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Population dynamics and damage intensity of brown planthopper (BPH) and *Nilaparvata lugens* (Stal.) provide information about the economic threshold status of *N. lugens* in Bali. This study enriched information on the genetic diversity of *N. lugens* isolates from eastern Indonesia, particularly Bali. It is the first report of *N. lugens* biotype Y in Indonesia. In addition, the latest information in this study is that rice varieties Situbagendit and Inpari 32, which were previously resistant to BPH, are now found to be susceptible to BPH. This information is critical as a basis for controlling *N. lugens* in Indonesia

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³² **The Brown Planthopper (***Nilaparvata lugens* **Stal.) Attack and Its** ³³ **Genetic Diversity on Rice in Bali, Indonesia**

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 $\begin{array}{c} 40 \\ 41 \\ 42 \\ 43 \\ 44 \\ 45 \\ 46 \\ 47 \end{array}$ 41 **Abstract.** The brown planthopper is an important pest on rice crops in Indonesia. The genetic diversity of BPH isolates in 42 western Indonesia has been extensively reported, whereas eastern Indonesia isolates have not been reported. This research aims to analyze genetic diversity and evaluate the BPH attack's intensity on Bali rice plants. The research method used was an observation of 44 attack percentage, population dynamics, attack intensity, and genetic diversity of BPH in 9 districts in Bali (Badung, Gianyar,
45 Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana). Molecula 46 *lugens* DNA in the mtCOI fragment. BPH attacks of >50% were found in the districts of Gianyar, Bangli, Jembrana, and Badung. The 47 BPH population was primarily found in Ciherang and IR-64 varieties of rice in the Badung Regency, with 43.67 BPH per rice hill. In general, rice varieties grown in all observation locations were susceptible to BPH, such 48 general, rice varieties grown in all observation locations were susceptible to BPH, such as Ciherang, IR-64, Inpari 32, and Situbagendit.
49 In the Ciherang and IR-64 varieties, the highest attack intensity average valu 49 In the Ciherang and IR-64 varieties, the highest attack intensity average value reached 30%. The sequence of *N. lugens* isolate from Bali 50 Jembrana showed the highest nucleotide and amino acid homology with *N. lugens* isolate FSD-034 from Pakistan (MK301229) biotype 51 Yof 99.5 -99.74% and 100%, respectively. This study found *N. lugens* biotype Y in rice 52 reported that Rice varieties Situbagendit and Inpari 32, previously resistant to BPH, are reported as susceptible to BPH.

53 **Keywords:** susceptible variety, Situbagendit, Inpari 32, genetic diversity, attack intensity

54 **Abbreviations** (if any): The BPH, Rice Plants

55 **Running title:** The Brown Planthopper (*Nilaparvata lugens* Stal.) Attack and Its Genetic Diversity on Rice in Bali, Indonesia

56

39

57 **INTRODUCTION**

 The brown planthopper (BPH) (*Nilaparvata lugens* Stal, Hemiptera: Delphacidae) is the most destructive rice 59 pest in Indonesia. Repeated outbreaks of BPH in Indonesia are caused by continuous rice cultivation, extensive use, and
60 over-application of insecticides (Baehaki and Meiava 2015). This pest is vascular monophagous in over-application of insecticides (Baehaki and Mejaya 2015). This pest is vascular monophagous in rice (Cheng et al. 2013; Ferrater et al. 2015). Feeding by nymphs and imago at the base of the plant causes rapid wilting and drying of the plant 62 (Bottrell and Schoenly 2012; Cheng et al. 2013; Bao and Zhang 2019). In addition, BPH is also a vector of Rice grassy stunt virus and Rice ragged stunt virus (Bao and Zhang 2019). At high population levels of N. *lugens* stunt virus and Rice ragged stunt virus (Bao and Zhang 2019). At high population levels of *N. lugens* can cause significant losses in rice production (Cheng et al. 2013; Zheng et al. 2013; Bao and Zhang 2019).

65 The BPH cannot tolerate winter in northern Asia, including Japan, Korea, and northern China (He et al. 2012; Fu et al. 2012; Fu et al. 2014). The population originally came from subtropical and tropical areas by flying long distances 67 during the summer (Fu et al. 2014; Hu et al. 2014). The intensification of rice production triggered the BPH outbreak in 68 Tropical Asia during the green revolution era in the 1970s and 1980s (Bottrell and Schoenly 2012). Until now, *N. lugens* is 69 the main problem causing rice harvest failure in several countries. Inaccurate identification and prolonged identification of η . *N. lugens* are obstacles to its field management strategy.

70 *N. lugens* are obstacles to its field management strategy.
71 Traditionally, BPH has been identified at Traditionally, BPH has been identified at the species level by morphological features using anatomical

21 characteristics, namely, wings, front, and external genitalia (Dupo and Barrion 2009). Accurate identification requ 72 characteristics, namely, wings, front, and external genitalia (Dupo and Barrion 2009). Accurate identification requires 73 extensive expertise and experience and yet sometimes can lead to errors. Morphological identification by an entomologist 74 can reduce the potential for errors. Practical morphological identification is only possible when dealing with small sample 75 sizes and well-preserved specimens. Therefore, it is crucial to utilize a new identification method that is accurate, fast,
77 Molecular techniques with high reproducibility and fast results offer an excellent alternati time-saving, and suitable for large numbers of specimens.

Molecular techniques with high reproducibility and fast results offer an excellent alternative to traditional 78 morphological classification. Several mitochondrial and nuclear genes have been used as genetic markers to differentiate 79 related species. These include the mitochondrial cytochrome c oxidase subunit 1 (CO1) gene, nuclear 12S-16S-18S **Commented [A1]:** arrange based on alphabet

80 ribosomal RNA genes, and ITS1 and ITS2 internal transcription spacers (Fukunaga et al. 2000; Brengues et al. 2014; Wang et al. 2016; Liu et al. 2018). ITS1 and ITS2 are nonfunctional spacers that separate the 81 Gomez-Polo et al. 2014; Wang et al. 2016; Liu et al. 2018). ITS1 and ITS2 are nonfunctional spacers that separate the
82 18S-5 8S and 5 8S-28S rRNA genes respectively (Ji et al. 2003; Liu et al. 2018). As ITS sequences 82 18S-5.8S and 5.8S-28S rRNA genes, respectively (Ji et al. 2003; Liu et al. 2018). As ITS sequences have low intra-species 83 variation but high variation between species, they are helpful for species classification and phylogenetic analysis for morphologically similar organisms, both in prokaryotes and eukaryotes (Liu et al. 2009). Finally, f 84 morphologically similar organisms, both in prokaryotes and eukaryotes (Liu et al. 2009). Finally, from the molecular 85 identification of the combined mitochondrial COI-COII and ten microsatellite marker loci (Winnie et 85 identification of the combined mitochondrial COI-COII and ten microsatellite marker loci (Winnie et al. 2020).
86 The genetic diversity of N. luggens has been reported in several countries such as China. South Kore

86 The genetic diversity of *N. lugens* has been reported in several countries such as China, South Korea, Pakistan, 87 India, and Malaysia (Jing et al. 2012; Zheng et al. 2021; Anant et al. 2021; Latif et al. 2012). The g 87 India, and Malaysia (Jing et al. 2012; Zheng et al. 2021; Anant et al. 2021; Latif et al. 2012). The genetic diversity of *N*.
88 *lugens* in Indonesia is widely reported in western Indonesia (Java Island) (Winnie et al 88 *lugens* in Indonesia is widely reported in western Indonesia (Java Island) (Winnie et al. 2020; Chaerani et al. 2021). 89 Reports on the genetic diversity of *N. lugens* in eastern Indonesia have not been found. Therefore, this study aims to
90 analyze genetic diversity and determine the intensity of RPH attacks on rice plants in eastern I analyze genetic diversity and determine the intensity of BPH attacks on rice plants in eastern Indonesia, especially Bali.

91 **MATERIALS AND METHODS**

92 **Brown Planthopper Sampling from Rice Dwarf Disease Endemic Areas**

93 Samples were taken from nine locations in Bali Province (Badung, Gianyar, Klungkung, Bangli, Karangasem, 94 Tabanan, Denpasar City, Buleleng, and Jembrana). The brown planthopper samples taken from rice plants were nymphs
95 and imagos. Nymphs and imagos were used for total DNA extraction. After arriving at the laboratory, th 95 and imagos. Nymphs and imagos were used for total DNA extraction. After arriving at the laboratory, the nymphs and imago were stored dry at -20°C. imago were stored dry at -20°C.

97
98 98 **Observation of BPH Attack Symptoms and Quantity of BPH Population/rice hill**
99 Observation of symptoms of BPH attack was carried out by observing symp

99 Observation of symptoms of BPH attack was carried out by observing symptoms of damage to rice plants due to 100 BPH attack. The abundance of the BPH/rice hill population was obtained by counting all nymphs and imagoes o 100 BPH attack. The abundance of the BPH/rice hill population was obtained by counting all nymphs and imagoes obtained.
101 Data on the population per cluster from 20 samples at each observation location were then averaged Data on the population per cluster from 20 samples at each observation location were then averaged.

102
103 103 **BPH Attack Percentage**

The percentage of BPH attacks is calculated using the following formula:
 $P = \frac{a}{b} \times 100\%$

105

 106 Note:
 107 P = A

107 $P =$ Attack percentage (%)
108 $a =$ Number of rice hills aff

- 108 $a =$ Number of rice hills affected by BPH
109 $b =$ Number of rice hills observed $b =$ Number of rice hills observed
- 110

111 **Damage Intensity**

112 Determination of scoring on symptoms of rice damage due to BPH attack is based on Table 1. The intensity of 113 damage due to a BPH attack is determined using the formula: damage due to a BPH attack is determined using the formula:

$$
I = \sum_{i=1}^{N i x V i} v x 100\%
$$

114 115 116

117

-
- 118 Note:
119 $I = D$
- 119 I = Damage intensity
120 Ni = The number of a $Ni = The number of affected rice hills on the score i$
-
- 121 Vi = Score i
122 N = The nun
- 122 $N =$ The number of rice hills observed
123 $Z =$ Highest score $Z =$ Highest score
- 124

125 **Total DNA Extraction from Brown Planthopper**

126 Total DNA extraction of brown planthopper was obtained from one individual imago or one individual nymph
127 based on the modified method of Goodwin et al. (1994). One individual imago was put into a microtube and then based on the modified method of Goodwin et al. (1994). One individual imago was put into a microtube and then added

128 with 100 μl of CTAB extraction buffer (2% CTAB, 1.4 M NaCl, 100 mM Tris-HCI, 20 mM EDTA, and 1% PVP (-40

-
- [°]C)). Next, 1 μl of proteinase K was added, then the insects were crushed using a micro-pistil, vortexed, and incubated in a water bath of 65°C for 3 minutes. After that, the tube was added with 100 μl CI (chloroform:
- 130 water bath of 65°C for 3 minutes. After that, the tube was added with 100 μl CI (chloroform: isoamyl alcohol) in a ratio of 15 minutes. The tube was then vortexed for 3 minutes and centrifuged at 10,000 rpm for 15 mi 131 24:1. The tube was then vortexed for 3 minutes and centrifuged at 10,000 rpm for 15 minutes. The supernatant formed was
- 132 transferred to a new microtube (60 μl) and then added with 3 M NaOAc (pH 5.2), as much as 1/10 of the total volume of

Commented [A2]: This formula need supporting reference

133 the supernatant. Isopropanol was added up to 2/3 of the total volume of the supernatant, then incubated at -20°C for one
134 night. The tube was centrifuged at 10,000 rpm for 10 min and the supernatant was discarded. T 134 night. The tube was centrifuged at 10,000 rpm for 10 min, and the supernatant was discarded. The pellets were washed
135 with 100 ul of 80% ethanol (cold) and centrifuged at 8000 rpm for 5 minutes. In the final step, t 135 with 100 μl of 80% ethanol (cold) and centrifuged at 8000 rpm for 5 minutes. In the final step, the supernatant was removed, and the pellet was dried for approximately 1 hour. It was then added with a solution of 20 μ 136 removed, and the pellet was dried for approximately 1 hour. It was then added with a solution of 20 μl TE and stored at - 20°C until used.

138
139

139 **Amplification of mtCOI Fragments Using the PCR Method** 140 **PCR reactants were manufactured with a total volume** 140 PCR reactants were manufactured with a total volume of 25 μl consisting of 12.5 μl Go Tag Green Master Mix
141 (Promega, US) and 9.5 μl ddH2O, DNA amplification of the mtCOI fragment was carried out using a pair of un 141 (Promega, US) and 9.5 μl ddH2O. DNA amplification of the mtCOI fragment was carried out using a pair of universal
142 primers mtCOI LCO 1490 (3'-GGTCAACAAATCATAAAGATATTGG-5') and HCO 2198 (5ΤΑΑΑCTTCA 142 primers mtCOI LCO 1490 (3'-GGTCAACAAATCATAAAGATATTGG-5') and HCO 2198 (STAAACTTCA
143 GGGTGACCA AAAAATCA-3') (Folmer et al. 1994) each 1 ul. and 1 ul DNA template. PCR reactions were carried out 143 GGGTGACCA AAAAATCA-3') (Folmer et al. 1994) each 1 μl, and 1 μl DNA template. PCR reactions were carried out
144 with a Perkin Elmer 480 Thermocycler (Applied Biosystem, US). The PCR reaction was initiated by initial 144 with a Perkin Elmer 480 Thermocycler (Applied Biosystem, US). The PCR reaction was initiated by initial denaturation
145 for 5 min at 94°C. The PCR was continued for 35 cycles in the following order: 94° C for 1 m 145 for 5 min at 94°C. The PCR was continued for 35 cycles in the following order: 94°C for 1 minute, 52° C for 35 seconds, 146 72°C for 1 minute 30 seconds, and a final extension of 72°C for 7 minutes. The PCR result 72°C for 1 minute 30 seconds, and a final extension of 72°C for 7 minutes. The PCR results were then analyzed in 1% 147 agarose gel. The DNA fragments of mtCOI were visualized using a UV transilluminator after being immersed in a 2%
148 ethidium bromide solution for 15 minutes and photographed with a digital camera. The result of amplif 148 ethidium bromide solution for 15 minutes and photographed with a digital camera. The result of amplification by PCR technique was in the form of mtCOI DNA fragments with a size of \pm 710 base pairs (pb). technique was in the form of mtCOI DNA fragments with a size of \pm 710 base pairs (pb).

150 151 **Analysis of DNA Sequence Results**

152 Nucleotide Sequencing DNA fragment purification and mtCOI nucleotide sequencing were performed at PT. 1st
153 Base, Malaysia. The results were then registered in the NCBI gene bank (http://www.ncbi.nlm.nih.gov). Analys 153 Base, Malaysia. The results were then registered in the NCBI gene bank (http://www.ncbi.nlm.nih.gov). Analysis of mtCOI DNA sequence data ChromasPro program was used to combine forward and reverse nucleotide sequences 154 mtCOI DNA sequence data ChromasPro program was used to combine forward and reverse nucleotide sequences to obtain
155 the mtCOI gene (ChromasPro version 2.01, 2006). The Bioedit program was used to compare mtCOI fragme 155 the mtCOI gene (ChromasPro version 2.01. 2006). The Bioedit program was used to compare mtCOI fragments between
156 samples (Multiple alignments) (Hall 1999). The phylogenetic relationship was built by comparing the mt 156 samples (Multiple alignments) (Hall 1999). The phylogenetic relationship was built by comparing the mtCOI sample
157 fragments from the brown planthopper from Indonesia with the mtCOI fragments already stored in the NC 157 fragments from the brown planthopper from Indonesia with the mtCOI fragments already stored in the NCBI GenBank
158 (http://www.ncbi.nlm.nih.gov). The criteria for retrieving mtCOI fragments at GenBank were fragments w 158 (http://www.ncbi.nlm.nih.gov). The criteria for retrieving mtCOI fragments at GenBank were fragments with a nucleotide
159 base length of ± 800 bo (Boykin et al. 2007) (Table 1). The phylogenetic tree was constructe 159 base length of \pm 800 bp (Boykin et al. 2007) (Table 1). The phylogenetic tree was constructed using the PAUP 4.0b10 program (Swofford 2002) with the maximum parsimony cladistic quantitative method. The cladogram wa 160 program (Swofford 2002) with the maximum parsimony cladistic quantitative method. The cladogram was compiled using
161 the Heuristic method. The cladogram used results from the strick consensus with the statistical boo 161 the Heuristic method. The cladogram used results from the strick consensus with the statistical bootstrap test to obtain a 162 100% probability. 100% probability.

163 **RESULTS AND DISCUSSION**

164 The brown planthopper causes direct and indirect damage to rice plants. Direct damage was in the form of stunted
165 and uneven growth of rice plants (Figure 1A and 1B), vellow plants (Figure 1C), and hopperburn caused 165 and uneven growth of rice plants (Figure 1A and 1B), yellow plants (Figure 1C), and hopperburn caused by fluid in rice
166 plant cells sucked by BPH nymphs, brachiptera (Fig. short wings), and macroptera (long wings) (166 plant cells sucked by BPH nymphs, brachiptera (Fig. short wings), and macroptera (long wings) (Figures 1E and 1F).
167 Indirect damage was caused by BPH, which acts as a vector of grass dwarf virus and empty dwarf viru 167 Indirect damage was caused by BPH, which acts as a vector of grass dwarf virus and empty dwarf virus, causing stunted
168 Ice plants (Figure 1D). Besides Bali or other parts of Indonesia. BPH attacks on rice crops were 168 rice plants (Figure 1D). Besides Bali or other parts of Indonesia, BPH attacks on rice crops were also reported in China,
169 where hopperburn affected 60% of all examined crops (Hu et al. 2014). 169 where hopperburn affected 60% of all examined crops (Hu et al. 2014).
170 A percentage of BPH attacks of more than 50% was found in

¹ ^A percentage of BPH attacks of more than 50% was found in Gianyar, Bangli, Jembrana, and Badung Regencies
171 (Table 2). The BPH population was primarily found in Ciherang and IR-64 varieties of rice in the Badung Re 171 (Table 2). The BPH population was primarily found in Ciherang and IR-64 varieties of rice in the Badung Regency, with 172 43.67 BPH per rice hill (Table 2). Baehaki and Meiava (2015) added that the economic threshold c 172 43.67 BPH per rice hill (Table 2). Baehaki and Mejaya (2015) added that the economic threshold could be measured 173 through the number or population of pests and planting age. BPH is said to have reached the economic threshold when the non-
174 population of this pest was found in the field as many as pine BPH per rice hill when the 174 population of this pest was found in the field, as many as nine BPH per rice hill when the rice age was less than 40 DAP or 175 18 BPH when the rice was more than 40 DAP (Baehaki and Meiava 2015). In general, rice vari 175 18 BPH when the rice was more than 40 DAP (Baehaki and Mejaya 2015). In general, rice varieties grown in all
176 observation locations in Bali were BPH susceptible varieties, such as Ciberang, IR-64, Innari 32, and Sit 176 observation locations in Bali were BPH susceptible varieties, such as Ciherang, IR-64, Inpari 32, and Situbagendit.
177 The dynamics of BPH development in the field can be influenced by several factors, including host

177 The dynamics of BPH development in the field can be influenced by several factors, including host plant factors
178 and natural enemies (Horgan et al. 2015; Kobayashi 2016). The host plant factors that affect the BPH p 178 and natural enemies (Horgan et al. 2015; Kobayashi 2016). The host plant factors that affect the BPH population are related to the age of the rice plant. When the observations were made, the rice plants were still in t 179 related to the age of the rice plant. When the observations were made, the rice plants were still in the vegetative phase, 180 aged 4-6 WAP. According to Jing et al. (2014), naturally. BPH usually comes to young rice f aged 4-6 WAP. According to Jing et al. (2014), naturally, BPH usually comes to young rice fields, and insects usually 181 come in the first two weeks after planting. Thus, the brown planthopper in rice cultivation might be the first generation of 182 planthoppers that have not yet reproduced because one BPH life cycle takes between 3-4 weeks (IRRI 2009).
183 BPH observations in Dennasar, Tabanan, Karangasem, and Klungkung cities were dominated b

183 **BPH** observations in Denpasar, Tabanan, Karangasem, and Klungkung cities were dominated by macroptera
184 imago (Table 2). According to Horgan et al. (2017), the planthopper that first came to the plantation was the m 184 imago (Table 2). According to Horgan et al. (2017), the planthopper that first came to the plantation was the macroptera
185 planthopper as a winged immigrant planthopper. Meanwhile, in Badung, Gianyar, Buleleng, Bangl 185 planthopper as a winged immigrant planthopper. Meanwhile, in Badung, Gianyar, Buleleng, Bangli, and Jembrana
186 regencies nymphal BPH was dominated by BPH and several individuals were in the imago phase of brachintera 186 regencies, nymphal BPH was dominated by BPH, and several individuals were in the imago phase of brachiptera and
187 macroptera The dominance of the nymph phase caused the population of BPH in Badung Gianyar Buleleng Ba 187 macroptera. The dominance of the nymph phase caused the population of BPH in Badung, Gianyar, Buleleng, Bangli, and
188 Jembrana districts to be the highest when compared to the cities of Denpasar, Tabanan, Karangasem, Jembrana districts to be the highest when compared to the cities of Denpasar, Tabanan, Karangasem, and Klungkung. The

