relationship between parasite species.

1. INTRODUCTION

Insect is object important thing to learn Because is destructive pests _ crops in agricultural areas and constitutes organism with amount the largest species that is about 91% of species arthropods or about 72% of whole species known animal. (Menta & Remelli, 2020) Frequent insects _ damage plant is group class Hexapods. Insect Hexapods have characteristic typical, that is own six legs. Type This own a number of order types , among others are : Diptera , Coleoptera , Lepidoptera , Orthoptera and Hemiptera (Li et al., 2019b).

Hey means " half " and pteron means " wing ". class insects included _ to in this order own wing experiencing future _ modification as a " hemelitron ", ie half part in the area base thick, meanwhile the rest structured like membranes, and wings behind similar thin membrane (membrane). That name given Because insect of this order own wing front that part the base hard like skin, however part the back is thin like membrane. Insect the Hemiptera group ever to invade the rice fields in the district Delanggu , Karanganom , Wonosari , Juwiring and Trucuk in 2011. Explosion _ Hemiptera pests are caused by several factors, factors main contributor _ to increasing several Hemiptera populations and attacks year final This is potency high biotic Hemiptera, factor abiotic and systems cultivation supporting paddy _ development Hemiptera population (Radhy, 2011).

There are several techniques that can used For know lift phylogeny between species among them is with count manually using _ formula index similarity Sorensen or also can done with use application *Multivariate Statistical Package*(Vidovic, n.d.). *The Multivariate Statistical Package* is an application that is often used by biologists, especially those who focus on taxonomy. MVSP is an analysis program strong multivariate _ For compatible with a PC that does various cluster and dendogram analysis. MVSP is used on hundreds of sites and more from 50 countries. Application This give the easy way For analyze data across a wide range field start from taxonomy, ecology, geology, sociology, genetics, and systematics MVSP fits perfectly used For know level density between species after species the identified especially formerly (Giribet & Edgecombe, 2019).

Characteristic typical main insect Hemiptera members are structure shaped mouth _ like needles. They use structure mouth This For stab network from eat it and then suck fluid in it. Hemiptera Alone is omnivore meaning _ they consume almost all type food start from fluid plants, seeds , insects else , until animals small like fish (Lytle, 2015). The process of morphological identification is to make observations details start from characteristic general until characteristic Specific Which owned every species. Activity identification can done with helpkey terminated nor without key terminated. Identification withthe help of the termination key will deliver the observed species to to taxon each, start taxon highest until Lowest,that is start *phyllum* until with species. As for identification withouthelp key determination still can done with objective For know percentage kinship between species in One level taxon, both class, order, family, or genus (Lee et al., 2019). Techniques to determine the level of kinship of species in an area taxon level, can done with various method, among them through tree phylogeny, cladogram, cladistic, And dendogram. Tree phylogeny, cladistic, and cladogram describe kinship relationships something species with grandma ancestor Which related with history evolution. As for dendogram is diagram which describes degree of closeness or kinship of the indicated species group with magnitude percentage (Edgecombe, 2020). Magnitude percentage Which obtained based on results calculation through comparison character morphology Which owned each species. There are several techniques that can used For know lift kinship between species among them is with count manually using _ formula index similarity Sorensen or also can done with use application *Multivariate Statistical Package*(Vidovic, n.d.).

The Multivariate Statistical Package is an application that is often used by biologists, especially those who focus on taxonomy. MVSP is an analysis program strong multivariate _ For compatible with a PC that does various cluster and dendogram analysis. MVSP is used on hundreds of sites and more from 50 countries. Analysis results using MVSP has published in various journals, including *Science, Nature, Ecology, Journal of Petroleum Geology,* and Journal *of Biogeography.* Application This give the easy way For analyze data across a wide range field start from taxonomy, ecology, geology, sociology, genetics, and systematics. MVSP fits perfectly used For know level density between species after species the identified especially formerly (Giribet & Edgecombe, 2019).Study about cluster analysis using MVSP yet Lots used, especially For know level Hemiptera kinship plays a role as pests on plants rice The purpose of this study is to determine the degree of kinship of the parasitic Hemiptera that attacks the rice fields in Majegan Distik, Tulung, Klaten..