189 presence of the brachiptera planthopper might be contributed to the increase in the nymph population (Baehaki and Mejaya
190 2015). According to Horgan et al. (2015), rapid population growth usually occurs in groups wi 2015). According to Horgan et al. (2015), rapid population growth usually occurs in groups with many young individuals.
191 The average intensity of BPH attack on Ciberang and IR-64 varieties of rice was higher than in oth

191 The average intensity of BPH attack on Ciherang and IR-64 varieties of rice was higher than in other varieties. In the Ciherang and IR-64 varieties of rice, the average value of the highest attack intensity was 30% (Fi 192 the Ciherang and IR-64 varieties of rice, the average value of the highest attack intensity was 30% (Figure 2). It is because farmers grow rice varieties Ciherang and IR-64 from year to year without any replacement of 193 farmers grow rice varieties Ciherang and IR-64 from year to year without any replacement of other varieties. Furthermore, 194 rice varieties Ciherang and IR-64 became very susceptible to BPH attacks. In addition, BPH i 194 rice varieties Ciherang and IR-64 became very susceptible to BPH attacks. In addition, BPH is a pest that begins to attack
195 rice plants from a voung age, even when the rice is still in the nursery 195 rice plants from a young age, even when the rice is still in the nursery.
196 Cording to Sawada et al. (1993), fluctuations in BPH pest

196 According to Sawada et al. (1993), fluctuations in BPH pest attacks are more influenced by the growth phase of the rice plant that is the host in the field. BPH pests are often found when rice plants are in the vegetat 197 the rice plant that is the host in the field. BPH pests are often found when rice plants are in the vegetative and generative stages (Bottrell and Schoenly 2012). Horgan et al. (2017) added that BPH pests could damage 198 stages (Bottrell and Schoenly 2012). Horgan et al. (2017) added that BPH pests could damage rice plants at all stages of
199 growth and act as vectors for grass and dwarf viruses. BPH attack was higher when rice was in 199 growth and act as vectors for grass and dwarf viruses. BPH attack was higher when rice was in the vegetative phase than in
200 the generative phase. It happens because the pests attack the young rice stalks. Considerin 200 the generative phase. It happens because the pests attack the young rice stalks. Considering the type of mouth of BPH, which is included in the suction, BPH can suck the liquid from the rice stems and cause the plant l 201 which is included in the suction, BPH can suck the liquid from the rice stems and cause the plant leaves to turn yellow
202 (Anant et al. 2021). According to Choi et al. (2019), during the vegetative phase, food availa 202 (Anant et al. 2021). According to Choi et al. (2019), during the vegetative phase, food availability in the form of nitrogen 203 is abundant in rice plants. Rice plants need nitrogen to form plant organs. Food is one of the factors that affect the life of 204 insects. Oiu et al. (2004) continued that the N element absorbed by plants also serves 204 insects. Qiu et al. (2004) continued that the N element absorbed by plants also serves as a source of nutrition for BPH. If 205 food is available with good quality (suitable for pests), then the insect pest populatio 205 food is available with good quality (suitable for pests), then the insect pest population will increase, and vice versa (Qiu et 206 al. 2004). 206 al. 2004).
207

207 The mtCOI DNA band was only successfully amplified from the total DNA extraction of one imago or nymph 208 and not more than one BPH imago. The mtCOI fragment that was successfully amplified corresponds to a size of +7 208 and not more than one BPH imago. The mtCOI fragment that was successfully amplified corresponds to a size of \pm 710 bp in all samples from nine districts in Bali, namely Badung, Gianyar, Klungkung, Bangli, Karangasem 209 in all samples from nine districts in Bali, namely Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar
210 City, Buleleng, and Jembrana (Figure 3). Nucleotide and amino acid sequence analysis showed high 210 City, Buleleng, and Jembrana (Figure 3). Nucleotide and amino acid sequence analysis showed high homology with *N*. 211 *lugens* sequences in the database at GenBank, 94.2 – 99.7% and 95.8 - 100%, respectively (Table 3 211 *lugens* sequences in the database at GenBank, 94.2 – 99.7% and 95.8 - 100%, respectively (Table 3). *N. lugens* sequences 212 from Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana showed the
213 highest nucleotide, and amino acid homology with N. lugens isolate FSD-034 from Pakistan (MK301229) bio 213 highest nucleotide, and amino acid homology with *N. lugens* isolate FSD-034 from Pakistan (MK301229) biotype Y, respectively. 99.5 -99.74% and 100% (Table 3). The results of the molecular detection of *N. lugens* usin 214 respectively. 99.5 -99.74% and 100% (Table 3). The results of the molecular detection of *N. lugens* using the PCR method 215 in Bali, Indonesia, are the first reports of the molecular character of *N. lugens* in Indonesia.

216 Samples from Indonesia formed a group with *N. lugens* biotype Y fragment mtCOI from Pakistan, India, South 217 Korea, and China (Figure 4). This study found *N. lugens* biotype Y in rice plants for the first time in I 217 Korea, and China (Figure 4). This study found *N. lugens* biotype Y in rice plants for the first time in Indonesia. The 218 Indonesian sample did not form separate groups according to the proximity of the district locations but formed a polytomy
219 cladogram (Figure 4). This polytomy cladogram shows that the *N. lugens* between regencies (219 cladogram (Figure 4). This polytomy cladogram shows that the *N. lugens* between regencies (Badung, Gianyar, 220 Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana) were observed to have the 220 Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana) were observed to have the same
221 ancestry. These results indicate high locomotion ability with genetic mixing between N. lugens in Bali i 221 ancestry. These results indicate high locomotion ability with genetic mixing between *N. lugens* in Bali isolates. Similar
222 conditions were also demonstrated in *N. lugens* among Asian isolates using mitochondrial s 222 conditions were also demonstrated in *N. lugens* among Asian isolates using mitochondrial sequences showing genetic
223 mixing. It can also be correlated with the theory of long-distance migration of *N. lugens*, which 223 mixing. It can also be correlated with the theory of long-distance migration of *N. lugens*, which migrates from the tropics (northern Vietnam) in April-May to temperate regions (China, Korea, and Japan) in June-July a 224 (northern Vietnam) in April-May to temperate regions (China, Korea, and Japan) in June-July as shown based on
225 meteorological studies (Otuka et al. 2008). The population of *N. lugens* is a long-distance migratory f 225 meteorological studies (Otuka et al. 2008). The population of *N. lugens* is a long-distance migratory flight from the tropics 226 to temperate Asia before modern pesticides are widely used in tropical rice. Due to the infrequent use of insecticides prior 227 to the 1960s in the tropics, factors other than insecticides may have triggered long-wing 227 to the 1960s in the tropics, factors other than insecticides may have triggered long-wing movements to form *N. lugens* nopulations (Bottrell and Schoenly 2012). 228 populations (Bottrell and Schoenly 2012).
229 In previous studies in Indonesia,

229 In previous studies in Indonesia, BPH biotypes 1, 2, 3, and 4 have been found. Chen et al. (2011) reported that the
230 brown planthopper is a highly adaptive insect because it can form new biotypes In early 1975 the I 230 brown planthopper is a highly adaptive insect because it can form new biotypes. In early 1975 the IR-26 rice variety from
231 IRRI Philippines was introduced. The IR-26 variety was unique because it contained a Bph1 re 231 IRRI Philippines was introduced. The IR-26 variety was unique because it contained a Bph1 resistant gene to anticipate
232 fluctuations in the brown planthopper population. However, in 1976 there was a great population 232 fluctuations in the brown planthopper population. However, in 1976 there was a great population explosion in several rice
233 production centers due to changes in the brown planthopper population from biotype 1 to biot 233 production centers due to changes in the brown planthopper population from biotype 1 to biotype 2. As an anticipatory measure against brown planthopper biotype 2, in 1980, the IR-42 rice variety (containing the bph2 re 234 measure against brown planthopper biotype 2, in 1980, the IR-42 rice variety (containing the bph2 resistant gene) was
235 introduced from IRRI Philippines. Unfortunately, in 1981 there was another explosion in the brow 235 introduced from IRRI Philippines. Unfortunately, in 1981 there was another explosion in the brown planthopper
236 population in Simalungun, North Sumatra, and several other areas due to changes in the brown planthopper 236 population in Simalungun, North Sumatra, and several other areas due to changes in the brown planthopper population
237 from biotype 2 to biotype 3. To deal with the brown planthopper biotype 3, rice variety IR-56 was 237 from biotype 2 to biotype 3. To deal with the brown planthopper biotype 3, rice variety IR-56 was introduced (containing the gene bph3 resistance) in 1983 and IR-64 (containing the bph1+ resistance gene) in 1986. The i 238 the gene bph3 resistance) in 1983 and IR-64 (containing the bph1+ resistance gene) in 1986. The introduction process
239 continues In 1991 the IR-74 variety (containing the bph3 resistant gene) was introduced In 2006 t 239 continues. In 1991, the IR-74 variety (containing the bph3 resistant gene) was introduced. In 2006, the resistance gene IR-
240 64 was broken because the brown planthopper population changed to biotype 4. The stability 240 64 was broken because the brown planthopper population changed to biotype 4. The stability of the biotype zero brown
241 blanthoppers persisted for 41 years before becoming brown planthopper biotype 1. The change of br 241 planthoppers persisted for 41 years before becoming brown planthopper biotype 1. The change of brown planthopper biotype 1 to biotype 2 only took 4 years, and the change of biotype 2 brown planthopper to biotype 3 with 242 biotype 1 to biotype 2 only took 4 years, and the change of biotype 2 brown planthopper to biotype 3 within 5 years. Until 243 2005, the brown planthopper biotype 3 was still dominated by biotype 3, and in 2006 the bio 243 2005, the brown planthopper biotype 3 was still dominated by biotype 3, and in 2006 the biotype 4 brown planthopper 244 began to develop. The long existence of the biotype 3 brown planthopper was caused by the development of the IR-64
245 (bph1+) variety over a long period. IR-64 is a resistant variety (durable resistance) that can with 245 (bph1+) variety over a long period. IR-64 is a resistant variety (durable resistance) that can withstand changes in brown planthoppers to a more virulent biotype.

Commented [A3]: It need supporting reference

247 The continuous cultivation of IR-64 rice varieties by farmers in Bali led to the emergence of a new biotype BPH,
248 namely Y Insects of biotype Y originated from biotype 1 by eating YHY15 resistant varieties for more 248 namely Y. Insects of biotype Y originated from biotype 1 by eating YHY15 resistant varieties for more than two years for
249 33 generations (Jing et al. 2012) Rice varieties YHY15 carry the Bnh15 resistance gene (Jing 249 33 generations (Jing et al. 2012). Rice varieties YHY15 carry the Bph15 resistance gene (Jing et al. 2012).
250 This study shows great potential in the population of N. lugens to adapt to previously resistant ri

250 This study shows great potential in the population of *N. lugens* to adapt to previously resistant rice varieties. This 251 study reported that rice varieties Situbagendit and Inpari 32, previously resistant to BPH, we 251 study reported that rice varieties Situbagendit and Inpari 32, previously resistant to BPH, were susceptible to BPH. This
252 sesearch can provide information to farmers not to continuously plant susceptible varieties, 252 research can provide information to farmers not to continuously plant susceptible varieties, which could cause BPH
253 epidemics in the field as well as the emergence of new more virulent BPH biotypes. Thus a new contr 253 epidemics in the field, as well as the emergence of new, more virulent BPH biotypes. Thus a new control strategy based on a forecasting system can be developed for the regional management of this insect. a forecasting system can be developed for the regional management of this insect.

255

256 **CONCLUTIONS**

257 *N. lugens* that attacks rice plants in Bali (Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar 258 City, Buleleng, and Jembrana) belongs to biotype Y. Symptoms of damage to rice plants are most severe in Badung
259 Regency. Apart from Ciherang and IR-64 varieties, Situbagendit and Inpari 32 varieties are susceptible 259 Regency. Apart from Ciherang and IR-64 varieties, Situbagendit and Inpari 32 varieties are susceptible to BPH attack.

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1 **TABLES LIST**

 $\begin{array}{c} 4 \\ 5 \\ 6 \end{array}$

 $\begin{array}{c} 1 \\ 2 \\ 3 \end{array}$

2 **Table 3.** Nucleotide (nt) and amino acid (aa) homology of *N. lugens* in rice from Bali, Indonesia, compared with *N. lugens* from other countries in GenBank

Isolate	Origin - of	Biotype	Accession	Homology nt (aa) $(\%)$ N. lugens IDN								
	isolate		number	Denpasar	Badung	Gianvar	Tabanan	Buleleng	Karangasem	Klungkung	Bangli	Jembrana
FSD-034	PAK		MK301229	99.5 (100)	99.6 (100)	99.5 (100)	99.5 (100)	99.6 (100)	99.5 (100)	99.7 (100)	99.5(100)	99.6 (100)
HZZ55	IND		MK032794	99.4 (100)	99.5 (100)	99.4 (100)	99.5(100)	99.4 (100)	99.5 (100)	99.6 (100)	99.5(100)	99.6 (100)
SAEVG Morph0111	IND		MN520923	99.4 (100)	99.5(100)	99.4 (100)	99.5 (100)	99.4 (100)	99.5 (100)	99.5(100)	99.5 (100)	99.6 (100)
KBPH	KOR		MK590088	99.3 (100)	99.5 (100)	99.4 (100)	99.4 (100)	99.3 (100)	99.4 (100)	99.4 (100)	99.4 (100)	99.5 (100)
KOREA BPH	KOR		LC461184	99.3 (100)	99.5 (100)	99.4 (100)	99.4 (100)	99.3 (100)	99.4 (100)	99.4 (100)	99.4 (100)	99.5 (100)
WUHAN-Y	CHN		KC333653	99.3 (100)	99.5 (100)	99.4 (100)	99.4 (100)	99.3 (100)	99.4 (100)	99.4 (100)	99.3 (100)	99.4 (100)
WUHAN-3	CHN		JN563997	97.8 (98.1)	97.2 (97.8)	97.5 (98.9)	97.5 (98.9)	97.4 (97.9)	97.8 (98.1)	97.5 (98.9)	97.2 (98.8)	97.6 (98.0)
WUHAN-2	CHN		JN563996	96.3 (97.5)	96.3 (97.5)	96.4 (97.5)	96.3 (97.5)	96.2(97.4)	96.4 (97.5)	96.3 (97.5)	96.2 (97.4)	96.3 (97.5)
WUHAN-1	CHN		JN563995	95.3 (96.7)	95.4 (96.7)	95.3 (96.7)	95.4 (96.7)	95.6 (96.8)	95.6 (96.8)	95.3 (96.7)	95.4 (96.7)	95.3 (96.7)
GX	CHN		LC461186	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)	95.4 (96.7)	95.5 (96.8)	95.5 (96.8)	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)
Gangavathi	IND		OL451531	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)	95.5 (96.8)	95.5 (96.8)	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)
WUHAN-L	CHN		KC333654	94.2 (95.8)	94.4 (96.2)	94.2 (95.8)	94.4 (96.2)	94.3 (96.0)	94.4 (96.2)	94.2 (95.8)	94.4 (96.2)	94.4 (96.2)
N. bakeri	CHN	$\overline{}$	JX266790	84.6 (85.6)	85.2 (86.1)	84.8 (85.9)	84.8 (85.9)	84.6 (85.6)	85.2 (86.1)	84.8 (85.9)	85.2 (86.1)	85.2(86.1)
Sogatella furcifera	CHN		HM160123	75.6 (76.9)	75.6 (76.9)	76.2 (77.8)	77.6 (78.4)	77.4 (78.4)	76.8 (77.8)	75.6 (76.9)	76.8 (77.8)	77.6 (78.4)

3 Notes: nt (nucleotide), aa (amino acid), IDN (Indonesia), PAK (Pakistan), IND (India), KOR (South Korea), CHN (China), *N. bakeri* and *Sogatella furcifera* from China was used as outgroups

4

 $\frac{1}{2}$

5

26

27 **Figure 2.** The attack intensity of *N. lugens* on rice in Bali Province

Figure 4. The cladogram of the mtCOI fragment of *N. lugens* from eastern Indonesia, Bali (Badung, Gianyar, Klungkung, Bangli,

Xarangasem, Tabanan, Denpasar City, Buleleng, and Jembrana) was compared with mtCOI fragment

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13
 14 14 **For possibility publication on the journal:**

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16

17 **Novelty:**

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Population dynamics and damage intensity of brown planthopper (BPH) and *Nilaparvata lugens* (Stal.) provide information about the economic threshold status of *N. lugens* in Bali. This study enriched information on the genetic diversity of *N. lugens* isolates from eastern Indonesia, particularly Bali. It is the first report of *N. lugens* biotype Y in Indonesia. In addition, the latest information in this study is that rice varieties Situbagendit and Inpari 32, which were previously resistant to BPH, are now found to be susceptible to BPH. This information is critical as a basis for controlling *N. lugens* in Indonesia

$\frac{19}{20}$ $Statements:$

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21

Place and date: Denpasar July 2022

29 (fill in your name, no need scanned autograph) Listihani Listihani

80 2018). As ITS sequences have low intra-species variation but high variation between species, they are helpful for species classification and phylogenetic analysis for morphologically similar organisms, both in prokaryot 81 classification and phylogenetic analysis for morphologically similar organisms, both in prokaryotes and eukaryotes (Liu et al. 2009). Finally, from the molecular identification of the combined mitochondrial COI-COII and 82 al. 2009). Finally, from the molecular identification of the combined mitochondrial COI-COII and ten microsatellite 83 marker loci (Winnie et al. $[2020]$. marker loci (Winnie et al. 2020).

85 **MATERIALS AND METHODS**

86 **Brown Planthopper Sampling from Rice Dwarf Disease Endemic Areas**

87 Samples were taken from nine locations in Bali Province (Badung, Gianyar, Klungkung, Bangli, Karangasem, 88 Tabanan, Denpasar City, Buleleng, and Jembrana). The brown planthopper samples taken from rice plants were nymp 88 Tabanan, Denpasar City, Buleleng, and Jembrana). The brown planthopper samples taken from rice plants were nymphs 89 and imagos. Nymphs and imagos were used for total DNA extraction. After arriving at the laboratory, the nymphs and imago were stored dry at -20°C. imago were stored dry at -20°C.

92 **Observation of BPH Attack Symptoms and Quantity of BPH Population/rice hill**

91
92
93
94 93 Observation of symptoms of BPH attack was carried out by observing symptoms of damage to rice plants due to 94 BPH attack. The abundance of the BPH/rice hill population was obtained by counting all nymphs and imagoes obtained.
95 Data on the population per cluster from 20 samples at each observation location were then averaged. Data on the population per cluster from 20 samples at each observation location were then averaged.

96
97 97 **BPH Attack Percentage**

The percentage of BPH attacks is calculated using the following formula:

$$
P = \frac{a}{b} \times 100\%
$$

 $\frac{99}{100}$ 100 Note:
101 $P = A$

84

101 $P =$ Attack percentage (%)
102 $a =$ Number of rice hills af

102 a = Number of rice hills affected by BPH
103 b = Number of rice hills observed

 $b =$ Number of rice hills observed

104 105 **Damage Intensity**

106 Determination of scoring on symptoms of rice damage due to BPH attack is based on Table 1. The intensity of damage due to a BPH attack is determined using the formula: damage due to a BPH attack is determined using the formula:

$$
I = \sum_{i=1}^{N i x V i} V x 100\%
$$

108 109

110

111

Commented [A11]: please explain the primary specifications!

Commented [A12]: please add to reference on the genetic diversity of N. lugens

- 112 Note:
113 $I = D$
- 113 I = Damage intensity
114 Ni = The number of a
- 114 $\text{Ni} = \text{The number of affected rice hills on the score i}$
115 $\text{Vi} = \text{Score}$ i
- 115 $Vi = Score i$
116 $N = The num$
- $N =$ The number of rice hills observed $117 \quad Z =$ Highest score
-

118
119 119 **Total DNA Extraction from Brown Planthopper**

120 Total DNA extraction of brown planthopper was obtained from one individual imago or one individual nymph.
121 One individual imago was put into a microtube and then added with 100 ul of CTAB extraction buffer (2% CTAB, 121 One individual imago was put into a microtube and then added with 100 μl of CTAB extraction buffer (2% CTAB, 1.4 M
122 NaCl 100 mM Tris-HCl 20 mM EDTA and 1% PVP (-40 °C)) Next 1 μl of proteinase K was added then the 122 NaCl, 100 mM Tris-HCI, 20 mM EDTA, and 1% PVP (-40 °C)). Next, 1 µl of proteinase K was added, then the insects were crushed using a micro-pistil, vortexed, and incubated in a water bath of 65 °C. After that, the tube 123 were crushed using a micro-pistil, vortexed, and incubated in a water bath of 65° C. After that, the tube was added with 100
124 ul CI (chloroform: isoamyl alcohol) in a ratio of 24:1. The tube was then vortexed f 124 μl CI (chloroform: isoamyl alcohol) in a ratio of 24:1. The tube was then vortexed for 3 minutes and centrifuged at 10,000 125 rpm for 15 minutes. The supernatant formed was transferred to a new microtube (60 μl) and then added with 3 M NaOAc 126 (pH 5.2), as much as 1/10 of the total volume of the supernatant. Isopropanol was added up to $2/3$ of the total volume of the supernatant, then incubated at -20° C for one night. The tube was centrifuged at 10.00 127 the supernatant, then incubated at -20°C for one night. The tube was centrifuged at 10,000 rpm for 10 min, and the supernatant was discarded. The pellets were washed with 100 μ l of 80% ethanol (cold) and centrifuged 128 supernatant was discarded. The pellets were washed with 100 μl of 80% ethanol (cold) and centrifuged at 8000 rpm for 5
129 minutes. In the final step, the supernatant was removed, and the pellet was dried for approxim 129 minutes. In the final step, the supernatant was removed, and the pellet was dried for approximately 1 hour. It was then added with a solution of 20 μ l TE and stored at -20°C until used. added with a solution of 20 μl TE and stored at -20°C until used.

131 **132 Amplification of mtCOI Fragments Using the PCR Method**
133 **PCR** reactants were manufactured with a total volument

133 PCR reactants were manufactured with a total volume of 25 μl consisting of 12.5 μl Go Tag Green Master Mix
134 and 9.5 μl ddH2O. DNA amplification of the mtCOI fragment was carried out using a pair of universal primer 134 and 9.5 μl ddH2O. DNA amplification of the mtCOI fragment was carried out using a pair of universal primers mtCOI 135 LCO 1490 (3'-GGTCAACAAATCATAAAGATATTGG-5') and HCO 2198 (5'TAAACTTCA GGGTGACCA 135 LCO 1490 (3'-GGTCAACAAATCATAAAGATATTGG-5') and HCO 2198 (5TAAACTTCA GGGTGACCA
136 AAAAATCA-3') (Folmer et al. 1994) each 1 ul. and 1 ul DNA template. PCR reactions were carried out with a Perkin 136 AAAAATCA-3') (Folmer et al. 1994) each 1 μl, and 1 μl DNA template. PCR reactions were carried out with a Perkin
137 Elmer 480 Thermocycler. The PCR reaction was initiated by initial denaturation for 5 min at 94°C. Th 137 Elmer 480 Thermocycler. The PCR reaction was initiated by initial denaturation for 5 min at 94°C. The PCR was continued for 35 cycles in the following order: 94° C for 1 minute. 52° C for 35 seconds. 72° C 138 continued for 35 cycles in the following order: 94° C for 1 minute, 52° C for 35 seconds, 72° C for 1 minute 30 seconds, and a final extension of 72° C for 7 minutes. The PCR results were then analyzed 139 a final extension of 72°C for 7 minutes. The PCR results were then analyzed in 1% agarose gel. The DNA fragments of the DNA fragments of the DNA fragments of the DNA fragments of the PCR resultion for 15 140 mtCOI were visualized using a UV transilluminator after being immersed in a 2% ethidium bromide solution for 15
141 minutes and photographed with a digital camera minutes and photographed with a digital camera.

142
143 143 **Analysis of DNA Sequence Results**

144 Nucleotide Sequencing DNA fragment purification and mtCOI nucleotide sequencing were performed at PT. 1st
145 Base Malaysia The results were then registered in the NCBI gene bank (http://www.nchi.nlm.nih.gov) Analysis 145 Base, Malaysia. The results were then registered in the NCBI gene bank (http://www.ncbi.nlm.nih.gov). Analysis of mtCOI DNA sequence data ChromasPro program was used to combine forward and reverse nucleotide sequences 146 mtCOI DNA sequence data ChromasPro program was used to combine forward and reverse nucleotide sequences to obtain
147 the mtCOI genel. The Bioedit program was used to compare mtCOI fragments between samples (Multiple a the mtCOI gene. The Bioedit program was used to compare mtCOI fragments between samples (Multiple alignments) 148 (Hall 1999). The phylogenetic relationship was built by comparing the mtCOI sample fragments from the brown
149 planthopper from Indonesia with the mtCOI fragments already stored in the NCBI GenBank 149 planthopper from Indonesia with the mtCOI fragments already stored in the NCBI GenBank
150 (http://www.ncbi.nlm.nih.gov). The criteria for retrieving mtCOI fragments at GenBank were fragments with a nucleotide 150 (http://www.ncbi.nlm.nih.gov). The criteria for retrieving mtCOI fragments at GenBank were fragments with a nucleotide base length of \pm 800 bp (Boykin et al. 2007) (Table 1). The phylogenetic tree was constructed using the PAUP 4.0b10 152 program (Swofford 2002) with the maximum parsimony cladistic quantitative method. The cladogram was compiled using
153 the Heuristic method. The cladogram used results from the strick consensus with the statistical boo 153 the Heuristic method. The cladogram used results from the strick consensus with the statistical bootstrap test to obtain a 164 100% probability 100% probability.

155 **RESULTS AND DISCUSSION**

156 The brown planthopper causes direct and indirect damage \underline{to} rice plants. Direct damage was in the form of stunted
157 and uneven growth of rice plants (Figure 1A and 1B), vellow plants (Figure 1C), and hopperburn 157 and uneven growth of rice plants (Figure 1A and 1B), yellow plants (Figure 1C), and hopperburn caused by fluid in rice
158 plant cells sucked by BPH nymphs, brachiptera (Fig. short wings), and macroptera (long wings) (158 plant cells sucked by BPH nymphs, brachiptera (Fig. short wings), and macroptera (long wings) (Figures 1E and 1F).
159 Indirect damage was caused by BPH, which acts as a vector of grass dwarf virus and empty dwarf viru 159 Indirect damage was caused by BPH, which acts as a vector of grass dwarf virus and empty dwarf virus, causing stunted 160 rice plants (Figure 1D). Besides Bali or other parts of Indonesia, BPH attacks on rice crops wer rice plants (Figure 1D). Besides Bali or other parts of Indonesia, BPH attacks on rice crops were also reported in China, 161 where hopperburn affected 60% of all examined crops.

162 A percentage of BPH attacks of more than 50% was found in Gianyar, Bangli, Jembrana, and Badung Regencies 163 (Table 2). The BPH population was primarily found in Ciherang and IR-64 varieties of rice in the Badung Regency, with 164 43.67 BPH per rice hill (Table 2). Baehaki and Mejaya (2015) added that the economic threshold could be measured through the number or population of pests and planting age. BPH is said to have reached the economic thr 165 through the number or population of pests and planting age. BPH is said to have reached the economic threshold when the 166 population of this pest was found in the field, as many as nine BPH per rice hill when the ric 166 population of this pest was found in the field, as many as nine BPH per rice hill when the rice age was less than 40 DAP or 167 18 BPH when the rice was more than 40 DAP (Baehaki and Mejaya 2015). In general, rice varieties grown in all 168 observation locations in Bali were BPH susceptible varieties, such as Ciherang, IR-64, Inpari 32, and Sit 168 observation locations in Bali were BPH susceptible varieties, such as Ciherang, IR-64, Inpari 32, and Situbagendit.

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169 The dynamics of BPH development in the field can be influenced by several factors, including host plant factors and natural enemies (Horgan et al. 2015; Kobayashi 2016). The host plant factors that affect the BPH popul 170 and natural enemies (Horgan et al. 2015; Kobayashi 2016). The host plant factors that affect the BPH population are related to the age of the rice plant. When the observations were made, the rice plants were still in t 171 related to the age of the rice plant. When the observations were made, the rice plants were still in the vegetative phase.
172 According to Jing et al. (2014), naturally, BPH usually comes to young rice fields, and ins 172 According to Jing et al. (2014), naturally, BPH usually comes to young rice fields, and insects usually come in the first two weeks after planting. Thus, the brown planthopper in rice cultivation might be the first gen 173 weeks after planting. Thus, the brown planthopper in rice cultivation might be the first generation of planthoppers that have not vert reproduced because one BPH life cycle takes between $3-4$ weeks (IRRI 2009). 174 have not yet reproduced because one BPH life cycle takes between 3-4 weeks (IRRI 2009).
175 **BPH** observations in Dennasar. Tabanan. Karangasem, and Klungkung cities w

175 BPH observations in Denpasar, Tabanan, Karangasem, and Klungkung cities were dominated by macroptera
176 imago, According to Horgan et al. (2017), the planthopper that first came to the plantation was the macroptera pl 176 imago. According to Horgan et al. (2017), the planthopper that first came to the plantation was the macroptera planthopper as a winged immigrant planthopper. In Badung, Gianyar, Buleleng, Bangli, and Jembrana regencies 177 as a winged immigrant planthopper. In Badung, Gianyar, Buleleng, Bangli, and Jembrana regencies, nymphal BPH was dominated by BPH, and several individuals were in the imago phase of brachiptera and macroptera. The domi 178 dominated by BPH, and several individuals were in the imago phase of brachiptera and macroptera. The dominance of the number of the number of the highest 179 nymph phase caused the population of BPH in Badung. Gianyar, 179 nymph phase caused the population of BPH in Badung, Gianyar, Buleleng, Bangli, and Jembrana districts to be the highest 180 when compared to the cities of Denpasar, Tabanan, Karangasem, and Klungkung. The presence of t 180 when compared to the cities of Denpasar, Tabanan, Karangasem, and Klungkung. The presence of the brachiptera
181 planthopper might be contributed to the increase in the nymph population (Baehaki and Mejaya 2015). 181 planthopper might be contributed to the increase in the nymph population (Baehaki and Mejaya 2015).
182 The average intensity of BPH attack on Ciherang and IR-64 varieties of rice was higher than

182 The average intensity of BPH attack on Ciherang and IR-64 varieties of rice was higher than in other varieties. In
183 the Ciherang and IR-64 varieties of rice, the average value of the highest attack intensity was 30% 183 the Ciherang and IR-64 varieties of rice, the average value of the highest attack intensity was 30% (Figure 2). It is because farmers grow rice varieties Ciherang and IR-64 from vear to vear without any replacement of 184 farmers grow rice varieties Ciherang and IR-64 from year to year without any replacement of other varieties. Furthermore, 185 rice varieties Ciherang and IR-64 became very susceptible to BPH attacks. In addition, BPH i 185 rice varieties Ciherang and IR-64 became very susceptible to BPH attacks. In addition, BPH is a pest that begins to attack 186 rice plants from a young age, even when the rice is still in the nursery. 186 rice plants from a young age, even when the rice is still in the nursery.
187 Cacording to Sawada et al. (1993), fluctuations in BPH pest

187 According to Sawada et al. (1993), fluctuations in BPH pest attacks are more influenced by the growth phase of
188 the rice plant that is the host in the field. BPH pests are often found when rice plants are in the veg 188 the rice plant that is the host in the field. BPH pests are often found when rice plants are in the vegetative and generative stages (Bottrell and Schoenly 2012). Horgan et al. (2017) added that BPH pests could damage 189 stages (Bottrell and Schoenly 2012). Horgan et al. (2017) added that BPH pests could damage rice plants at all stages of growth and act as vectors for grass and dwarf viruses. BPH attack was higher when rice was in the 190 growth and act as vectors for grass and dwarf viruses. BPH attack was higher when rice was in the vegetative phase than in the generative phase. It happens because the pests attack the young rice stalks. Considering th 191 the generative phase. It happens because the pests attack the young rice stalks. Considering the type of mouth of BPH, which is included in the suction. BPH can suck the liquid from the rice stems and cause the plant l 192 which is included in the suction, BPH can suck the liquid from the rice stems and cause the plant leaves to turn yellow
193 (Anant et al. 2021). According to Choi et al. (2019), during the vegetative phase, food availa 193 (Anant et al. 2021). According to Choi et al. (2019), during the vegetative phase, food availability in the form of nitrogen 194 is abundant in rice plants. Rice plants need nitrogen to form plant organs. Food is one of the factors that affect the life of insects. Out et al. (2004) continued that the N element absorbed by plants also serves as a 195 insects. Qiu et al. (2004) continued that the N element absorbed by plants also serves as a source of nutrition for BPH. If 196 food is available with good quality, then the insect pest population will increase, and vice versa (Qiu et al. 2004).
197 The mtCOI DNA band was only successfully amplified from the total DNA extraction of one imago

197 The mtCOI DNA band was only successfully amplified from the total DNA extraction of one imago or nymph
198 and not more than one BPH imago. The mtCOI fragment that was successfully amplified corresponds in all samples 198 and not more than one BPH imago. The mtCOI fragment that was successfully amplified corresponds $\ln|\text{all samples from}}$ nine districts in Bali, namely Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Bulelen 199 nine districts in Bali, namely Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and
200 Jembrana (Figure 3). Nucleotide and amino acid sequence analysis showed high homology with N. lug 200 Jembrana (Figure 3). Nucleotide and amino acid sequence analysis showed high homology with *N. lugens* sequences in the database at GenBank, 94.2 – 99.7% and 95.8 - 100% (Table 3). *N. lugens* sequences from Badung, Gi 201 database at GenBank, 94.2 – 99.7% and 95.8 - 100% (Table 3). *N. lugens* sequences from Badung, Gianyar, Klungkung, 202 Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana showed the highest nucleotide, and amino acid
203 homology with N. lugens isolate FSD-034 from Pakistan (MK301229) biotype Y, respectively. 99.5 -99.74 203 homology with *N. lugens* isolate FSD-034 from Pakistan (MK301229) biotype Y, respectively. 99.5 -99.74% and 100%, 204 respectively (Table 3). The results of the molecular detection of *N. lugens* using the PCR method in Bali, Indonesia, are 205 the first reports of the molecular character of *N. lugens* in Indonesia. 205 the first reports of the molecular character of *N. lugens* in Indonesia.
206 Samples from Indonesia formed a group with *N. lugens* bi

206 Samples from Indonesia formed a group with *N. lugens* biotype Y fragment mtCOI from Pakistan, India, South 207 Korea, and China (Figure 4). This study found *N. lugens* biotype Y in rice plants for the first time in I 207 Korea, and China (Figure 4). This study found *N. lugens* biotype Y in rice plants for the first time in Indonesia. The 208 Indonesian sample did not form separate groups according to the proximity of the district loc 208 Indonesian sample did not form separate groups according to the proximity of the district locations but formed a polytomy
209 cladogram (Figure 4). This polytomy cladogram shows that the *N. lugens* between regencies (209 cladogram (Figure 4). This polytomy cladogram shows that the *N. lugens* between regencies (Badung, Gianyar, 210 Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana) were observed to have the 210 Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana) were observed to have the same
211 ancestry These results indicate high locomotion ability with genetic mixing between N *lugens* in Bali i 211 ancestry. These results indicate high locomotion ability with genetic mixing between *N. lugens* in Bali isolates. Similar conditions were also demonstrated in *N. lugens* among Asian isolates using mitochondrial seque 212 conditions were also demonstrated in *N. lugens* among Asian isolates using mitochondrial sequences showing genetic 213 mixing. It can also be correlated with the theory of long-distance migration of *N. lugens*, which 213 mixing. It can also be correlated with the theory of long-distance migration of *N. lugens*, which migrates from the tropics (northern Vietnam) in April-May to temperate regions (China, Korea, and Japan) in June-July a 214 (northern Vietnam) in April-May to temperate regions (China, Korea, and Japan) in June-July as shown based on 215 meteorological studies (Otuka et al. 2008).
216 In previous studies in Indonesia.

216 In previous studies in Indonesia, BPH biotypes 1, 2, 3, and 4 have been found. Chen et al. (2011) reported that the 217 brown planthopper is a highly adaptive linesed. In early 1975 the IR-26 rice variety from IRRI Phi 217 brown planthopper is a highly adaptive insect. In early 1975 the IR-26 rice variety from IRRI Philippines was introduced.
218 The IR-26 variety was unique because it contained a Bph1 resistant gene to anticipate fluctu 218 The IR-26 variety was unique because it contained a Bph1 resistant gene to anticipate fluctuations in the brown
219 planthopper population. However, in 1976 there was a great population explosion in several rice produc 219 planthopper population. However, in 1976 there was a great population explosion in several rice production centers due to changes in the brown planthopper population from biotype 1 to biotype 2. As an anticipatory meas 220 changes in the brown planthopper population from biotype $\hat{1}$ to biotype 2. As an anticipatory measure against brown 221 planthopper biotype 2, in 1980, the IR-42 rice variety (containing the bph2 resistant gene) w 221 planthopper biotype 2, in 1980, the IR-42 rice variety (containing the bph2 resistant gene) was introduced from IRRI
222 Philippines. Unfortunately, in 1981 there was another explosion in the brown planthopper populati 222 Philippines. Unfortunately, in 1981 there was another explosion in the brown planthopper population in Simalungun, 223 North Sumatra, and several other areas due to changes in the brown planthopper population from biot 223 North Sumatra, and several other areas due to changes in the brown planthopper population from biotype 2 to biotype 3.
224 To deal with the brown planthopper biotype 3, rice variety IR-56 was introduced (containing the 224 To deal with the brown planthopper biotype 3, rice variety IR-56 was introduced (containing the gene bph3 resistance) in 225 1983 and IR-64 (containing the bph1+ resistance gene) in 1986. The introduction process conti 225 1983 and IR-64 (containing the bph1+ resistance gene) in 1986. The introduction process continues. In 1991, the IR-74 variety (containing the bph3 resistant gene) was introduced. In 2006, the resistance gene IR-64 was variety (containing the bph3 resistant gene) was introduced. In 2006, the resistance gene IR-64 was broken because the 227 brown planthopper population changed to biotype 4. The stability of the biotype zero brown planthoppers persisted for 41
228 vears before becoming brown planthopper biotype 1. The change of brown planthopper biotype 1 228 years before becoming brown planthopper biotype 1. The change of brown planthopper biotype 1 to biotype 2 only took 4

Commented [A23]: add a little explanation about the insect population

Commented [A24]: suitable for pests

Commented [A25]: to a size of ±710 bp in all.

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Commented [A27]: Add to explanation population of N. lugens **Commented [A28]:** why can be highly adaptive insect, Because.

229 years, and the change of biotype 2 brown planthopper to biotype 3 within 5 years. Until 2005, the brown planthopper 2 300 biotype 3 was still dominated by biotype 3 and in 2006 the biotype 4 brown planthopper began to 230 biotype 3 was still dominated by biotype 3, and in 2006 the biotype 4 brown planthopper began to develop.
231 The continuous cultivation of IR-64 rice varieties by farmers in Bali led to the emergence of a ne

231 The continuous cultivation of IR-64 rice varieties by farmers in Bali led to the emergence of a new biotype BPH,
232 namely Y. Insects of biotype Y originated from biotype 1 by eating YHY15 resistant varieties for more 232 namely Y. Insects of biotype Y originated from biotype 1 by eating YHY15 resistant varieties for more than two years for 233 generations (Jing et al. 2012). Rice varieties YHY15 carry the Bph15 resistance gene (Jing et 233 33 generations (Jing et al. 2012). Rice varieties YHY15 carry the Bph15 resistance gene (Jing et al. 2012).
234 This study shows great notential in the population of N *lugens* to adant to previously resistant rights

234 This study shows great potential in the population of *N. lugens* to adapt to previously resistant rice varieties. This
235 study reported that rice varieties Situbagendit and Inpari 32, previously resistant to BPH, we 235 study reported that rice varieties Situbagendit and Inpari 32, previously resistant to BPH, were susceptible to BPH. This
236 research can provide information to farmers not to continuously plant susceptible varieties, 236 research can provide information to farmers not to continuously plant susceptible varieties, which could cause BPH
237 epidemics in the field, as well as the emergence of new, more virulent BPH biotypes. Thus a new con 237 epidemics in the field, as well as the emergence of new, more virulent BPH biotypes. Thus a new control strategy based on a forecasting system can be developed for the regional management of this insect a forecasting system can be developed for the regional management of this insect. 239

240 **CONCLUTIONS**

241 *N. lugens* that attacks rice plants in Bali (Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar 242 City, Buleleng, and Jembrana) belongs to biotype Y. Symptoms of damage to rice plants are most severe in Badung 243 Regency. Apart from Ciherang and IR-64 varieties, Situbagendit and Inpari 32 varieties are susceptible to BPH attack.