2. MATERIALS AND METHODS

2.1. Ditermine Species

Determine species results catch Which will in count his kinship from the order Hemiptera as pest of plant, consisting from family Gerridae , Reduviidae , Pentatomidae , Coreidea , Rhopalidae , Rudiviidae , Pyrrhocoridae , Pentadomidae , Reduvidae , and Pyrhocoridae.

2.1.1. *Determine the sampling point at the location*

Sampling was carried out at 5 points covering the largest rice fields in 5 areas, including Klirong, Klalung, Daden, Sanggrahan, and Nandan.

2.1.1.1. *Sub sub-chapters*

The formulas used in the data calculation are written using the equation editor or other standard applications. Formulas shall may not be in the form of images or screen capture results from other sources. The formula is written by including the source of reference.
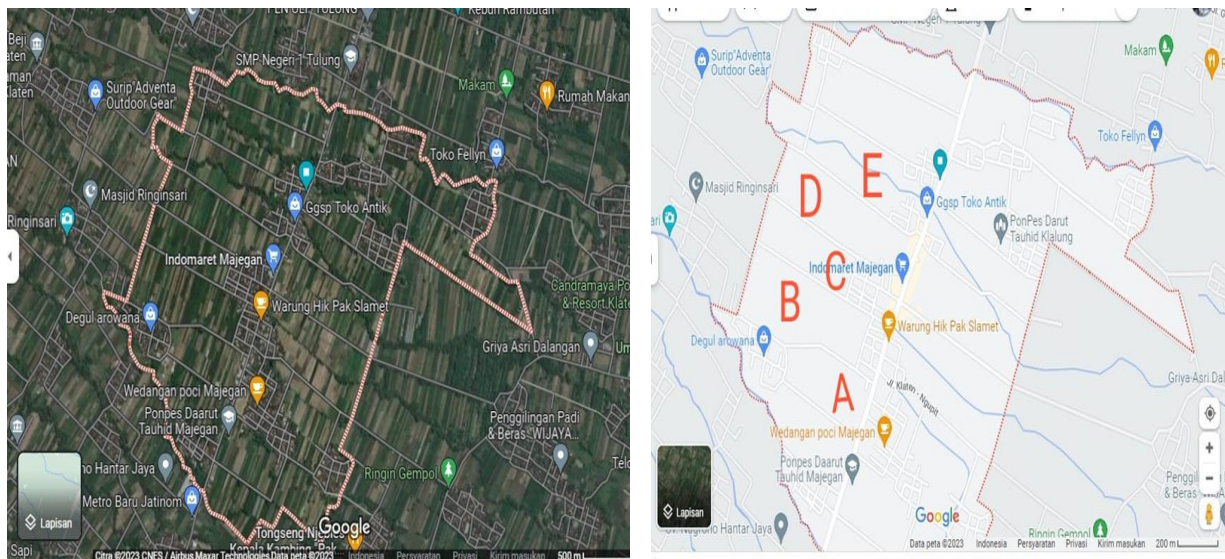

Figure 1. Hemiptera species sampling points

Description :
- A   = Rice field area of Klirong
- B   = Rice field area of Klalung
- C   = Rice field area of Daden
- D   = Rice field area of Sanggrahan
- E   = Paddy field area of Nadan

2.1.1.2. *Identifying Species*

After determine species Which will counted level kinship, Then determine character morphology Which will made base identification. Identification done withhelp insect determinant key and Boror

2.1.1.3. *Kinship Analysis*

Analysis kinship using MVSP (*Multivariate Statistical Package) software*. The data obtained through this application are the percentage of kinship levels between Hemiptera species and the dendogram which shows the kinship clusters between species.

3. RESULTS AND DISCUSSION

3.1. *Identification of Species*

Morphological identification was carried out based on 30 specific characters of Hemiptera. Some families of Hemiptera are parasitic, including Gerridae, Reduviidae, Pentatomidae,

Coreidea, Rhopalidae, Rudiviiidae, Pyrrhocoridae, Pentadomidae, Reduvidae, and Pyrhocoridae. There are 9 species from this family that have been identified in table 1 below.