244 **ACKNOWLEDGEMENTS**

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1 **TABLES LIST**

Score	Appearance	Description
Ω	Healthy	No planthopper was found in any rice hill.
	Very light damage	The rice hills occupied by the planthoppers did not show dead midribs, few exuviae, and the rice stalks had not yet overgrown with Dematium and Cladosporium fungi that followed the brown planthopper attack.
3	Slightly damaged	The rice hills occupied by the planthoppers have shown dead midribs, many exuviae, and the rice stems are overgrown with Dematium and Cladosporium fungi that follow the brown planthopper attack.
5	Heavily damaged	Rice hills inhabited by planthoppers showed damage marked by many dead midribs, many exuviae, stunted and black-looking tillers, and overgrown with Dematium and Cladosporium fungi.
7	Partially dead	Some of the stems in the rice hill die, or the rice hill withers due to planthoppers attack.
9	Hopperburn	Rice hills die from hopperburn

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Table 2. Population and symptoms of BPH attack on rice plants in Bali

2 **Table 3.** Nucleotide (nt) and amino acid (aa) homology of *N. lugens* in rice from Bali, Indonesia, compared with *N. lugens* from other countries in GenBank

Isolate	Origin - of	Biotype	Accession	Homology nt (aa) (%) N. lugens_IDN_								
	isolate		number	Denpasar	Badung	Gianyar	Tabanan	Buleleng	Karangasem	Klungkung	Bangli	Jembrana
FSD-034	PAK		MK301229	99.5 (100)	99.6 (100)	99.5 (100)	99.5 (100)	99.6 (100)	99.5 (100)	99.7 (100)	99.5 (100)	99.6 (100)
HZZ55	IND		MK032794	99.4 (100)	99.5 (100)	99.4 (100)	99.5(100)	99.4 (100)	99.5 (100)	99.6 (100)	99.5 (100)	99.6 (100)
SAEVG Morph0111	IND		MN520923	99.4 (100)	99.5 (100)	99.4 (100)	99.5(100)	99.4 (100)	99.5 (100)	99.5(100)	99.5 (100)	99.6 (100)
KBPH	KOR		MK590088	99.3 (100)	99.5 (100)	99.4 (100)	99.4 (100)	99.3 (100)	99.4 (100)	99.4 (100)	99.4 (100)	99.5 (100)
KOREA BPH	KOR		LC461184	99.3 (100)	99.5 (100)	99.4 (100)	99.4 (100)	99.3 (100)	99.4 (100)	99.4 (100)	99.4 (100)	99.5 (100)
WUHAN-Y	CHN		KC333653	99.3 (100)	99.5 (100)	99.4 (100)	99.4 (100)	99.3 (100)	99.4 (100)	99.4 (100)	99.3 (100)	99.4 (100)
WUHAN-3	CHN		JN563997	97.8(98.1)	97.2 (97.8)	97.5 (98.9)	97.5 (98.9)	97.4 (97.9)	97.8 (98.1)	97.5 (98.9)	97.2 (98.8)	97.6 (98.0)
WUHAN-2	CHN		JN563996	96.3 (97.5)	96.3 (97.5)	96.4 (97.5)	96.3 (97.5)	96.2(97.4)	96.4 (97.5)	96.3 (97.5)	96.2 (97.4)	96.3 (97.5)
WUHAN-1	CHN		JN563995	95.3 (96.7)	95.4 (96.7)	95.3 (96.7)	95.4 (96.7)	95.6 (96.8)	95.6 (96.8)	95.3 (96.7)	95.4 (96.7)	95.3 (96.7)
GX	CHN		LC461186	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)	95.4 (96.7)	95.5 (96.8)	95.5 (96.8)	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)
Gangavathi	IND		OL451531	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)	95.5 (96.8)	95.5 (96.8)	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)
WUHAN-L	CHN		KC333654	94.2 (95.8)	94.4 (96.2)	94.2 (95.8)	94.4 (96.2)	94.3 (96.0)	94.4 (96.2)	94.2 (95.8)	94.4 (96.2)	94.4 (96.2)
N. bakeri	CHN	$\overline{}$	JX266790	84.6 (85.6)	85.2(86.1)	84.8 (85.9)	84.8 (85.9)	84.6 (85.6)	85.2 (86.1)	84.8 (85.9)	85.2 (86.1)	85.2(86.1)
Sogatella furcifera	CHN		HM160123	75.6 (76.9)	75.6 (76.9)	76.2 (77.8)	77.6 (78.4)	77.4 (78.4)	76.8 (77.8)	75.6 (76.9)	76.8 (77.8)	77.6 (78.4)

3 Notes: nt (nucleotide), aa (amino acid), IDN (Indonesia), PAK (Pakistan), IND (India), KOR (South Korea), CHN (China), *N. bakeri* and *Sogatella furcifera* from China was used as outgroups

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27 **Figure 2.** The attack intensity of *N. lugens* on rice in Bali Province

Figure 4. The cladogram of the mtCOI fragment of *N. lugens* from eastern Indonesia, Bali (Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana) was compared with mtCOI fragments

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Population dynamics and damage intensity of brown planthopper (BPH) and *Nilaparvata lugens* (Stal.) provide information about the economic threshold status of *N. lugens* in Bali. This study enriched information on the genetic diversity of *N. lugens* isolates from eastern Indonesia, particularly Bali. It is the first report of *N. lugens* biotype Y in Indonesia. In addition, the latest information in this study is that rice varieties Situbagendit and Inpari 32, which were previously resistant to BPH, are now found to be susceptible to BPH. This information is critical as a basis for controlling *N. lugens* in Indonesia

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³² **The Brown Planthopper (***Nilaparvata lugens* **Stal.) Attack and Its** ³³ **Genetic Diversity on Rice in Bali, Indonesia LISTIHANI LISTIHANI1♥ , PUTU EKA PASMIDI ARIATI¹ , I GUSTI AYU DIAH YUNITI¹** 34 **, DEWA GEDE WIRYANGGA SELANGGA**

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 ¹ Faculty of Agriculture and Business, University of Mahasaraswati Denpasar ² Faculty of Agriculture, Udayana University 38 email: listihani9@gmail.com 39 $\frac{40}{41}$ **Abstract.** The brown planthopper is **an** important pest on rice crops in Indonesia. The genetic diversity of BPH isolates in analyze genetic diversity and evaluate the BPH attack's intensity on Bali rice plants. The resea western Indonesia has been extensively reported, whereas eastern Indonesia isolates have not been reported. This research aims to analyze genetic diversity and evaluate the BPH attack's intensity on Bali rice plants. The research method used was an observation of attack percentage, population dynamics, attack intensity, and genetic diversity of BPH in 9 districts in Bali (Badung, Gianyar, 45 Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana). Molecular identification was carried out on *N. lugens* DNA in the mtCOI fragment. BPH attacks of >50% were found in the districts of Gianyar, Bangli, Jembrana, and Badung. The 47 BPH population was primarily found in Ciherang and IR-64 varieties of rice in the Badung Regency, with 43.67 BPH per rice hill. In general, rice varieties grown in all observation locations were susceptible to BPH, such 48 general, rice varieties grown in all observation locations were susceptible to BPH, such as Ciherang, IR-64, Inpari 32, and Situbagendit.
49 In the Ciherang and IR-64 varieties, the highest attack intensity average valu 49 In the Ciherang and IR-64 varieties, the highest attack intensity average value reached 30%. The sequence of *N. lugens* isolate from Bali 50 Jembrana showed the highest nucleotide and amino acid homology with N. lugens isolate FSD-034 from Pakistan (MK301229) biotype
51 Y of 99.5 -99.74% and 100%, respectively. This study found N. lugens biotype Y in rice pl 52 reported that Rice varieties Situbagendit and Inpari 32, previously resistant to BPH, are reported as susceptible to BPH. 53 **Keywords:** 54 **Abbreviations** (if any): The BPH, Rice Plants 55 **Running title:** The Brown Planthopper (*Nilaparvata lugens* Stal.) Attack and Its Genetic Diversity on Rice in Bali, Indonesia 57 **INTRODUCTION** 58 The brown planthopper (BPH) *(Nilaparvata lugens* Stal, Hemiptera: Delphacidae) is the most destructive rice
59 pest in Indonesia. Repeated outbreaks of BPH in Indonesia are caused by continuous rice cultivation, extens 59 pest in Indonesia. Repeated outbreaks of BPH in Indonesia are caused by continuous rice cultivation, extensive use, and
60 over-application of insecticides (Baehaki and Meiava 2015). This pest is vascular monophagous in 60 over-application of insecticides (Baehaki and Mejaya 2015). This pest is vascular monophagous in rice (Cheng et al. 2013; 61 Ferrater et al. 2015). Feeding by nymphs and imago at the base of the plant causes rapid wilting and drying of the plant
62 (Bottrell and Schoenly 2012: Cheng et al. 2013: Bao and Zhang 2019). In addition. BPH is also a 62 (Bottrell and Schoenly 2012; Cheng et al. 2013; Bao and Zhang 2019). In addition, BPH is also a vector of *Rice grassy* 63 *stunt virus* and *Rice ragged stunt virus* (Bao and Zhang 2019). At high population levels of *N. lugens* can cause significant 64 losses in rice production (Cheng et al. 2013; Zheng et al. 2013; Bao and Zhang 2019).
65 **The BPH cannot tolerate winter in northern Asia, including Japan, Korea, an** 65 The BPH cannot tolerate winter in northern Asia, including Japan, Korea, and northern China (He et al. 2012; Fu et al. 2012; Fu et al. 2014). The population originally came from subtropical and tropical areas by flying long distances 67 during the summer (Fu et al. 2014; Hu et al. 2014). BPH infestation in temperate climates originated from annual 68 migrations from tropical Asia and China (He et al. 2012). During autumn, BPH re-migrates (north-to-south) and BPH
69 populations have been studied in China and India (Bottrell and Schoenly 2012). Such return migration m 69 populations have been studied in China and India (Bottrell and Schoenly 2012). Such return migration may help explain
The movies of the studied in China and India (Bottrell and Schoenly 2012). Such return migration may 70 **how long-distance migration is maintained in the winter.**
71 **homogleman The intensification of rice production triggered** The intensification of rice production triggered the BPH outbreak in Tropical Asia during the green revolution era

²¹ in the 1970s and 1980s (Bottrell and Schoenly 2012). Until now, *N. lugens* is the main problem causi 72 in the 1970s and 1980s (Bottrell and Schoenly 2012). Until now, *N. lugens* is the main problem causing rice harvest failure 73 in several countries. Inaccurate identification and prolonged identification of *N. lugens* are obstacles to its field 74 management strategy.

75 Traditionally 75 Traditionally, BPH has been identified at the species level by morphological features using anatomical 76 characteristics, namely, wings, front, and external genitalia (Dupo and Barrion 2009). Accurate identification requires
77 extensive expertise and experience and vet sometimes can lead to errors. Morphological identific words

56

extensive expertise and experience and yet sometimes can lead to errors. Morphological identification by an entomologist 78 can reduce the potential for errors. Practical morphological identification is only possible when dealing with small sample

Commented [u1]: The introduction at least consists of 600

79 sizes and well-preserved specimens. Therefore, it is crucial to utilize a new identification method that is accurate, fast, $\frac{1}{2}$ time-saving and suitable for large numbers of specimens 80 time-saving, and suitable for large numbers of specimens.
81 Molecular techniques with high reproducibility

81 Molecular techniques with high reproducibility and fast results offer an excellent alternative to traditional
82 morphological classification. Several mitochondrial and nuclear genes have been used as genetic markers to 82 morphological classification. Several mitochondrial and nuclear genes have been used as genetic markers to differentiate related species. These include the mitochondrial cytochrome c oxidase subunit 1 (CO1) gene, nuclea 83 related species. These include the mitochondrial cytochrome c oxidase subunit 1 (CO1) gene, nuclear 12S-16S-18S
84 ribosomal RNA genes, and ITS1 and ITS2 internal transcription spacers (Fukunaga et al. 2000; Brengues et 84 ribosomal RNA genes, and ITS1 and ITS2 internal transcription spacers (Fukunaga et al. 2000; Brengues et al. 2014; Wang et al. 2016; Liu et al. 2018). ITS1 and ITS2 are nonfunctional spacers that separate the 85 Gomez-Polo et al. 2014; Wang et al. 2016; Liu et al. 2018). ITS1 and ITS2 are nonfunctional spacers that separate the
86 18S-5.8S and 5.8S-28S rRNA genes, respectively (Ji et al. 2003; Liu et al. 2018). As ITS sequences 86 18S-5.8S and 5.8S-28S rRNA genes, respectively (Ji et al. 2003; Liu et al. 2018). As ITS sequences have low intra-species variation but high variation between species, they are helpful for species classification and phy 87 variation but high variation between species, they are helpful for species classification and phylogenetic analysis for morphologically similar organisms, both in prokaryotes and eukaryotes (Liu et al. 2009). Finally, f 88 morphologically similar organisms, both in prokaryotes and eukaryotes (Liu et al. 2009). Finally, from the molecular 89 identification of the combined mitochondrial COI-COII and ten microsatellite marker loci (Winnie et

89 identification of the combined mitochondrial COI-COII and ten microsatellite marker loci (Winnie et al. 2020).
90 **The genetic diversity of N.** *lugens* has been reported in several countries such as China, South Kore 90 The genetic diversity of *N. lugens* has been reported in several countries such as China, South Korea, Pakistan,
91 **India, and Malaysia (Jing et al. 2012: Zheng et al. 2021: Anant et al. 2021: Latif et al. 2012). The** 91 India, and Malaysia (Jing et al. 2012; Zheng et al. 2021; Anant et al. 2021; Latif et al. 2012). The genetic diversity of *N.* 92 *lugens* in Indonesia is widely reported in western Indonesia (Java Island) (Winnie et al. 2020; Chaerani et al. 2021).

93 **Reports on the genetic diversity of** *N. lugens* **in eastern Indonesia have not been found. Therefore, this study aims to 94** analyze genetic diversity and determine the intensity of RPH attacks on rice plants in eastern analyze genetic diversity and determine the intensity of BPH attacks on rice plants in eastern Indonesia, especially Bali.

95 **MATERIALS AND METHODS**

96 **Brown Planthopper Sampling from Rice Dwarf Disease Endemic Areas**

97 Samples were taken from nine locations in Bali Province (Badung, Gianyar, Klungkung, Bangli, Karangasem, 98 Tabanan, Denpasar City, Buleleng, and Jembrana). The brown planthopper samples taken from rice plants were nymp 98 Tabanan, Denpasar City, Buleleng, and Jembrana). The brown planthopper samples taken from rice plants were nymphs 99 and imagos. Nymphs and imagos were used for total DNA extraction. After arriving at the laboratory, the nymphs and imago were stored dry at -20°C. imago were stored dry at -20°C.

101

102 **Observation of BPH Attack Symptoms and Quantity of BPH Population/rice hill**

103 Observation of symptoms of BPH attack was carried out by observing symptoms of damage to rice plants due to 104 BPH attack. The abundance of the BPH/rice hill population was obtained by counting all nymphs and imagoes BPH attack. The abundance of the BPH/rice hill population was obtained by counting all nymphs and imagoes obtained. 105 Data on the population per cluster from 20 samples at each observation location were then averaged.

106
107 107 **BPH Attack Percentage**

108 The percentage of BPH attacks is calculated using the following formula:

109
110

- 110 Note:
111 $P = A$
- 111 $P =$ Attack percentage (%)
112 $a =$ Number of rice hills af
- 112 $a =$ Number of rice hills affected by BPH
113 $b =$ Number of rice hills observed $b =$ Number of rice hills observed

114

115 **Damage Intensity**

116 Determination of scoring on symptoms of rice damage due to BPH attack is based on Table 1. The intensity of 117 damage due to a BPH attack is determined using the formula (Erdiansyah and Damanhuri 2018):

$$
I = \sum_{i=1}^{N} \frac{N i x V i}{N x Z} x 100\%
$$

118 119

120

121

122 Note:
123 $I = D_i$ 123 I = Damage intensity
124 Ni = The number of

124 Ni = The number of affected rice hills on the score i
125 Vi = Score i

125 Vi = Score i
126 N = The nun

126 $N =$ The number of rice hills observed
127 $Z =$ Highest score $Z =$ Highest score

$\frac{128}{129}$ 129 **Total DNA Extraction from Brown Planthopper**

Total DNA extraction of brown planthopper was obtained from one individual imago or one individual nymph 131 based on the modified method of Goodwin et al. (1994). One individual imago was put into a microtube and then added 132 with 100 μl of CTAB extraction buffer (2% CTAB, 1.4 M NaCl, 100 mM Tris-HCI, 20 mM EDTA, and 1% PVP (-40
133 °C)) Next 1 μl of proteinase K was added then the insects were crushed using a micro-pistil vortexed and inc ^oC)). Next, 1 μl of proteinase K was added, then the insects were crushed using a micro-pistil, vortexed, and incubated in a ratio of 65° C for 3 minutes. After that the tube was added with 100 ul CI (chloroform: i 134 water bath of 65°C for 3 minutes. After that, the tube was added with 100 µl CI (chloroform: isoamyl alcohol) in a ratio of 135 24:1. The tube was then vortexed for 3 minutes and centrifuged at 10,000 rpm for 15 minut 135 24:1. The tube was then vortexed for 3 minutes and centrifuged at 10,000 rpm for 15 minutes. The supernatant formed was transferred to a new microtube (60 μ) and then added with 3 M NaOAc (pH 5.2), as much as 1/10 transferred to a new microtube (60 µl) and then added with 3 M NaOAc (\overline{p} H 5.2), as much as 1/10 of the total volume of the supernation. Isopropanol was added up to 2/3 of the total volume of the supernation then inc 137 the supernatant. Isopropanol was added up to $2/3$ of the total volume of the supernatant, then incubated at -20° C for one needs to -138 isometrifused at $10,000$ rpm for $10,000$ rpm and the supernatant was di 138 night. The tube was centrifuged at 10,000 rpm for 10 min, and the supernatant was discarded. The pellets were washed with 100 μ l of 80% ethanol (cold) and centrifuged at 8000 rpm for 5 minutes. In the final step, th 139 with 100 μl of 80% ethanol (cold) and centrifuged at 8000 rpm for 5 minutes. In the final step, the supernatant was removed, and the pellet was dried for approximately 1 hour. It was then added with a solution of 20 μ 140 removed, and the pellet was dried for approximately 1 hour. It was then added with a solution of 20 μl TE and stored at - 20° C until used.

142
143 143 **Amplification of mtCOI Fragments Using the PCR Method**

144 PCR reactants were manufactured with a total volume of 25 μl consisting of 12.5 μl Go Tag Green Master Mix
145 Promega, US) and 9.5 μl ddH2O. DNA amplification of the mtCOI fragment was carried out using a pair of uni ga, US) and 9.5 μl ddH2O. DNA amplification of the mtCOI fragment was carried out using a pair of universal 146 primers mtCOI LCO 1490 (3'-GGTCAACAAATCATAAAGATATTGG-5') and HCO 2198 (5TAAACTTCA
147 GGGTGACCA AAAAATCA-3') (Folmer et al. 1994) each 1 ul. and 1 ul DNA template. PCR reactions were carried out 147 GGGTGACCA AAAAATCA-3') (Folmer et al. 1994) each 1 μ l, and 1 μ I DNA template. PCR reactions were carried out with a Perkin Elmer 480 Thermocycler (Applied Biosystem, US). The PCR reaction was initiated by initia 148 with a Perkin Elmer 480 Thermocycler (Applied Biosystem, US). The PCR reaction was initiated by initial denaturation
149 for 5 min at 94°C. The PCR was continued for 35 cycles in the following order: 94°C for 1 minute 149 for 5 min at 94°C. The PCR was continued for 35 cycles in the following order: 94°C for 1 minute, 52° C for 35 seconds, and a final extension of 72°C for 7 minutes. The PCR results were then analyzed in 1% 150 72°C for 1 minute 30 seconds, and a final extension of 72°C for 7 minutes. The PCR results were then analyzed in 1%
151 agarose gel. The DNA fragments of mtCOI were visualized using a UV transilluminator after being i 151 agarose gel. The DNA fragments of mtCOI were visualized using a UV transilluminator after being immersed in a 2%
152 ethidium bromide solution for 15 minutes and photographed with a digital camera. The result of amplif 152 ethidium bromide solution for 15 minutes and photographed with a digital camera. The result of amplification by PCR 153 technique was in the form of mtCOI DNA fragments with a size of \pm 710 base pairs (pb). technique was in the form of mtCOI DNA fragments with a size of \pm 710 base pairs (pb).

154
155 155 **Analysis of DNA Sequence Results**

156 Nucleotide Sequencing DNA fragment purification and mtCOI nucleotide sequencing were performed at PT. 1st 157 Base, Malaysia. The results were then registered in the NCBI gene bank (http://www.ncbi.nlm.nih.gov). Analys 157 Base, Malaysia. The results were then registered in the NCBI gene bank (http://www.ncbi.nlm.nih.gov). Analysis of mtCOI DNA sequence data ChromasPro program was used to combine forward and reverse nucleotide sequences 158 mtCOI DNA sequence data ChromasPro program was used to combine forward and reverse nucleotide sequences to obtain
159 the mtCOI gene (ChromasPro version 2.01, 2006). The Bioedit program was used to compare mtCOI fragme 159 the mtCOI gene (ChromasPro version 2.01. 2006). The Bioedit program was used to compare mtCOI fragments between
160 samples (Multiple alignments) (Hall 1999). The phylogenetic relationship was built by comparing the mt 160 samples (Multiple alignments) (Hall 1999). The phylogenetic relationship was built by comparing the mtCOI sample
161 fragments from the brown planthopper from Indonesia with the mtCOI fragments already stored in the NC 161 fragments from the brown planthopper from Indonesia with the mtCOI fragments already stored in the NCBI GenBank
162 (http://www.ncbi.nlm.nih.gov). The criteria for retrieving mtCOI fragments at GenBank were fragments w 162 (http://www.ncbi.nlm.nih.gov). The criteria for retrieving mtCOI fragments at GenBank were fragments with a nucleotide base length of \pm 800 bp (Boykin et al. 2007) (Table 1). The phylogenetic tree was constructed u 163 base length of \pm 800 bp (Boykin et al. 2007) (Table 1). The phylogenetic tree was constructed using the PAUP 4.0b10 program (Swofford 2002) with the maximum parsimony cladistic quantitative method. The cladogram wa 164 program (Swofford 2002) with the maximum parsimony cladistic quantitative method. The cladogram was compiled using
165 the Heuristic method. The cladogram used results from the strick consensus with the statistical boo 165 the Heuristic method. The cladogram used results from the strick consensus with the statistical bootstrap test to obtain a 166 100% probability. 100% probability.

167 **RESULTS AND DISCUSSION**

168 The brown planthopper causes direct and indirect damage to rice plants. Direct damage was in the form of stunted
169 and uneven growth of rice plants (Figure 1A and 1B), vellow plants (Figure 1C), and hopperburn caused 169 and uneven growth of rice plants (Figure 1A and 1B), yellow plants (Figure 1C), and hopperburn caused by fluid in rice
170 plant cells sucked by BPH nymphs, brachiptera (Fig. short wings), and macroptera (long wings) (170 plant cells sucked by BPH nymphs, brachiptera (Fig. short wings), and macroptera (long wings) (Figures 1E and 1F).
171 Indirect damage was caused by BPH, which acts as a vector of grass dwarf virus and empty dwarf viru 171 Indirect damage was caused by BPH, which acts as a vector of grass dwarf virus and empty dwarf virus, causing stunted
172 ice plants (Figure 1D). Besides Bali or other parts of Indonesia, BPH attacks on rice crops were 172 rice plants (Figure 1D). Besides Bali or other parts of Indonesia, BPH attacks on rice crops were also reported in China,
173 where hopperburn affected 60% of all examined crops (Hu et al. 2014) 173 where hopperburn affected 60% of all examined crops (Hu et al. 2014).
174 A percentage of BPH attacks of more than 50% was found in

174 A percentage of BPH attacks of more than 50% was found in Gianyar, Bangli, Jembrana, and Badung Regencies
175 (Table 2). The BPH population was primarily found in Ciherang and IR-64 varieties of rice in the Badung Rege 175 (Table 2). The BPH population was primarily found in Ciherang and IR-64 varieties of rice in the Badung Regency, with 176 43.67 BPH per rice hill (Table 2). Baehaki and Mejaya (2015) added that the economic threshol 176 43.67 BPH per rice hill (Table 2). Baehaki and Mejaya (2015) added that the economic threshold could be measured
177 through the number or population of pests and planting age. BPH is said to have reached the economic 177 through the number or population of pests and planting age. BPH is said to have reached the economic threshold when the population of this pest was found in the field, as many as nine BPH per rice hill when the rice ag 178 population of this pest was found in the field, as many as nine BPH per rice hill when the rice age was less than 40 DAP or
179 18 BPH when the rice was more than 40 DAP (Baehaki and Meiava 2015). In general, rice vari 179 18 18 BPH when the rice was more than 40 DAP (Baehaki and Mejaya 2015). In general, rice varieties grown in all
180 observation locations in Bali were BPH susceptible varieties, such as Ciherang, IR-64, Inpari 32, and 180 observation locations in Bali were BPH susceptible varieties, such as Ciherang, IR-64, Inpari 32, and Situbagendit.
181 The dynamics of BPH development in the field can be influenced by several factors, including host

181 The dynamics of BPH development in the field can be influenced by several factors, including host plant factors
182 and natural enemies (Horgan et al. 2015; Kobayashi 2016). The host plant factors that affect the RPH p 182 and natural enemies (Horgan et al. 2015; Kobayashi 2016). The host plant factors that affect the BPH population are related to the age of the rice plant. When the observations were made, the rice plants were still in t 183 related to the age of the rice plant. When the observations were made, the rice plants were still in the vegetative phase,
184 aged 4-6 WAP. According to Jing et al. (2014), naturally, BPH usually comes to voung rice f 184 aged 4-6 WAP. According to Jing et al. (2014), naturally, BPH usually comes to young rice fields, and insects usually come in the first two weeks after planting. Thus, the brown planthopper in rice cultivation might be 185 come in the first two weeks after planting. Thus, the brown planthopper in rice cultivation might be the first generation of
186 planthoppers that have not **ver** reproduced because one BPH life cycle takes between 3-4 186 planthoppers that have not **yet** reproduced because one BPH life cycle takes between 3-4 weeks (IRRI 2009).
187 **BPH** observations in Denpasar, Tabanan, Karangasem, and Klungkung cities were dominated **t**

187 **BPH** observations in Denpasar, Tabanan, Karangasem, and Klungkung cities were dominated by macroptera
188 imago (Table 2), According to Horgan et al. (2017), the planthopper that first came to the plantation was the m imago (Table 2). According to Horgan et al. (2017), the planthopper that first came to the plantation was the macroptera 189 planthopper as a winged immigrant planthopper. **Meanwhile,** in Badung, Gianyar, Buleleng, Bangli, and Jembrana
190 regencies, nymphal BPH was dominated by BPH, and several individuals were in the imago phase of brachip 190 regencies, nymphal BPH was dominated by BPH, and several individuals were in the imago phase of brachiptera and
191 macroptera. The dominance of the nymph phase caused the population of BPH in Badung. Gianyar. Buleleng 191 macroptera. The dominance of the nymph phase caused the population of BPH in Badung, Gianyar, Buleleng, Bangli, and
192 Jembrana districts to be the highest when compared to the cities of Denpasar, Tabanan, Karangasem, 192 Jembrana districts to be the highest when compared to the cities of Denpasar, Tabanan, Karangasem, and Klungkung. The presence of the brachiptera planthopper might be contributed to the increase in the nymph population 193 presence of the brachiptera planthopper might be contributed to the increase in the nymph population (Baehaki and Mejaya
194 2015). According to Horgan et al. (2015), rapid population growth usually occurs in groups wi 194 2015). According to Horgan et al. (2015), rapid population growth usually occurs in groups with many young individual
195 195 The average intensity of RPH attack on Ciberang and IR-64 varieties of rice was higher than

195 The average intensity of BPH attack on Ciherang and IR-64 varieties of rice was higher than in other varieties. In the Ciherang and IR-64 varieties of rice, the average value of the highest attack intensity was 30% (Fi 196 the Ciherang and IR-64 varieties of rice, the average value of the highest attack intensity was 30% (Figure 2). It is because farmers grow rice varieties Ciherang and IR-64 from year to year without any replacement of 197 farmers grow rice varieties Ciherang and IR-64 from year to year without any replacement of other varieties. Furthermore, 198 rice varieties Ciherang and IR-64 became very susceptible to BPH attacks. In addition, BPH i 198 rice varieties Ciherang and IR-64 became very susceptible to BPH attacks. In addition, BPH is a pest that begins to attack
199 rice plants from a voung age, even when the rice is still in the nursery. 199 rice plants from a young age, even when the rice is still in the nursery.
200 According to Sawada et al. (1993), fluctuations in BPH pest

200 According to Sawada et al. (1993), fluctuations in BPH pest attacks are more influenced by the growth phase of the rice plant that is the host in the field. BPH pests are often found when rice plants are in the vegetat 201 the rice plant that is the host in the field. BPH pests are often found when rice plants are in the vegetative and generative stages (Bottrell and Schoenly 2012). Horgan et al. (2017) added that BPH pests could damage 202 stages (Bottrell and Schoenly 2012). Horgan et al. (2017) added that BPH pests could damage rice plants at all stages of 203 growth and act as vectors for grass and dwarf viruses. **BPH attack was higher when rice was in the vegetative phase than in**
204 **the generative phase (Horgan et al. 2015).** It happens because the pests attack the voun 204 **the generative phase (Horgan et al. 2015).** It happens because the pests attack the young rice stalks. Considering the type of mouth of BPH, which is included in the suction, BPH can suck the liquid from the rice stem 205 of mouth of BPH, which is included in the suction, BPH can suck the liquid from the rice stems and cause the plant leaves
206 to turn yellow (Anant et al. 2021). According to Choi et al. (2019), during the vegetative p 206 to turn yellow (Anant et al. 2021). According to Choi et al. (2019), during the vegetative phase, food availability in the 207 form of nitrogen is abundant in rice plants. Rice plants need nitrogen to form plant organs 207 form of nitrogen is abundant in rice plants. Rice plants need nitrogen to form plant organs. Food is one of the factors that 208 affect the life of insects. Out et al. (2004) continued that the N element absorbed by pl 208 affect the life of insects. Qiu et al. (2004) continued that the N element absorbed by plants also serves as a source of nutrition for BPH. If food is available with good quality (suitable for pests), then the insect p 209 nutrition for BPH. If food is available with good quality (suitable for pests), then the insect pest population will increase, $\frac{210}{\pi}$ and vice versa (Qiu et al. 2004). 210 and vice versa (Qiu et al. 2004).
211 The mtCOI DNA band

211 The mtCOI DNA band was only successfully amplified from the total DNA extraction of one imago or nymph 212 and not more than one BPH imago. The mtCOI fragment that was successfully amplified corresponds to a size of 212 and not more than one BPH imago. The mtCOI fragment that was successfully amplified corresponds to a size of \pm 710 bp 213 in all samples from nine districts in Bali, namely Badung, Gianyar, Klungkung, Bangli, Karang 213 in all samples from nine districts in Bali, namely Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar
214 City, Buleleng, and Jembrana (Figure 3). Nucleotide and amino acid sequence analysis showed high 214 City, Buleleng, and Jembrana (Figure 3). Nucleotide and amino acid sequence analysis showed high homology with *N*.
215 *lugens* sequences in the database at GenBank. 94.2 – 99.7% and 95.8 - 100%. **respectively** (Tabl 215 *lugens* sequences in the database at GenBank, 94.2 – 99.7% and 95.8 - 100%, respectively (Table 3). *N. lugens* sequences 216 from Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana showed the 217 highest nucleotide, and amino acid homology with N. *lugens* isolate FSD-034 from Pakistan (MK301229) b 217 highest nucleotide, and amino acid homology with *N. lugens* isolate FSD-034 from Pakistan (MK301229) biotype Y
218 respectively 99.5-99.74% and 100% (Table 3). The results of the molecular detection of *N. lugens* usi 218 respectively. 99.5 -99.74% and 100% (Table 3). The results of the molecular detection of *N. lugens* using the PCR method 219 in Bali, Indonesia, are the first reports of the molecular character of *N. lugens* in Indonesia.

220 Samples from Indonesia formed a group with *N. lugens* biotype Y fragment mtCOI from Pakistan, India, South 221 Korea, and China (Figure 4). This study found *N. lugens* biotype Y in rice plants for the first time in I 221 Korea, and China (Figure 4). This study found *N. lugens* biotype Y in rice plants for the first time in Indonesia. The
222 Indonesian sample did not form separate groups according to the proximity of the district loca 222 Indonesian sample did not form separate groups according to the proximity of the district locations but formed a polytomy cladogram (Figure 4). This polytomy cladogram shows that the *N. lugens* between regencies (Bad 223 cladogram (Figure 4). This polytomy cladogram shows that the *N. lugens* between regencies (Badung, Gianyar, 224 Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana) were observed to have the same
225 ancestry. These results indicate high locomotion ability with genetic mixing between N. lugens in Bali i 225 ancestry. These results indicate high locomotion ability with genetic mixing between *N. lugens* in Bali isolates. Similar conditions were also demonstrated in *N. lugens* among Asian isolates using mitochondrial seque 226 conditions were also demonstrated in *N. lugens* among Asian isolates using mitochondrial sequences showing genetic 227 mixing. It can also be correlated with the theory of long-distance migration of *N. lugens*, which 227 mixing. It can also be correlated with the theory of long-distance migration of *N. lugens*, which migrates from the tropics
228 (northern Vietnam) in April-May to temperate regions (China, Korea, and Japan) in June-Ju 228 (northern Vietnam) in April-May to temperate regions (China, Korea, and Japan) in June-July as shown based on
229 meteorological studies (Otuka et al. 2008). The population of *N. lugens* is a long-distance migratory f 229 meteorological studies (Otuka et al. 2008). The population of *N. lugens* is a long-distance migratory flight from the tropics
230 to temperate Asia before modern pesticides are widely used in tropical rice. Due to the 230 to temperate Asia before modern pesticides are widely used in tropical rice. Due to the infrequent use of insecticides prior 231 to the 1960s in the tropics factors other than insecticides may have triggered long-wing 231 to the 1960s in the tropics, factors other than insecticides may have triggered long-wing movements to form *N. lugens*
232 nopulations (Bottrell and Schoenly 2012). 232 populations (Bottrell and Schoenly 2012).
233 In previous studies in Indonesia,

233 In previous studies in Indonesia, BPH biotypes 1, 2, 3, and 4 have been found. Chen et al. (2011) reported that the 254 brown planthopper is a highly adaptive insect **because it can form new biotypes**. In early 1975 th 234 brown planthopper is a highly adaptive insect **because it can form new biotypes**. In early 1975 the IR-26 rice variety from
235 IRRI Philippines was introduced. The IR-26 variety was unique because it contained a Bph1 235 IRRI Philippines was introduced. The IR-26 variety was unique because it contained a Bph1 resistant gene to anticipate 236 fluctuations in the brown planthopper population. However, in 1976 there was a great population explosion in several rice
237 production centers due to changes in the brown planthopper population from biotype 1 to biot 237 production centers due to changes in the brown planthopper population from biotype 1 to biotype 2. As an anticipatory measure against brown planthopper biotype 2, in 1980, the IR-42 rice variety (containing the bph2 re 238 measure against brown planthopper biotype 2, in 1980, the IR-42 rice variety (containing the bph2 resistant gene) was
239 introduced from IRRI Philippines. Unfortunately, in 1981 there was another explosion in the bro 239 introduced from IRRI Philippines. Unfortunately, in 1981 there was another explosion in the brown planthopper population in Simalungun. North Sumatra, and several other areas due to changes in the brown planthopper pop 240 population in Simalungun, North Sumatra, and several other areas due to changes in the brown planthopper population 241 from biotype 2 to biotype 3. To deal with the brown planthopper biotype 3, rice variety IR-56 was 241 from biotype 2 to biotype 3. To deal with the brown planthopper biotype 3, rice variety IR-56 was introduced (containing the pene bph3 resistance) in 1983 and IR-64 (containing the bph1+ resistance gene) in 1986. The i 242 the gene bph3 resistance) in 1983 and IR-64 (containing the bph1+ resistance gene) in 1986. The introduction process
243 continues. In 1991, the IR-74 variety (containing the bph3 resistant gene) was introduced. In 200 continues. In 1991, the IR-74 variety (containing the bph³ resistant gene) was introduced. In 2006, the resistance gene IR-244 64 was broken because the brown planthopper population changed to biotype 4. The stability of the biotype zero brown
245 planthoppers persisted for 41 years before becoming brown planthopper biotype 1. The change of br 245 planthoppers persisted for 41 years before becoming brown planthopper biotype 1. The change of brown planthopper 246 biotype 1 to biotype 2 only took 4 years, and the change of biotype 2 brown planthopper to biotype 3 biotype 1 to biotype 2 only took 4 years, and the change of biotype 2 brown planthopper to biotype 3 within 5 years. Until 247 2005, the brown planthopper biotype 3 was still dominated by biotype 3, and in 2006 the biotype 4 brown planthopper 248 began to develop. The long existence of the biotype 3 brown planthopper was caused by the development of the IR-64
249 (bph1+) variety over a long period. IR-64 is a resistant variety (durable resistance) that can withstand changes in brown
250 planthoppers to a more virulent biotype 250 **planthoppers to a more virulent biotype**
251 **he continuous cultivation of**

251 The continuous cultivation of IR-64 rice varieties by farmers in Bali led to the emergence of a new biotype BPH,
252 namely Y. Insects of biotype Y originated from biotype 1 by eating YHY15 resistant varieties for more 252 namely Y. Insects of biotype Y originated from biotype 1 by eating YHY15 resistant varieties for more than two years for
253 33 generations (Jing et al. 2012). Rice varieties YHY15 carry the Bph15 resistance gene (Jing 253 33 generations (Jing et al. 2012). Rice varieties YHY15 carry the Bph15 resistance gene (Jing et al. 2012).
254 This study shows great notential in the nopulation of N *lugens* to adant to previously resistant rice

254 This study shows great potential in the population of *N. lugens* to adapt to previously resistant rice varieties. This study reported that rice varieties Situbagendit and Inpari 32, previously resistant to BPH, were s 255 study reported that rice varieties Situbagendit and Inpari 32, previously resistant to BPH, were susceptible to BPH. This 256 research can provide information to farmers not to continuously plant susceptible varieties, which could cause BPH 257 epidemics in the field, as well as the emergence of new, more virulent BPH biotypes. Thus a new control strategy based on a forecasting system can be developed for the regional management of this insect a forecasting system can be developed for the regional management of this insect. 259

260 **CONCLUTIONS**

261 *N. lugens* that attacks rice plants in Bali (Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar 262 City, Buleleng, and Jembrana) belongs to biotype Y. Symptoms of damage to rice plants are most severe in Badung 263 Regency. Apart from Ciherang and IR-64 varieties, Situbagendit and Inpari 32 varieties are susceptible to BPH attack.