Table 1. Identified Species of Hemiptera

No	Species Code	Species Name	Family
1	A	*Gerris lacusticus*	Gerridae
2	B	*Leptoglossus clypealis*	Coreidea
3	C	*Dysdercus cingulatus*	Pyrrhocoridae
4	D	*Narvesus carolinensis*	Reduviidae
5	E	*Triatoma sanguisuga*	Reduvidae
6	F	*Arilus cristatus*	Rudiviidae
7	G	*Thyanta custator*	Pentatomidae
8	H	*Padops cinctipes*	Pyrhocoridae
9	I	*Boisea trivittata*	Rhopalidae

3.1.1. Cluster Analysis And Dendogram

MVSP (*Multi-Variate Statistical Package*) is Popular multivariate analysis *software* is a program that allows calculations from index kinship between species. MVSP is a statistical program for the best statistical analysis, not only for its analytical capabilities, but also for ease of use for presenting data and checking kinship assumptions in a biodiversity (Ogasawara & Kon, 2021). There are various methods of data analysis. One way is to use the Bray Curtis method. Bray Curtis distance, or commonly called Sorensen distance is a normalization method that is widely used in botany, ecology, taxonomy , and systematics to measure differences. In the Bray Curtis method, the number 0 indicates an identical similarity and the number 1 indicates a very absolute difference between the species being compared(Bhargava & Yablonovitch, 2015). Contrary to Bray Curtis, the Jaccard method is used to analyze the kinship between species based on their similarities. The inventor of this method is Paul Jaccard. The highest score in the Jaccard analysis is 1 which means the specimens being compared are identical and the lowest is 0 which means the specimens have nothing in common (Vidovic, n.d.).

Table 2. Cluster Analysis of Parasite Hemiptera

Node	Group 1	Group 2	Simil. (%)
1	D	F	86.957
2	C	E	86.364
3	Node 2	G	83.721
4	Node 1	H	79.545
5	Node 3	I	75.502
6	B	Node 5	70.826
7	A	Node 4	66.140
8	Node 7	Node 6	60.458

The results of the cluster analysis showed that the 9 species of Hemiptera were divided into 2 different groups. Species D and F show the highest similarity and it can be interpreted that the two are closely related. The lowest degree of similarity is between species at node 7 and node 8, which are independent of each cluster. Node 7 is represented by species B while node 8 is represented by species A. Thus the most distantly related species are species B and A. To draw

conclusions about phylogeny, systematicians must gather information on the morphology, genes, and biochemistry ofrelevant organisms. It's important to focus on traits which are the result of a common ancestor, because they are just traits here's what reflect connection evolutionary (Song et al., 2019)

Helden & Leather (2004), stated that stated that Partially big distribution kingdom animal most based on morphology, physiology, And pattern development. Symmetry, metamer, development caelom, and the type of cleavage in the egg is widely discussed as a basis determine kinship. Dendrograms is a tree-shaped diagram showing the degrees of equality in between members something group creature life (Vidovic, n.d., 2020). Clustering hierarchies build a cluster hierarchy or in other words a cluster tree, which is also known as a dendrogram. Each cluster node contain clusters child; clusters you Which share   point Which covered by the parent they (Montgomery et al., 2020).
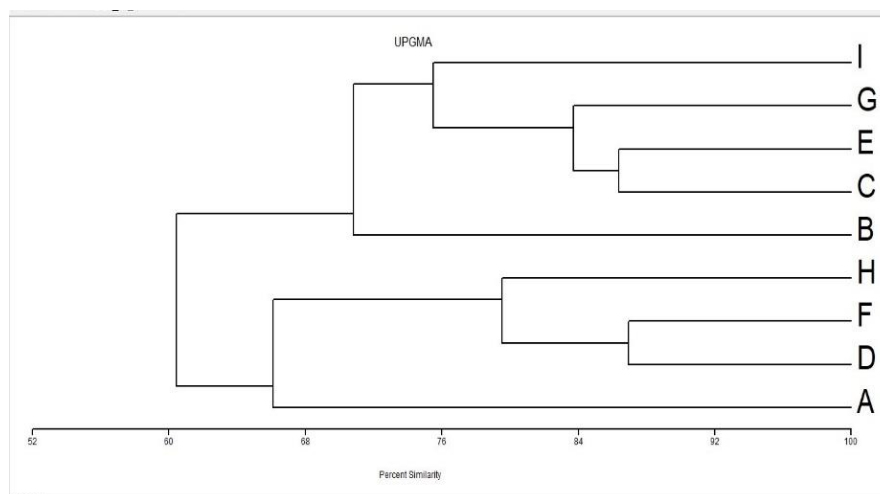

Figure 1. Dendogram

The closest relatives are *Narvesus carolinensis* and *Arilus cristatus*, with a similarity rate of 86.9%. The life cycle of *Narvesus* carolinensis is about 35-56 days. Usually these insects are active in the morning and evening. During the day they usually hide under plants or grass. What is unique about walang sangit is that when disturbed it will emit a distinctive odor ('scorching' smell). The population density of the stink bug will usually increase when the plants are in bloom, the weather is warm and drizzling (on the other hand, heavy rains can reduce the population). This insect usually attacks the milk-ripe rice by sucking the liquid of the rice seeds. The puncture mark will be a dark spot. Rice that is attacked by stink bugs will decrease in weight and even become empty. *Arilus cristatus* usually measures 1-1.25 inches. This species includes a powerful killer. It has long legs, antennae, a stubby beak with large eyes, a slender head.

Figure 2. *Narvesus carolinensis*   **Figure 3**. *Arilus cristatus*

While the species that have the most distant kinship are *Narvesus carolinensis* and *Gerris lacusticus* with 60.4%. *Gerris lacusticus* is a group of predatory insects which all belong to the Gerridae tribe. Its members, about 340 species, many of which are difficult to distinguish. In literature it is also known erroneously as the "water spider", although it is not a spider at all. The name "anggang-anggang" itself comes from its movement back and forth while floating.

Figure 5. *Gerris lacusticus*

This insect is very easy to recognize because of its habit of always walking/jumping on the surface of the water. Movement is fast, can reach 1.5 m/s. Most live in calm waters, but there are five species (from the genus Halobates) that are known to live on the surface of the ocean. From the surface of the water, the algae target prey (usually other insects) that are near the surface. This animal has become a model in biophysical research regarding the ability of surface pressure to support weight.

4. CONCLUSIONS

The results of morphological identification obtained 9 species of parasitic Hemiptera in the rice field area of Majegan village, Tulung, Klaten, Central Java, namely: *Gerris lacusticus,*

Leptoglossus clypealis, Dysdercus cingulatus, Narvesus carolinensis, Triatoma sanguisuga, Arilus cristatus, Thyanta custator, Padops cinctipes and *Boisea trivittata.* The most closely related species is *Narvesus carolinensis* and *Arilus cristatus*, with a similarity rate of 86.9%. While the species that have the most distant kinship are *Narvesus carolinensis* and *Gerris lacusticus* that is equal to 60.4%. The high degree of similarity indicates a close relationship between parasite species. Future research could focus on developing natural enemies for the Hemyptera parasite.

5. ACKNOWLEDGMENTS

6. REFERENCES

Bhargava, S., & Yablonovitch, E. (2015). Lowering HAMR near-field transducer temperature via inverse electromagnetic design. IEEE Transactions on Magnetics, 51(4). https://doi.org/10.1109/TMAG.2014.2355215

Edgecombe, G. D. (2020). Arthropod Origins: Integrating Paleontological and Molecular Evidence. https://doi.org/10.1146/annurev-ecolsys-011720

Giribet, G., & Edgecombe, G. D. (2019). The Phylogeny and Evolutionary History of Arthropods. In Current Biology (Vol. 29, Issue 12, pp. R592–R602). Cell Press. https://doi.org/10.1016/j.cub.2019.04.057

Helden, A. J., & Leather, S. R. (2004). Biodiversity on urban roundabouts-Hemiptera, management and the species-area relationship. Basic and Applied Ecology, 5(4), 367–377. https://doi.org/10.1016/j.baae.2004.06.004

Hong, F., Han, H. L., Pu, P., Wei, D., Wang, J., & Liu, Y. (2019). Effects of five host plant species on the life history and population growth parameters of myzus persicae (Hemiptera: Aphididae). Journal of Insect Science, 19(5). https://doi.org/10.1093/jisesa/iez094

Høye, T. T. (2020). Arthropods and climate change – arctic challenges and opportunities. In Current Opinion in Insect Science (Vol. 41, pp. 40–45). Elsevier Inc. https://doi.org/10.1016/j.cois.2020.06.002