264 **ACKNOWLEDGEMENTS**

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1 **TABLES LIST**

Score	Appearance	Description
Ω	Healthy	No planthopper was found in any rice hill.
	Very light	The rice hills occupied by the planthoppers did not show dead midribs, few exuviae, and the rice
	damage	stalks had not yet overgrown with Dematium and Cladosporium fungi that followed the brown planthopper attack.
3	Slightly damaged	The rice hills occupied by the planthoppers have shown dead midribs, many exuviae, and the rice stems are overgrown with Dematium and Cladosporium fungi that follow the brown planthopper attack.
5	Heavily damaged	Rice hills inhabited by planthoppers showed damage marked by many dead midribs, many exuviae, stunted and black-looking tillers, and overgrown with Dematium and Cladosporium fungi.
7	Partially dead	Some of the stems in the rice hill die, or the rice hill withers due to planthoppers attack.
9	Hopperburn	Rice hills die from hopperburn

 $\begin{array}{c} 4 \\ 5 \\ 6 \end{array}$

 $\begin{array}{c} 1 \\ 2 \\ 3 \end{array}$

Table 2. Population and symptoms of BPH attack on rice plants in Bali

2 **Table 3.** Nucleotide (nt) and amino acid (aa) homology of *N. lugens* in rice from Bali, Indonesia, compared with *N. lugens* from other countries in GenBank

Isolate	Origin -ot	Biotype	Accession		Homology nt (aa) $(\%)$ N. lugens IDN							
	isolate		number	Denpasar	Badung	Gianyar	Tabanan	Buleleng	Karangasem	Klungkung	Bangli	Jembrana
FSD-034	PAK		MK301229	99.5 (100)	99.6 (100)	99.5 (100)	99.5 (100)	99.6 (100)	99.5 (100)	99.7 (100)	99.5 (100)	99.6 (100)
HZZ55	IND		MK032794	99.4 (100)	99.5 (100)	99.4 (100)	99.5(100)	99.4 (100)	99.5 (100)	99.6 (100)	99.5(100)	99.6 (100)
SAEVG_Morph0111	IND		MN520923	99.4 (100)	99.5 (100)	99.4 (100)	99.5 (100)	99.4 (100)	99.5 (100)	99.5 (100)	99.5 (100)	99.6 (100)
KBPH	KOR		MK590088	99.3 (100)	99.5 (100)	99.4 (100)	99.4 (100)	99.3 (100)	99.4 (100)	99.4 (100)	99.4 (100)	99.5 (100)
KOREA BPH	KOR		LC461184	99.3 (100)	99.5 (100)	99.4 (100)	99.4 (100)	99.3 (100)	99.4 (100)	99.4 (100)	99.4 (100)	99.5 (100)
WUHAN-Y	CHN		KC333653	99.3 (100)	99.5 (100)	99.4 (100)	99.4 (100)	99.3 (100)	99.4 (100)	99.4 (100)	99.3 (100)	99.4 (100)
WUHAN-3	CHN		JN563997	97.8 (98.1)	97.2 (97.8)	97.5 (98.9)	97.5 (98.9)	97.4 (97.9)	97.8 (98.1)	97.5 (98.9)	97.2 (98.8)	97.6 (98.0)
WUHAN-2	CHN		JN563996	96.3 (97.5)	96.3 (97.5)	96.4 (97.5)	96.3 (97.5)	96.2(97.4)	96.4 (97.5)	96.3 (97.5)	96.2 (97.4)	96.3 (97.5)
WUHAN-1	CHN		JN563995	95.3 (96.7)	95.4 (96.7)	95.3 (96.7)	95.4 (96.7)	95.6 (96.8)	95.6 (96.8)	95.3 (96.7)	95.4 (96.7)	95.3 (96.7)
GX	CHN		LC461186	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)	95.4 (96.7)	95.5 (96.8)	95.5 (96.8)	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)
Gangavathi	IND		OL451531	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)	95.5 (96.8)	95.5 (96.8)	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)
WUHAN-L	CHN		KC333654	94.2 (95.8)	94.4 (96.2)	94.2 (95.8)	94.4 (96.2)	94.3 (96.0)	94.4 (96.2)	94.2 (95.8)	94.4 (96.2)	94.4 (96.2)
N. bakeri	CHN	$\overline{}$	JX266790	84.6 (85.6)	85.2(86.1)	84.8 (85.9)	84.8 (85.9)	84.6 (85.6)	85.2 (86.1)	84.8 (85.9)	85.2 (86.1)	85.2(86.1)
Sogatella furcifera	CHN		HM160123	75.6 (76.9)	75.6 (76.9)	76.2 (77.8)	77.6 (78.4)	77.4 (78.4)	76.8 (77.8)	75.6 (76.9)	76.8 (77.8)	77.6 (78.4)

3 Notes: nt (nucleotide), aa (amino acid), IDN (Indonesia), PAK (Pakistan), IND (India), KOR (South Korea), CHN (China), *N. bakeri* and *Sogatella furcifera* from China was used as outgroups

4

 $\frac{1}{2}$

5

6

 $\begin{array}{c} 8 \\ 9 \\ 10 \end{array}$ **Figure 1.** Symptoms of BPH attack on rice plants in Bali: A. rice plant growth is stunted; B. uneven plant growth (spots); C. yellow plant; D. dwarf rice plants; E. plants die like burning (hopperburn); F. BPH brachiptera

Figure 2. The attack intensity of *N. lugens* on rice in Bali Province

FIGURES LIST

 $\frac{15}{16}$ 16 Figure 3. DNA amplification of *N. lugens* in rice plants in Bali using primers LCO 1490/HCO 2198. 1. Denpasar City, 2. Bagung, 3. 17 (Gianyar, 4. Tabanan, 5. Buleleng, 6. Karangasemt, 7. Klungkung, 8. Bagung, 8. 17 (Gi

19 Figure 4. The cladogram of the mtCOI fragment of *N. lugens* from eastern Indonesia, Bali (Badung, Gianyar, Klungkung, Bangli, 20
20 Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana) was compared with mtCOI fr 21 that had been deposited on the NCBI website. N. bakeri and Sogatella furcifera from China were used as outgroups. The numbers on the branching cladograms represent bootstrap values with 100% probability. IDN (Indonesia)

30 **SUBMISSION CHECKLIST**

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Further considerations

The brown planthopper (*Nilaparvata lugens* **Stal.) attack and its genetic diversity on rice in Bali, Indonesia**

 Abstract. The brown planthopper *(Nilaparvata lugens Stal.)* is an important pest on rice crops in Indonesia. The genetic diversity of BPH isolates in western Indonesia has been extensively reported, whereas eastern In 10 BPH isolates in western Indonesia has been extensively reported, whereas eastern Indonesia isolates have not been reported. This research aims to analyze genetic diversity and evaluate the BPH attack's intensity on Bali 11 research aims to analyze genetic diversity and evaluate the BPH attack's intensity on Bali rice plants. The research method used was an observation of attack percentage, population dynamics, attack intensity, and geneti 12 observation of attack percentage, population dynamics, attack intensity, and genetic diversity of BPH in 9 districts in Bali (Badung, 13 Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jemb 13 Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana). Molecular identification was carried out 14 on N. *lugens* DNA in the mtCOI fragment. BPH attacks of >50% were found in the distri 14 on *N. lugens* DNA in the mtCOI fragment. BPH attacks of >50% were found in the districts of Gianyar, Bangli, Jembrana, and Badung.
15 The BPH population was primarily found in Ciherang and IR-64 varieties of rice in th 15 The BPH population was primarily found in Ciherang and IR-64 varieties of rice in the Badung Regency, with 43.67 BPH per rice hill.
16 In general, rice varieties grown in all observation locations were susceptible to BP 16 In general, rice varieties grown in all observation locations were susceptible to BPH, such as Ciherang, IR-64, Inpari 32, and Situbagendit. In the Ciherang and IR-64 varieties, the highest attack intensity average valu Situbagendit. In the Ciherang and IR-64 varieties, the highest attack intensity average value reached 30%. The sequence of *N. lugens* 18 isolate from Bali Jembrana showed the highest nucleotide and amino acid homology with *N. lugens* isolate FSD-034 from Pakistan (MK301229) biotype Y of 99.5 -99.74% and 100%, respectively. This study found *N. lugens* b (MK301229) biotype Y of 99.5 -99.74% and 100%, respectively. This study found *N. lugens* biotype Y in rice plants for the first time in Indonesia. This study reported that Rice varieties Situbagendit and Inpari 32, previously resistant to BPH, are reported as susceptible to BPH.

Keywords: attack intensity, genetic diversity, Inpari 32, Situbagendit, susceptible variety

Running title: The Brown Planthopper Attack and Its Genetic Diversity

 $7\,$

INTRODUCTION

 The brown planthopper (BPH) (*Nilaparvata lugens* Stal, Hemiptera: Delphacidae) is the most destructive rice pest in Indonesia. Repeated outbreaks of BPH in Indonesia are caused by continuous rice cultivation, extensive use, and over- application of insecticides (Baehaki 2012). This pest is vascular monophagous in rice (Cheng et al. 2013; Ferrater et al. 2013; Triwidodo 2020). Feeding by nymphs and imago at the base of the plant causes rapid wilting and drying of the plant (Bottrell and Schoenly 2012; Cheng et al. 2013; Bao and Zhang 2019). In addition, BPH is also a vector of *Rice grassy stunt virus* and *Rice ragged stunt virus* (Bao and Zhang 2019). At high population levels of *N. lugens* can cause significant losses in rice production (Cheng et al. 2013; Zheng et al. 2013; Bao and Zhang 2019).

 The BPH cannot tolerate winter in northern Asia, including Japan, Korea, and northern China (He et al. 2012; Fu et al. 2012; Fu et al. 2014). The population originally came from subtropical and tropical areas by flying long distances during the summer (Fu et al. 2014; Hu et al. 2014). BPH infestation in temperate climates originated from annual migrations from tropical Asia and China (He et al. 2012). During autumn, BPH re-migrates (north-to-south) and BPH populations have been studied in China and India (Bottrell and Schoenly 2012). Such return migration may help explain how long-distance migration is maintained in the winter.

 The intensification of rice production triggered the BPH outbreak in Tropical Asia during the green revolution era in the 1970s and 1980s (Bottrell and Schoenly 2012). Until now, *N. lugens* is the main problem causing rice harvest failure in several countries. Inaccurate identification and prolonged identification of *N. lugens* are obstacles to its field management strategy.

 Traditionally, BPH has been identified at the species level by morphological features using anatomical characteristics, namely, wings, front, and external genitalia (Lv et al. 2015). Accurate identification requires extensive expertise and experience and yet sometimes can lead to errors. Morphological identification by an entomologist can reduce the potential for errors. Practical morphological identification is only possible when dealing with small sample sizes and well-preserved specimens. Therefore, it is crucial to utilize a new identification method that is accurate, fast, time-saving, and suitable for large numbers of specimens.

 Molecular techniques with high reproducibility and fast results offer an excellent alternative to traditional morphological classification. Several mitochondrial and nuclear genes have been used as genetic markers to differentiate related species. These include the mitochondrial cytochrome c oxidase subunit 1 (CO1) gene, nuclear 12S-16S-18S 51 ribosomal RNA genes, and ITS1 and ITS2 internal transcription spacers (Brengues et al. 2014; Gomez-Polo et al. 2014; 52 Yu et al. 2014; Wang et al. 2016; Zheng et al. 2021). ITS1 and ITS2 are nonfunctional spacers that separate the 18S-5.8S

 and 5.8S-28S rRNA genes, respectively (Wang et al. 2016; Zheng et al. 2021). As ITS sequences have low intra-species variation but high variation between species, they are helpful for species classification and phylogenetic analysis for morphologically similar organisms, both in prokaryotes and eukaryotes (Zheng et al. 2021). Finally, from the molecular identification of the combined mitochondrial COI-COII and ten microsatellite marker loci (Winnie et al. 2020).

 The genetic diversity of *N. lugens* has been reported in several countries such as China, South Korea, Pakistan, India, 58 and Malaysia (*Jing et al. 2012; Latif et al. 2012; Anant et al. 2021; Zheng et al. 2021*). The genetic diversity of *N. lugens* in 59 Indonesia is widely reported in western Indonesia (Java Island) (Winnie et al. 2020: 59 Indonesia is widely reported in western Indonesia (Java Island) (Winnie et al. 2020; Chaerani et al. 2021). Reports on the genetic diversity of N. *lugens* in eastern Indonesia have not been found. Therefore, this study genetic diversity of *N. lugens* in eastern Indonesia have not been found. Therefore, this study aims to analyze genetic diversity and determine the intensity of BPH attacks on rice plants in eastern Indonesia, especially Bali.

MATERIALS AND METHODS

Brown Planthopper Sampling from Rice Dwarf Disease Endemic Areas

Samples were taken from nine locations at the rice cultivation center in Bali Province (Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana). The brown planthopper samples taken from rice plants were nymphs and imagos. Nymphs and imagos were used for total DNA extraction. After arriving at the laboratory, 67 the nymphs and imago were stored dry at -20° C.

Observation of BPH Attack Symptoms and Quantity of BPH Population/rice hill

 Observation of symptoms of BPH attack was carried out by observing symptoms of damage to rice plants due to BPH 71 attack. The abundance of the BPH/rice hill population was obtained by counting all nymphs and imagoes obtained. Data on the population per cluster from 20 samples or 20 rice hills at each observation fields were then averaged. For each location, 3 fields of rice cultivation center were taken which were used for observation

BPH Attack Percentage

The percentage of BPH attacks is calculated using the following formula:
 $P = \frac{a}{b} \times 100\%$

 $\frac{77}{78}$ Note:

79 $P =$ Attack percentage $(\%)$

80 $a =$ Number of rice hills affected by BPH

b = Number of rice hills observed

Damage Intensity

 Determination of scoring on symptoms of rice damage due to BPH attack is based on Table 1. The intensity of damage due to a BPH attack is determined using the formula (Erdiansyah and Damanhuri 2018):

$$
I = \sum_{i=1}^{n} \frac{N i x V i}{N x Z} x 100\%
$$

 Note:

- 89 $I =$ Damage intensity
- 90 $Ni = The number of affected rice hills on the score i$
91 $Vi = Score i$
-
- 91 $Vi = Score i$
92 $N = The num$ 92 $N =$ The number of rice hills observed
93 $Z =$ Highest score
	- $Z =$ Highest score

Total DNA Extraction from Brown Planthopper

 Total DNA extraction of brown planthopper was obtained from one individual imago or one individual nymph based 97 on the modified method of Goodwin et al. (1994). One individual imago was put into a microtube and then added $\frac{100}{100 \mu}$ 98 of CTAB (Cethyl Trimethyl Ammonium Bromida) extraction buffer (2% CTAB, 1.4 M NaCl, 100 mM Tris-HCI, 20 mM 99 EDTA (Ethylenediaminetetraacetic acid), and 1% PVP (-40 °C)). Next, 1 μl of proteinase K was added, then the insects were crushed using a micro-pistil, vortexed, and incubated in a water bath of 65°C for 3 minutes. After that, the tube was added with 100 μl CI (chloroform: isoamyl alcohol) in a ratio of 24:1. The tube was then vortexed for 3 minutes and centrifuged at 10,000 rpm for 15 minutes. The supernatant formed was transferred to a new microtube (60 μl) and then added with 3 M NaOAc (pH 5.2), as much as 1/10 of the total volume of the supernatant. Isopropanol was added up to 2/3 104 of the total volume of the supernatant, then incubated at -20 $^{\circ}$ C for one night. The tube was centrifuged at 10,000 rpm for 10 min, and the supernatant was discarded. The pellets were washed with 100 μl of 80% ethanol (cold) and centrifuged at 8000 rpm for 5 minutes. In the final step, the supernatant was removed, and the pellet was dried for approximately 1 hour. 107 It was then added to a solution of 20 μ l TE and stored at -20 \degree C until used.

Amplification of mtCOI Fragments Using the PCR Method

 PCR reactants were manufactured with a total volume of 25 μl consisting of 12.5 μl Go Tag Green Master Mix 111 (Promega, US) and 9.5 μl ddH2O. DNA amplification of the mtCOI fragment was carried out using a pair of universal
112 primers mtCOI LCO 1490 (3'-GGTCAACAAATCATAAAGATATTGG-5') and HCO 2198 (5 ΤΑΑΑCTTCA 112 primers mtCOI LCO 1490 (3'-GGTCAACAAATCATAAAGATATTGG-5') and HCO 2198 (5'TAAACTTCA
113 GGGTGACCA AAAAATCA-3') (Folmer et al. 1994) each 1 ul. and 1 ul DNA template. PCR reactions were carried out GGGTGACCA AAAAATCA-3') (Folmer et al. 1994) each 1 μl, and 1 μl DNA template. PCR reactions were carried out 114 with a Perkin Elmer 480 Thermocycler (Applied Biosystem, US). The PCR reaction was initiated by initial denaturation
115 for 5 min at 94°C. The PCR was continued for 35 cycles in the following order: 94°C for 1 minute 115 for 5 min at 94°C. The PCR was continued for 35 cycles in the following order: 94° C for 1 minute, 52° C for 35 seconds, 116 72° C for 1 minute 30 seconds, and a final extension of 72° C for 7 minute 72°C for 1 minute 30 seconds, and a final extension of 72°C for 7 minutes. The PCR results were then analyzed in 1% agarose gel. The DNA fragments of mtCOI were visualized using a UV transilluminator after being immersed in a 2% ethidium bromide solution for 15 minutes and photographed with a digital camera. The result of amplification by PCR 119 technique was in the form of mtCOI DNA fragments with a size of \pm 710 base pairs (pb).

Analysis of DNA Sequence Results

 Nucleotide Sequencing DNA fragment purification and mtCOI nucleotide sequencing were performed at PT. 1st Base, Malaysia. The results were then registered in the NCBI gene bank (http://www.ncbi.nlm.nih.gov). Analysis of mtCOI DNA sequence data ChromasPro program was used to combine forward and reverse nucleotide sequences to obtain the mtCOI gene (ChromasPro version 2.01. 2006). The Bioedit program was used to compare mtCOI fragments between 126 samples (Multiple alignments). The phylogenetic relationship was built by comparing the mtCOI sample fragments from
127 the brown planthopper from Indonesia with the mtCOI fragments already stored in the NCBI GenBank 127 the brown planthopper from Indonesia with the mtCOI fragments already stored in the NCBI GenBank
128 (http://www.ncbi.nlm.nih.gov). The criteria for retrieving mtCOI fragments at GenBank were fragments with a nucleotid (http://www.ncbi.nlm.nih.gov). The criteria for retrieving mtCOI fragments at GenBank were fragments with a nucleotide 129 base length of \pm 710 bp (Boykin et al. 2007) (Table 3; Figure 3). The phylogenetic tree was constructed using the PAUP 4.0b10 program with the maximum parsimony cladistic quantitative method. The cladogram was compiled using the Heuristic method. The cladogram used results from the strick consensus with the statistical bootstrap test to obtain a 100% probability.

RESULTS AND DISCUSSION

134 The brown planthopper causes direct and indirect damage to rice plants. Direct damage was in the form of stunted and 135 uneven growth of rice plants (Figure 1A and 1B), yellow plants (Figure 1C), and hopperburn caused uneven growth of rice plants (Figure 1A and 1B), yellow plants (Figure 1C), and hopperburn caused by fluid in rice plant cells sucked by BPH nymphs, brachiptera (Fig. short wings), and macroptera (long wings) (Figures 1E and 1F). Indirect 137 damage was caused by BPH, which acts as a vector of *Rice grassy stunt virus* and *Rice ragged stunt virus*, causing stunted
138 rice plants (Figure 1D). Besides Bali or other parts of Indonesia. BPH attacks on rice cr rice plants (Figure 1D). Besides Bali or other parts of Indonesia, BPH attacks on rice crops were also reported in China, where hopperburn affected 60% of all examined crops (Hu et al. 2014). Transmission of the stunt virus by the brown planthoppers occurs persistently (Horgan et al. 2015). Virus infection causes damage to plants because viruses use plant proteins for replication, resulting in loss of crop production (Listihani et al. 2020; Damayanti et al. 2022; Listihani et al. 2022; Pandawani et al. 2022; Selangga and Listihani 2022; Selangga et al. 2022). Therefore, infection with RGSV and RRSV in rice plants causes rice to lack nutrients to the point of stunting.

 A percentage of BPH attacks of more than 50% was found in Gianyar, Bangli, Jembrana, and Badung Regencies (Table 2). The BPH population was primarily found in Ciherang and IR-64 varieties of rice in the Badung Regency, with 43.67 BPH per rice hill (Table 2). Baehaki (2012) added that the economic threshold could be measured through the number or population of pests and planting age. BPH is said to have reached the economic threshold when the population of this pest was found in the field, as many as nine BPH per rice hill when the rice age was less than 40 DAP or 18 BPH when the rice was more than 40 DAP (Baehaki 2012). In general, rice varieties grown in all observation locations in Bali were BPH susceptible varieties, such as Ciherang, IR-64, Inpari 32, and Situbagendit.

 The dynamics of BPH development in the field can be influenced by several factors, including host plant factors and natural enemies (Ferrater et al. 2015; Horgan et al. 2015; Kobayashi 2016). The host plant factors that affect the BPH population are related to the age of the rice plant. When the observations were made, the rice plants were still in the vegetative phase, aged 4-6 WAP. According to Jing et al. (2014), naturally, BPH usually comes to young rice fields, and insects usually come in the first two weeks after planting. Thus, the brown planthopper in rice cultivation might be the first generation of planthoppers that have not yet reproduced because one BPH life cycle takes between 3-4 weeks (IRRI 2009).

 BPH observations in Denpasar, Tabanan, Karangasem, and Klungkung cities were dominated by macroptera imago (Table 2). According to Horgan et al. (2017), the planthopper that first came to the plantation was the macroptera planthopper as a winged immigrant planthopper. Meanwhile, in Badung, Gianyar, Buleleng, Bangli, and Jembrana regencies, nymphal BPH was dominated by BPH, and several individuals were in the imago phase of brachiptera and macroptera. The dominance of the nymph phase caused the population of BPH in Badung, Gianyar, Buleleng, Bangli, and Jembrana districts to be the highest when compared to the cities of Denpasar, Tabanan, Karangasem, and Klungkung. The presence of the brachiptera planthopper might be contributed to the increase in the nymph population (Baehaki 2012). Rapid population growth usually occurs in groups with many young individuals (Horgan et al. 2015; Triwidodo and Listihani 2020).

 The average intensity of BPH attack on Ciherang and IR-64 varieties of rice was higher than in other varieties. In the Ciherang and IR-64 varieties of rice, the average value of the highest attack intensity was 30% (Figure 2). It is because 168 farmers grow rice varieties Ciherang and IR-64 from year to year without any replacement of other varieties. Furthermore,
169 rice varieties Ciherang and IR-64 became very susceptible to BPH attacks. In addition. BPH i 169 rice varieties Ciherang and IR-64 became very susceptible to BPH attacks. In addition, BPH is a pest that begins to attack 170 rice plants from a voung age, even when the rice is still in the nursery. rice plants from a young age, even when the rice is still in the nursery.