Jactel, H., Koricheva, J., & Castagneyrol, B. (2019). Responses of forest insect pests to climate change: not so simple. In Current Opinion in Insect Science (Vol. 35, pp. 103–108). Elsevier Inc. https://doi.org/10.1016/j.cois.2019.07.010

Lee, D. H., Park, Y. L., & Leskey, T. C. (2019). A review of biology and management of Lycorma delicatula (Hemiptera: Fulgoridae), an emerging global invasive species. In Journal of Asia-Pacific Entomology (Vol. 22, Issue 2, pp. 589–596). Elsevier B.V. https://doi.org/10.1016/j.aspen.2019.03.004

Li, F., Zhao, X., Li, M., He, K., Huang, C., Zhou, Y., Li, Z., & Walters, J. R. (2019a). Insect genomes: progress and challenges. In Insect Molecular Biology (Vol. 28, Issue 6, pp. 739–758). Blackwell Publishing Ltd. https://doi.org/10.1111/imb.12599

Li, F., Zhao, X., Li, M., He, K., Huang, C., Zhou, Y., Li, Z., & Walters, J. R. (2019b). Insect genomes: progress and challenges. In Insect Molecular Biology (Vol. 28, Issue 6, pp. 739–758). Blackwell Publishing Ltd. https://doi.org/10.1111/imb.12599

Lytle, D. A. (2015). Order Hemiptera. In Thorp and Covich's Freshwater Invertebrates: Ecology and General Biology: Fourth Edition (Vol. 1, pp. 951–963). Elsevier Inc. https://doi.org/10.1016/B978-0-12-385026-3.00037-1

Ma, C.-S., Ma, G., & Pincebourde, S. (2020). Survive a Warming Climate: Insect Responses to Extreme High Temperatures. Annual Review of Entomology Annu. Rev. Entomol. 2021, 66, 163–184. https://doi.org/10.1146/annurev-ento-041520

Menta, C., & Remelli, S. (2020). Soil health and arthropods: From complex system to worthwhile investigation. In Insects (Vol. 11, Issue 1). MDPI AG. https://doi.org/10.3390/insects11010054

Montgomery, G. A., Dunn, R. R., Fox, R., Jongejans, E., Leather, S. R., Saunders, M. E., Shortall, C. R., Tingley, M. W., & Wagner, D. L. (2020). Is the insect apocalypse upon us? How to find out. In Biological Conservation (Vol. 241). Elsevier Ltd. https://doi.org/10.1016/j.biocon.2019.108327

Moreira, F. F. F., Rodrigues, H. D. D., Sites, R. W., Silva Cordeiro, I. da R., & Magalhães, O. M. (2018). Order Hemiptera. In Thorp and Covich's Freshwater Invertebrates (pp. 175–216). Elsevier. https://doi.org/10.1016/b978-0-12-804223-6.00007-x

Ogasawara, Y., & Kon, M. (2021). Two clustering methods based on the Ward's method and dendrograms with interval-valued dissimilarities for interval-valued data. International Journal of Approximate Reasoning, 129, 103–121. https://doi.org/10.1016/j.ijar.2020.11.001

Song, N., Zhang, H., & Zhao, T. (2019). Insights into the phylogeny of Hemiptera from increased mitogenomic taxon sampling. Molecular Phylogenetics and Evolution, 137, 236–249. https://doi.org/10.1016/j.ympev.2019.05.009

Valdez, J. W. (2020). Arthropods as vertebrate predators: A review of global patterns. In Global Ecology and Biogeography (Vol. 29, Issue 10, pp. 1691–1703). Blackwell Publishing Ltd. https://doi.org/10.1111/geb.13157

Vidovic, S. U. (n.d.). Tree congruence: quantifying similarity between dendrogram topologies.

Wagner, D. L. (2019). Insect Declines in the Anthropocene. https://doi.org/10.1146/annurev-ento-011019

Wang, J., Wu, Y., Dai, R., & Yang, M. (2020). Comparative mitogenomes of six species in the subfamily Iassinae (Hemiptera: Cicadellidae) and phylogenetic analysis. International Journal of Biological Macromolecules, 149, 1294–1303. https://doi.org/10.1016/j.ijbiomac.2020.01.270

Wong, M. K. L., Guénard, B., & Lewis, O. T. (2019). Trait-based ecology of terrestrial arthropods. Biological Reviews, 94(3), 999–1022. https://doi.org/10.1111/brv.12488