171 According to Vu et al. (2014), fluctuations in BPH pest attacks are more influenced by the growth phase of the rice
172 plant that is the host in the field. BPH pests are often found when rice plants are in the vegetat 172 plant that is the host in the field. BPH pests are often found when rice plants are in the vegetative and generative stages (Bottrell and Schoenly 2012). Horgan et al. (2017) added that BPH pests could damage rice plan (Bottrell and Schoenly 2012). Horgan et al. (2017) added that BPH pests could damage rice plants at all stages of growth 174 and act as vectors for grass and dwarf viruses. BPH attack was higher when rice was in the vegetative phase than in the generative phase (Horgan et al. 2015). It happens because the pests attack the young rice stalks. generative phase (Horgan et al. 2015). It happens because the pests attack the young rice stalks. Considering the type of mouth of BPH, which is included in the suction, BPH can suck the liquid from the rice stems and cause the plant leaves to turn yellow (Anant et al. 2021). According to Choi et al. (2019) and Sutrawati et al. (2021), during the vegetative phase, food availability in the form of nitrogen is abundant in rice plants. Rice plants need nitrogen to form plant organs. Food is one of the factors that affect the life of insects. Horgan (2018) continued that the N element absorbed by plants also serves as a source of nutrition for BPH. If food is available with good quality (suitable for pests), then the insect pest population will increase, and vice versa (Horgan 2018; Triwidodo and Listihani 2020).

182 The mtCOI DNA band was successfully amplified from the total DNA extraction of one imago or nymph of BPH. The 183 mtCOI fragment that was successfully amplified corresponds to a size of ±710 bp in all samples from nine districts in Bali, 184 namely Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, a namely Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana (Figure 3).
185 Nucleotide and amino acid sequence analysis showed high homology with N. lugens sequences in the databas Nucleotide and amino acid sequence analysis showed high homology with *N. lugens* sequences in the database at GenBank, 94.2 – 99.7% and 95.8 - 100%, respectively (Table 3). *N. lugens* sequences from Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana showed the highest nucleotide, and amino acid homology with *N. lugens* isolate FSD-034 from Pakistan (MK301229) biotype Y, respectively. 99.5 -99.74% and 100% (Table 3). The results of the molecular detection of *N. lugens* using the PCR method in Bali, Indonesia, are the first reports 190 of the molecular character of *N. lugens* in Indonesia.
191 Samples from Indonesia formed a group with *N*.

 Samples from Indonesia formed a group with *N. lugens* biotype Y fragment mtCOI from Pakistan, India, South Korea, 192 and China (Figure 4). This study found *N. lugens* biotype Y in rice plants for the first time in Indonesia. The Indonesian
193 sample did not form separate groups according to the proximity of the district locations b 193 sample did not form separate groups according to the proximity of the district locations but formed a polytomy cladogram
194 (Figure 4). This polytomy cladogram shows that the N. lugens between regencies (Badung, Giany (Figure 4). This polytomy cladogram shows that the *N. lugens* between regencies (Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana) were observed to have the same ancestry. These results indicate high locomotion ability with genetic mixing between *N. lugens* in Bali isolates. Similar conditions were also demonstrated in *N. lugens* among Asian isolates using mitochondrial sequences showing genetic mixing. It can also be correlated with the theory of long-distance migration of *N. lugens*, which migrates from the tropics (northern Vietnam) in April-May to temperate regions (China, Korea, and Japan) in June-July as shown based on meteorological studies (Otuka et al. 2008). The population of *N. lugens* is a long-distance migratory flight from the tropics to temperate Asia before modern pesticides are widely used in tropical rice. Due to the infrequent use of insecticides prior to the 1960s in the tropics, factors other than insecticides may have triggered long-wing movements to form *N. lugens* populations (Bottrell 203 and Schoenly 2012).
204 In previous studies

 In previous studies in Indonesia, BPH biotypes 1, 2, 3, and 4 have been found. Kobayashi et al. (2014) reported that the 205 brown planthopper is a highly adaptive insect because it can form new biotypes. In early 1975 the IR-26 rice variety from 206 IRRI Philippines was introduced. The IR-26 variety was unique because it contained a Bph1 re IRRI Philippines was introduced. The IR-26 variety was unique because it contained a Bph1 resistant gene to anticipate fluctuations in the brown planthopper population. However, in 1976 there was a great population explosion in several rice production centers due to changes in the brown planthopper population from biotype 1 to biotype 2. As an anticipatory measure against brown planthopper biotype 2, in 1980, the IR-42 rice variety (containing the bph2 resistant gene) was introduced from IRRI Philippines. Unfortunately, in 1981 there was another explosion in the brown planthopper population in Simalungun, North Sumatra, and several other areas due to changes in the brown planthopper population from biotype 2 to biotype 3. To deal with the brown planthopper biotype 3, rice variety IR-56 was introduced (containing the gene bph3 resistance) in 1983 and IR-64 (containing the bph1+ resistance gene) in 1986. The introduction process 214 continues. In 1991, the IR-74 variety (containing the bph3 resistant gene) was introduced. In 2006, the resistance gene IR-
215 64 was broken because the brown planthopper population changed to biotype 4 (Baehaki 2012) 64 was broken because the brown planthopper population changed to biotype 4 (Baehaki 2012). The stability of the biotype zero brown planthoppers persisted for 41 years before becoming brown planthopper biotype 1. The change of brown planthopper biotype 1 to biotype 2 only took 4 years, and the change of biotype 2 brown planthopper to biotype 3 within 5 years. Until 2005, the brown planthopper biotype 3 was still dominated by biotype 3, and in 2006 the biotype 4 brown planthopper began to develop. The long existence of the biotype 3 brown planthopper was caused by the development of the IR-64 (bph1+) variety over a long period. IR-64 is a resistant variety (durable resistance) that can withstand changes in brown planthoppers to a more virulent biotype.

222 The continuous cultivation of IR-64 rice varieties by farmers in Bali led to the emergence of a new biotype BPH, 223 namely Y. Insects of biotype Y originated from biotype 1 by eating YHY15 resistant varieties for more than two years for 224 33 generations (Jing et al. 2012). Rice varieties YHY15 carry the Bph15 resistance gene (Jing et al. 2012).
225 This study shows great potential in the population of *N. lugens* to adapt to previously resistant rice va

225 This study shows great potential in the population of *N. lugens* to adapt to previously resistant rice varieties. This study reported that rice varieties Situbagendit and Inpari 32, previously resistant to BPH, were s 226 reported that rice varieties Situbagendit and Inpari 32, previously resistant to BPH, were susceptible to BPH. This research 227 can provide information to farmers not to continuously plant susceptible varieties, which could cause BPH epidemics in the field, as well as the emergence of new, more virulent BPH biotypes. Thus a new control strategy 228 the field, as well as the emergence of new, more virulent BPH biotypes. Thus a new control strategy based on a forecasting system can be developed for the regional management of this insect. system can be developed for the regional management of this insect.

230 In conclusion, *N. lugens* that attacks rice plants in Bali (Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, 231 Denpasar City, Buleleng, and Jembrana) belongs to biotype Y. Symptoms of damage to rice plants a 231 Denpasar City, Buleleng, and Jembrana) belongs to biotype Y. Symptoms of damage to rice plants are most severe in
232 Badung Regency, Apart from Ciherang and IR-64 varieties. Situbagendit and Inpari 32 varieties are su 232 Badung Regency. Apart from Ciherang and IR-64 varieties, Situbagendit and Inpari 32 varieties are susceptible to BPH attack.

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1 **TABLES LIST**

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Sumber: Baehaki (2012)

6 **Table 2.** Population and symptoms of BPH attack on rice plants in Bali

Location	Rice varieties	Rice plant age (DAP)	BPH attack percentage $(\%)$	BPH population abundance (individues/rice hills)
Denpasar City	Situbagendit, Inpari 32	35	35.43	7.41
Badung	Ciherang, IR-64	42	73.61	43.67
Gianyar	Ciherang, Inpari 32	45	52.26	12.49
Tabanan	Inpari 32	41	37.94	9.26
Buleleng	Ciherang, IR-64	33	46.82	11.28
Karangasem	Situbagendit	30	32.73	7.92
Klungkung	Inpari 32	43	35.89	8.53
Bangli	Ciherang, IR-64	42	52.80	14.83
Jembrana	Ciherang, Inpari 32	36	57.32	11.95

Note: DAP= day after planting

 $\frac{1}{2}$

2 **Table 3.** Nucleotide (nt) and amino acid (aa) homology of *N. lugens* in rice from Bali, Indonesia, compared with *N. lugens* from other countries in GenBank

Isolate	Origin - of	Biotype	Accession					Homology nt (aa) $(\%)$ N. lugens IDN				
	isolate		number	Denpasar	Badung	Gianyar	Tabanan	Buleleng	Karangasem	Klungkung	Bangli	Jembrana
FSD-034	PAK		MK301229	99.5 (100)	99.6 (100)	99.5 (100)	99.5 (100)	99.6 (100)	99.5 (100)	99.7 (100)	99.5 (100)	99.6 (100)
HZZ55	IND		MK032794	99.4 (100)	99.5 (100)	99.4 (100)	99.5 (100)	99.4 (100)	99.5 (100)	99.6 (100)	99.5 (100)	99.6 (100)
SAEVG_Morph0111	IND		MN520923	99.4 (100)	99.5 (100)	99.4 (100)	99.5 (100)	99.4 (100)	99.5 (100)	99.5 (100)	99.5 (100)	99.6 (100)
KBPH	KOR		MK590088	99.3 (100)	99.5 (100)	99.4 (100)	99.4 (100)	99.3 (100)	99.4 (100)	99.4 (100)	99.4 (100)	99.5 (100)
KOREA BPH	KOR		LC461184	99.3 (100)	99.5 (100)	99.4 (100)	99.4 (100)	99.3 (100)	99.4 (100)	99.4 (100)	99.4 (100)	99.5 (100)
WUHAN-Y	CHN		KC333653	99.3 (100)	99.5 (100)	99.4 (100)	99.4 (100)	99.3 (100)	99.4 (100)	99.4 (100)	99.3 (100)	99.4 (100)
WUHAN-3	CHN		JN563997	97.8 (98.1)	97.2 (97.8)	97.5 (98.9)	97.5 (98.9)	97.4 (97.9)	97.8 (98.1)	97.5 (98.9)	97.2 (98.8)	97.6 (98.0)
WUHAN-2	CHN		JN563996	96.3 (97.5)	96.3 (97.5)	96.4 (97.5)	96.3 (97.5)	96.2 (97.4)	96.4 (97.5)	96.3 (97.5)	96.2 (97.4)	96.3 (97.5)
WUHAN-1	CHN		JN563995	95.3 (96.7)	95.4 (96.7)	95.3 (96.7)	95.4 (96.7)	95.6 (96.8)	95.6 (96.8)	95.3 (96.7)	95.4 (96.7)	95.3 (96.7)
GX	CHN		LC461186	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)	95.4 (96.7)	95.5 (96.8)	95.5 (96.8)	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)
Gangavathi	IND		OL451531	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)	95.5 (96.8)	95.5 (96.8)	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)
WUHAN-L	CHN		KC333654	94.2 (95.8)	94.4 (96.2)	94.2 (95.8)	94.4 (96.2)	94.3 (96.0)	94.4 (96.2)	94.2 (95.8)	94.4 (96.2)	94.4 (96.2)
N. bakeri	CHN	$\overline{}$	JX266790	84.6 (85.6)	85.2 (86.1)	84.8 (85.9)	84.8 (85.9)	84.6 (85.6)	85.2 (86.1)	84.8 (85.9)	85.2 (86.1)	85.2 (86.1)
Sogatella furcifera	CHN		HM160123	75.6 (76.9)	75.6 (76.9)	76.2 (77.8)	77.6 (78.4)	77.4 (78.4)	76.8 (77.8)	75.6 (76.9)	76.8 (77.8)	77.6 (78.4)

3 Notes: nt (nucleotide), aa (amino acid), IDN (Indonesia), PAK (Pakistan), IND (India), KOR (South Korea), CHN (China), *N. bakeri* and *Sogatella furcifera* from China was used as outgroups

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5

6

FIGURES LIST

 Figure 1. Symptoms of BPH attack on rice plants in Bali: A. rice plant growth is stunted; B. uneven plant growth (spots); C. yellow plant; D. dwarf rice plants; E. plants die like burning (hopperburn); F. BPH brachiptera and macroptera were found on rice stalks.

Observation locations in 9 Regency in Bali

 $\frac{15}{16}$ 16 **Figure 3.** DNA amplification of *N. lugens* in rice plants in Bali using primers LCO 1490/HCO 2198. 1. Denpasar City, 2. Bagung, 3. 17 Gianyar, 4. Tabanan, 5. Buleleng, 6. Karangasemt, 7. Klungkung, 8. Bangli, 9. Jembrana, and M. DNA marker 1 kb (Thermo Scientific)

24 25

18

19 **Figure 4.** The cladogram of the mtCOI fragment of *N. lugens* from eastern Indonesia, Bali (Badung, Gianyar, Klungkung, Bangli, 20 Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana) was compared with mtCOI fragments from several regions of the world
21 that had been deposited on the NCBI website. N. bakeri and Sogatella furcifera from Chin 21 that had been deposited on the NCBI website. *N. bakeri* and *Sogatella furcifera* from China were used as outgroups. The numbers on the branching cladograms represent bootstrap values with 100% probability. IDN (Indone branching cladograms represent bootstrap values with 100% probability. IDN (Indonesia), PAK (Pakistan), IND (India), KOR (South Korea), and CHN (China), isolates marked with black dots are Bali isolates.

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The brown planthopper (*Nilaparvata lugens***) attack and its genetic diversity on rice in Bali, Indonesia**

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Abstract. Listihani L, Ariati PEP, Yuniti IGAD, Selangga DGW. 2022. The brown planthopper (Nilaparvata lugens) attack and its *genetic diversity on rice in Bali, Indonesia. Biodiversitas 23: 4696-4704.* The brown planthopper (*Nilaparvata lugens*) is an important pest on rice crops in Indonesia. The genetic diversity of BPH isolates in western Indonesia has been extensively reported, whereas eastern Indonesia isolates have not been reported. This research aims to analyze genetic diversity and evaluate the BPH attack's intensity on Bali rice plants. The research method used was an observation of attack percentage, population dynamics, attack intensity, and genetic diversity of BPH in 9 districts in Bali (Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana). Molecular identification was carried out on *N. lugens* DNA in the mtCOI fragment. BPH attacks of >50% were found in the districts of Gianyar, Bangli, Jembrana, and Badung. The BPH population was primarily found in Ciherang and IR-64 varieties of rice in the Badung Regency, with 43.67 BPH per rice hill. In general, rice varieties grown in all observation locations were susceptible to BPH, such as Ciherang, IR-64, Inpari 32, and Situbagendit. In the Ciherang and IR-64 varieties, the highest attack intensity average value reached 30%. The sequence of *N. lugens* isolate from Bali Jembrana showed the highest nucleotide and amino acid homology with *N. lugens* isolate FSD-034 from Pakistan (MK301229) biotype Y of 99.5 -99.74% and 100%, respectively. This study found *N. lugens* biotype Y in rice plants for the first time in Indonesia. This study reported that Rice varieties Situbagendit and Inpari 32, previously resistant to BPH, are reported as susceptible to BPH.

Keywords: Attack intensity, genetic diversity, Inpari 32, Situbagendit, susceptible variety

INTRODUCTION

The brown planthopper (BPH) (*Nilaparvata lugens*, Hemiptera: Delphacidae) is the most destructive rice pest in Indonesia. Repeated outbreaks of BPH in Indonesia are caused by continuous rice cultivation, extensive use, and over-application of insecticides (Baehaki 2012). This pest is vascular monophagous in rice (Cheng et al. 2013; Ferrater et al. 2013; Triwidodo 2020). Feeding by nymphs and imago at the base of the plant causes rapid wilting and drying of the plant (Bottrell and Schoenly 2012; Cheng et al. 2013; Bao and Zhang 2019). In addition, BPH is also a vector of Rice grassy stunt virus and Rice ragged stunt virus (Bao and Zhang 2019). High population levels of *N. lugens* can cause significant losses in rice production (Cheng et al. 2013; Zheng et al. 2013; Bao and Zhang 2019).

The BPH cannot tolerate winter in northern Asia, including Japan, Korea, and northern China (Fu et al. 2012; He et al. 2012; Fu et al. 2014). The population originally came from subtropical and tropical areas by flying long distances during the summer (Fu et al. 2014; Hu et al. 2014). BPH infestation in temperate climates originated from annual migrations from tropical Asia and China (He et al. 2012). During autumn, BPH re-migrates (north-tosouth) and BPH populations have been studied in China and India (Bottrell and Schoenly 2012). Such return migration may help explain how long-distance migration is maintained in the winter.

The intensification of rice production triggered the BPH outbreak in Tropical Asia during the green revolution era in the 1970s and 1980s (Bottrell and Schoenly 2012). Until now, *N. lugens* is the main problem causing rice harvest failure in several countries. Inaccurate identification and prolonged identification of *N. lugens* are obstacles to its field management strategy.

Traditionally, BPH has been identified at the species level by morphological features using anatomical characteristics, namely, wings, front, and external genitalia (Lv et al. 2015). Accurate identification requires extensive expertise and experience and yet sometimes can lead to errors. Morphological identification by an entomologist can reduce the potential for errors. Practical morphological identification is only possible when dealing with small sample sizes and well-preserved specimens. Therefore, it is crucial to utilize a new identification method that is accurate, fast, time-saving, and suitable for large numbers of specimens.

Molecular techniques with high reproducibility and fast results offer an excellent alternative to traditional morphological classification. Several mitochondrial and nuclear genes have been used as genetic markers to differentiate related species. These include the mitochondrial cytochrome c oxidase subunit 1 (CO1) gene,

nuclear 12S-16S-18S ribosomal RNA genes, and ITS1 and ITS2 internal transcription spacers (Brengues et al. 2014; Gomez-Polo et al. 2014; Yu et al. 2014; Wang et al. 2016; Zheng et al. 2021). ITS1 and ITS2 are nonfunctional spacers that separate the 18S-5.8S and 5.8S-28S rRNA genes, respectively (Wang et al. 2016; Zheng et al. 2021). As ITS sequences have low intra-species variation but high variation between species, they are helpful for species classification and phylogenetic analysis for morphologically similar organisms, both in prokaryotes and eukaryotes (Zheng et al. 2021). Finally, from the molecular identification of the combined mitochondrial COI-COII and ten microsatellite marker loci (Winnie et al. 2020).

The genetic diversity of *N. lugens* has been reported in several countries, such as China, South Korea, Pakistan, India, and Malaysia (Jing et al. 2012; Latif et al. 2012; Anant et al. 2021; Zheng et al. 2021). The genetic diversity of *N. lugens* in Indonesia is widely reported in western Indonesia (Java Island) (Winnie et al. 2020; Chaerani et al. 2021). Reports on the genetic diversity of *N. lugens* in eastern Indonesia have not been found. Therefore, this study aims to analyze genetic diversity and determine the intensity of BPH attacks on rice plants in eastern Indonesia, especially Bali.

MATERIALS AND METHODS

Brown planthopper sampling from rice dwarf disease endemic areas

Samples were taken from nine locations at the rice cultivation center in Bali Province (Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana). The brown planthopper samples taken from rice plants were nymphs and imagos. Nymphs and imagos were used for total DNA extraction. After arriving at the laboratory, the nymphs and imago were stored dry at -20°C.

Observation of BPH attack symptoms and quantity of BPH population/rice hills

Observation of symptoms of BPH attack was carried out by observing symptoms of damage to rice plants due to BPH attack. The abundance of the BPH/rice hills population was obtained by counting all nymphs and imagoes obtained. Data on the population per cluster from 20 samples or 20 rice hills at each observation fields were then averaged. For each location, 3 fields of rice cultivation center were taken, which were used for observation.

BPH attack percentage

The percentage of BPH attacks is calculated using the following formula:

$$
P = \frac{a}{b} \times 100\%
$$

Where:

P : Attack percentage $(\%)$

a : Number of rice hills affected by BPH

b : Number of rice hills observed

Damage intensity

Determination of scoring on symptoms of rice damage due to BPH attack is based on Table 1. The intensity of damage due to a BPH attack is determined using the formula (Erdiansyah and Damanhuri 2018):

$$
I = \sum_{i=1}^{N} \frac{N i x V i}{N x Z} x 100\%
$$

Where:

- I : Damage intensity
- Ni : The number of affected rice hills on the score i
- Vi : Score i
N : The nui
- N : The number of rice hills observed

Z : Highest score
- : Highest score

Total DNA extraction from brown planthopper

Total DNA extraction of brown planthopper was obtained from one individual imago or one individual nymph based on the modified method of Goodwin et al. (1994). One individual imago was put into a microtube and then added to 100 μL of CTAB (Cethyl Trimethyl Ammonium Bromida) extraction buffer (2% CTAB, 1.4 M NaCl, 100 mM Tris-HCI, 20 mM EDTA (Ethylenediaminetetraacetic acid), and 1% PVP (-40°C). Next, 1 μL of proteinase K was added, then the insects were crushed using a micro-pistil, vortexed, and incubated in a water bath of 65°C for 3 minutes.

Table 1. The damage score of rice plants due to BPH attack (Baehaki 2012)

After that, the tube was added with 100 μL CI (chloroform: isoamyl alcohol) in a ratio of 24:1. The tube was then vortexed for 3 minutes and centrifuged at 10,000 rpm for 15 minutes. The supernatant formed was transferred to a new microtube (60 μL) and then added with 3 M NaOAc (pH 5.2), as much as 1/10 of the total volume of the supernatant. Isopropanol was added up to 2/3 of the total volume of the supernatant, then incubated at -20°C for one night. The tube was centrifuged at 10,000 rpm for 10 min, and the supernatant was discarded. The pellets were washed with 100 μL of 80% ethanol (cold) and centrifuged at 8000 rpm for 5 minutes. In the final step, the supernatant was removed, and the pellet was dried for approximately 1 hour. It was then added to a solution of 20 μL TE and stored at -20°C until used.

Amplification of mtCOI fragments using the PCR method

PCR reactants were manufactured with a total volume of 25 μL consisting of 12.5 μL Go Tag Green Master Mix (Promega, US) and $9.5 \mu L$ ddH₂O. DNA amplification of the mtCOI fragment was carried out using a pair of
universal primers mtCOI LCO 1490 (3'universal primers mtCOI LCO 1490 (3'- GGTCAACAAATCATAAAGATATTGG-5') and HCO 2198 (5'-TAAACTTCAGGGTGACCAAAAAATCA-3') (Folmer et al. 1994) each 1 μL, and 1 μL DNA template. PCR reactions were carried out with a Perkin Elmer 480 Thermocycler (Applied Biosystem, US). The PCR reaction was initiated by initial denaturation for 5 min at 94°C. The PCR was continued for 35 cycles in the following order: 94°C for 1 minute, 52°C for 35 seconds, 72°C for 1 minute 30 seconds, and a final extension of 72°C for 7 minutes. The PCR results were then analyzed in 1% agarose gel. The DNA fragments of mtCOI were visualized using a UV transilluminator after being immersed in a 2% ethidium bromide solution for 15 minutes and photographed with a digital camera. The result of amplification by PCR technique was in the form of mtCOI DNA fragments with a size of \pm 710 base pairs (bp).

Analysis of DNA sequence results

Nucleotide sequencing DNA fragment purification and mtCOI nucleotide sequencing were performed at PT. 1st Base, Malaysia. The results were then registered in the NCBI gene bank (http://www.ncbi.nlm.nih.gov). Analysis of mtCOI DNA sequence data ChromasPro program was used to combine forward and reverse nucleotide sequences to obtain the mtCOI gene (ChromasPro version 2.01. 2006). The Bioedit program was used to compare mtCOI fragments between samples (Multiple alignments). The phylogenetic relationship was built by comparing the mtCOI sample fragments from the brown planthopper from Indonesia with the mtCOI fragments already stored in the NCBI GenBank (http://www.ncbi.nlm.nih.gov). The criteria for retrieving mtCOI fragments at GenBank were fragments with a nucleotide base length of ± 710 bp (Boykin et al. 2007) (Table 3, Figure 3). The phylogenetic tree was constructed using the PAUP 4.0b10 program with the maximum parsimony cladistic quantitative method. The cladogram was compiled using the Heuristic method. The cladogram used results from the strict consensus with the statistical bootstrap test to obtain a 100% probability.

RESULTS AND DISCUSSION

The brown planthopper causes direct and indirect damage to rice plants. Direct damage was in the form of stunted and uneven growth of rice plants (Figure 1A and 1B), yellow plants (Figure 1C), and hopperburn caused by fluid in rice plant cells sucked by BPH nymphs, brachyptera (short wings), and macroptera (long wings) (Figures 1E and 1F). Indirect damage was caused by BPH, which acts as a vector of Rice grassy stunt virus and Rice ragged stunt virus, causing stunted rice plants (Figure 1D). Besides Bali or other parts of Indonesia, BPH attacks on rice crops were also reported in China, where hopperburn affected 60% of all examined crops (Hu et al. 2014). Transmission of the stunt virus by the brown planthoppers occurs persistently (Horgan et al. 2015). Virus infection causes damage to plants because viruses use plant proteins for replication, resulting in loss of crop production (Listihani et al. 2020; Damayanti et al. 2022; Listihani et al. 2022; Pandawani et al. 2022; Selangga and Listihani 2022; Selangga et al. 2022). Therefore, infection with RGSV and RRSV in rice plants causes the rice to lack nutrients to the point of stunting.

A percentage of BPH attacks of more than 50% was found in Gianyar, Bangli, Jembrana, and Badung Regencies (Table 2). The BPH population was primarily found in Ciherang and IR-64 varieties of rice in the Badung Regency, with 43.67 BPH per rice hill. Baehaki (2012) added that the economic threshold could be measured through the number or population of pests and planting age. BPH is said to have reached the economic threshold when the population of this pest was found in the field, as many as nine BPH per rice hill when the rice age was less than 40 DAP or 18 BPH when the rice was more than 40 DAP (Baehaki 2012). In general, rice varieties grown in all observation locations in Bali were BPH susceptible varieties, such as Ciherang, IR-64, Inpari 32, and Situbagendit.

The dynamics of BPH development in the field can be influenced by several factors, including host plant factors and natural enemies (Ferrater et al. 2015; Horgan et al. 2015; Kobayashi 2016). The host plant factors that affect the BPH population are related to the age of the rice plant. When the observations were made, the rice plants were still in the vegetative phase, aged 4-6 WAP. According to Jing et al. (2014), naturally, BPH usually comes to young rice fields, and insects usually come in the first two weeks after planting. Thus, the brown planthopper in rice cultivation might be the first generation of planthoppers that have not yet reproduced because one BPH life cycle takes between 3-4 weeks (IRRI 2009).

Figure 1. Symptoms of BPH attack on rice plants in Bali. A. Rice plant growth is stunted; B. Uneven plant growth (spots); C. Yellow plant; D. Dwarf rice plants; E. Plants die like burning (hopperburn); F. BPH brachiptera and macroptera were found on rice stalks

Table 2. Population and symptoms of BPH attack on rice plants in Bali, Indonesia

Location	Rice varieties	Rice plant age (DAP)		BPH population abundance (individues/rice hills)
Denpasar City	Situbagendit, Inpari 32	35	35.43	7.41
Badung	Ciherang, IR-64	42	73.61	43.67
Gianyar	Ciherang, Inpari 32	45	52.26	12.49
Tabanan	Inpari 32	41	37.94	9.26
Buleleng	Ciherang, IR-64	33	46.82	11.28
Karangasem	Situbagendit	30	32.73	7.92
Klungkung	Inpari 32	43	35.89	8.53
Bangli	Ciherang, IR-64	42	52.80	14.83
Jembrana	Ciherang, Inpari 32	36	57.32	11.95

Note: DAP: day after planting

BPH observations in Denpasar, Tabanan, Karangasem, and Klungkung districts were dominated by macroptera imago (Table 2). According to Horgan et al. (2017), the planthopper that first came to the plantation was the macroptera planthopper as a winged immigrant planthopper. Meanwhile, in Badung, Gianyar, Buleleng, Bangli, and Jembrana districts, nymphs BPH was dominated by BPH, and several individuals were in the imago phase of brachyptera and macroptera. The dominance of the nymph phase caused the population of BPH in Badung, Gianyar, Buleleng, Bangli, and Jembrana districts to be the highest when compared to the districts of Denpasar, Tabanan, Karangasem, and Klungkung. The presence of the brachyptera planthopper might be contributed to the increase in the nymph population (Baehaki 2012). Rapid population growth usually occurs in groups with many young individuals (Horgan et al. 2015; Triwidodo and Listihani 2020).

The average intensity of BPH attack on Ciherang and IR-64 varieties of rice was higher than in other varieties. In the Ciherang and IR-64 varieties of rice, the average value of the highest attack intensity was 30% (Figure 2). It is because farmers grow rice varieties Ciherang and IR-64 from year to year without any replacement of other varieties. Furthermore, rice varieties Ciherang and IR-64 became very susceptible to BPH attacks. In addition, BPH is a pest that begins to attack rice plants from a young age, even when the rice is still in the nursery.

According to Vu et al. (2014), fluctuations in BPH pest attacks are more influenced by the growth phase of the rice plant that is the host in the field. BPH pests are often found when rice plants are in the vegetative and generative stages (Bottrell and Schoenly 2012). Horgan et al. (2017) added that BPH pests could damage rice plants at all stages of growth and act as vectors for grass and dwarf viruses. BPH attack was higher when rice was in the vegetative phase than in the generative phase (Horgan et al. 2015). It happens because the pests attack the young rice stalks. Considering the type of mouth of BPH, which is included in the suction, BPH can suck the liquid from the rice stems and cause the plant leaves to turn yellow (Anant et al. 2021). According to Choi et al. (2019) and Sutrawati et al. (2021), during the vegetative phase, food availability in the form of nitrogen is abundant in rice plants. Rice plants need nitrogen to form plant organs. Food is one of the factors that affect the life of insects. Horgan (2018) continued that the N element absorbed by plants also serves as a source of nutrition for BPH. If food is available with good quality (suitable for pests), then the insect pest population will increase, and vice versa (Horgan 2018; Triwidodo and Listihani 2020).

The mtCOI DNA band was successfully amplified from the total DNA extraction of one imago or nymph of BPH. The mtCOI fragment that was successfully amplified corresponds to a size of \pm 710 bp in all samples from nine districts in Bali, namely Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana (Figure 3). Nucleotide and amino acid sequence analysis showed high homology with *N. lugens* sequences in the database at GenBank, 94.2-99.7% and 95.8-100%, respectively (Table 3). *Nilaparvata lugens* sequences from Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana showed the highest nucleotide, and amino acid homology with *N. lugens* isolate FSD-034 from Pakistan (MK301229) biotype Y, respectively. 99.5-99.74% and 100% (Table 3). The results of the molecular detection of *N. lugens* using the PCR method in Bali, Indonesia, are the first reports of the molecular character of *N. lugens* in Indonesia.

Samples from Indonesia formed a group with *N. lugens* biotype Y fragment mtCOI from Pakistan, India, South Korea, and China (Figure 4). This study found *N. lugens* biotype Y in rice plants for the first time in Indonesia. The Indonesian sample did not form separate groups according to the proximity of the district locations but formed a polytomy cladogram (Figure 4). This polytomy cladogram shows that the *N. lugens* between regencies (Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana) were observed to have the same ancestry. These results indicate high locomotion ability with genetic mixing between *N. lugens* in Bali isolates. Similar conditions were also demonstrated in *N. lugens* among Asian isolates using mitochondrial sequences showing genetic mixing. It can also be correlated with the theory of long-distance migration of *N. lugens*, which migrates from the tropics (northern Vietnam) in April-May to temperate regions (China, Korea, and Japan) in June-July as shown based on meteorological studies (Otuka et al. 2008). The population of *N. lugens* is a long-distance migratory flight from the tropics to temperate Asia before modern pesticides are widely used in tropical rice. Due to the infrequent use of insecticides prior to the 1960s in the tropics, factors other than insecticides may have triggered long-wing movements to form *N. lugens* populations (Bottrell and Schoenly 2012).

Observation locations in 9 Regency in Bali

Figure 2. The attack intensity of *Nilaparvata lugens* on rice in Bali Province, Indonesia

Figure 3. DNA amplification of *Nilaparvata lugens* in rice plants in Bali using primers LCO 1490/HCO 2198. 1. Denpasar City; 2. Bagung; 3. Gianyar; 4. Tabanan; 5. Buleleng; 6. Karangasemt; 7. Klungkung; 8. Bangli; 9. Jembrana and M. DNA marker 1 kb (Thermo Scientific)

Isolate	Origin of		Accession		Homology nt (aa) $(\%)$ Nilaparvata lugens IDN							
	isolate	Biotype	number	Denpasar	Badung	Gianyar	Tabanan	Buleleng	Karangasem	Klungkung	Bangli	Jembrana
FSD-034	PAK	Y	MK301229	99.5 (100)	99.6 (100)	99.5 (100)	99.5 (100)	99.6 (100)	99.5 (100)	99.7 (100)	99.5 (100)	99.6 (100)
HZZ ₅₅	IND		MK032794	99.4 (100)	99.5 (100)	99.4 (100)	99.5 (100)	99.4 (100)	99.5 (100)	99.6 (100)	99.5 (100)	99.6 (100)
SAEVG_Morph0111	IND		MN520923	99.4 (100)	99.5 (100)	99.4 (100)	99.5 (100)	99.4 (100)	99.5 (100)	99.5 (100)	99.5 (100)	99.6 (100)
KBPH	KOR		MK590088	99.3 (100)	99.5 (100)	99.4 (100)	99.4 (100)	99.3 (100)	99.4 (100)	99.4 (100)	99.4 (100)	99.5 (100)
KOREA BPH	KOR		LC461184	99.3 (100)	99.5 (100)	99.4 (100)	99.4 (100)	99.3 (100)	99.4 (100)	99.4 (100)	99.4 (100)	99.5 (100)
WUHAN-Y	CHN	Y	KC333653	99.3 (100)	99.5 (100)	99.4 (100)	99.4 (100)	99.3 (100)	99.4 (100)	99.4 (100)	99.3 (100)	99.4 (100)
WUHAN-3	CHN		JN563997	97.8 (98.1)	97.2 (97.8)	97.5 (98.9)	97.5 (98.9)	97.4 (97.9)	97.8 (98.1)	97.5 (98.9)	97.2 (98.8)	97.6 (98.0)
WUHAN-2	CHN		JN563996	96.3 (97.5)	96.3 (97.5)	96.4 (97.5)	96.3 (97.5)	96.2 (97.4)	96.4 (97.5)	96.3 (97.5)	96.2 (97.4)	96.3 (97.5)
WUHAN-1	CHN		JN563995	95.3 (96.7)	95.4 (96.7)	95.3 (96.7)	95.4 (96.7)	95.6 (96.8)	95.6 (96.8)	95.3 (96.7)	95.4 (96.7)	95.3 (96.7)
GX	CHN		LC461186	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)	95.4 (96.7)	95.5 (96.8)	95.5 (96.8)	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)
Gangavathi	IND		OL451531	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)	95.5 (96.8)	95.5 (96.8)	95.3 (96.7)	95.3 (96.7)	95.3 (96.7)
WUHAN-L	CHN	L.	KC333654	94.2 (95.8)	94.4 (96.2)	94.2 (95.8)	94.4 (96.2)	94.3 (96.0)	94.4 (96.2)	94.2 (95.8)	94.4 (96.2)	94.4 (96.2)
Nilaparvata bakeri	CHN		JX266790	84.6 (85.6)	85.2(86.1)	84.8 (85.9)	84.8 (85.9)	84.6 (85.6)	85.2(86.1)	84.8 (85.9)	85.2 (86.1)	85.2(86.1)
Sogatella furcifera	CHN	$\mathbf{1}$	HM160123 \cdots nire	75.6 (76.9)	75.6 (76.9) $T \cap \mathcal{D}$	76.2 (77.8)	77.6 (78.4) α	77.4 (78.4)	76.8 (77.8)	75.6 (76.9)	76.8 (77.8)	77.6 (78.4)

Table 3. Nucleotide (nt) and amino acid (aa) homology of *Nilaparvata lugens* in rice from Bali, Indonesia, compared with *Nilaparvata lugens* from other countries in GenBank

Notes: nt (nucleotide); aa (amino acid); IDN (Indonesia); PAK (Pakistan); IND (India); KOR (South Korea); CHN (China); *Nilaparvata bakeri* and *Sogatella furcifera* from China was used as outgroups

Figure 4. The cladogram of the mtCOI fragment of *Nilaparvata lugens* from eastern Indonesia, Bali (Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana) was compared with mtCOI fragments from several regions of the world that had been deposited on the NCBI website. *Nilaparvata bakeri* and *Sogatella furcifera* from China were used as outgroups. The numbers on the branching cladograms represent bootstrap values with 100% probability. IDN (Indonesia), PAK (Pakistan), IND (India), KOR (South Korea), and CHN (China), isolates marked with black dots are Bali isolates

In previous studies in Indonesia, BPH biotypes 1, 2, 3, and 4 have been found. Kobayashi et al. (2014) reported that the brown planthopper is a highly adaptive insect because it can form new biotypes. In early 1975 the IR-26 rice variety from IRRI Philippines was introduced. The IR-26 variety was unique because it contained a Bph1 resistant gene to anticipate fluctuations in the brown planthopper population. However, in 1976 there was a great population explosion in several rice production centers due to changes in the brown planthopper population from biotype 1 to biotype 2. As an anticipatory measure against brown planthopper biotype 2, in 1980, the IR-42 rice variety (containing the bph2 resistant gene) was introduced from IRRI Philippines. Unfortunately, in 1981 there was another explosion in the brown planthopper population in Simalungun, North Sumatra, and several other areas due to changes in the brown planthopper population from biotype 2 to biotype 3. To deal with the brown planthopper biotype 3, rice variety IR-56 was introduced (containing the gene bph3 resistance) in 1983 and IR-64 (containing the bph1+ resistance gene) in 1986. The introduction process continues. In 1991, the IR-74 variety (containing the bph3 resistant gene) was introduced. In 2006, the resistance gene IR-64 was broken because the brown planthopper population changed to biotype 4 (Baehaki 2012). The stability of the biotype zero brown planthoppers persisted for 41 years before becoming brown planthopper biotype 1. The change of brown planthopper biotype 1 to biotype 2 only took 4 years, and the change of biotype 2 brown planthopper to biotype 3 within 5 years. Until 2005, the brown planthopper biotype 3 was still dominated by biotype 3, and in 2006 the biotype 4 brown planthopper began to develop. The long existence of the biotype 3 brown planthopper was caused by the development of the IR-64 (bph1+) variety over a long period. IR-64 is a resistant variety (durable resistance) that can withstand changes in brown planthoppers to a more virulent biotype.

The continuous cultivation of IR-64 rice varieties by farmers in Bali led to the emergence of a new biotype BPH, namely Y. Insects of biotype Y originated from biotype 1 by eating YHY15 resistant varieties for more than two years for 33 generations (Jing et al. 2012). Rice varieties YHY15 carry the Bph15 resistance gene (Jing et al. 2012).

This study shows great potential in the population of *N. lugens* to adapt to previously resistant rice varieties. This study reported that rice varieties Situbagendit and Inpari 32, previously resistant to BPH, were susceptible to BPH. This research can provide information to farmers not to continuously plant susceptible varieties, which could cause BPH epidemics in the field, as well as the emergence of new, more virulent BPH biotypes. Thus a new control strategy based on a forecasting system can be developed for the regional management of this insect.

In conclusion, *N. lugens* that attack rice plants in Bali (Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana) belongs to biotype Y. Symptoms of damage to rice plants are most severe in Badung Regency. Apart from Ciherang and IR-64

varieties, Situbagendit and Inpari 32 varieties are susceptible to BPH attack.

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The brown planthopper (*Nilaparvata lugens* **Stal.) attack and its genetic diversity on rice in Bali, Indonesia**

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Abstract. Listihani L, Ariati PEP, Yuniti IGAD, Selangga DGW. 2022. The brown planthopper (Nilaparvata lugens Stal.) attack and its
genetic diversity on rice in Bali, Indonesia. Biodiversitas 23: xxxx. The brown planthop pest on rice crops in Indonesia.. The genetic diversity of BPH isolates in western Indonesia has been extensively reported, whereas eastern Indonesia isolates have not been reported. This research aims to analyze genetic diversity and evaluate the BPH attack's intensity on Bali rice plants. The research method used was an observation of attack percentage, population dynamics, attack intensity, and genetic diversity of BPH in 9 districts in Bali (Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana). Molecular identification was carried out on *N. lugens* DNA in the mtCOI fragment. BPH attacks of >50% were found in the districts of Gianyar, Bangli, Jembrana, and Badung. The BPH population was primarily found in Ciherang and IR-64 varieties of
rice in the Badung Regency, with 43.67 BPH per rice hill. In general, rice varieties grown i to BPH, such as Ciherang, IR-64, Inpari 32, and Situbagendit. In the Ciherang and IR-64 varieties, the highest attack intensity average value reached 30%. The sequence of *N. lugens* isolate from Bali Jembrana showed the highest nucleotide and amino acid homology with
N. lugens isolate FSD-034 from Pakistan (MK301229) biotype Y of 99.5 -99.74% and 100%, biotype Y in rice plants for the first time in Indonesia. This study reported that Rice varieties Situbagendit and Inpari 32, previously resistant to BPH, are reported as susceptible to BPH.

Keywords: attack intensity, genetic diversity, Inpari 32, Situbagendit, susceptible variety

INTRODUCTION

The brown planthopper (BPH) (*Nilaparvata lugens* Stal, Hemiptera: Delphacidae) is the most destructive rice pest in Indonesia. Repeated outbreaks of BPH in Indonesia are caused by continuous rice cultivation, extensive use, and over-application of insecticides (Baehaki 2012). This pest is vascular monophagous in rice (Cheng et al. 2013; Ferrater et al. 2013; Triwidodo 2020). Feeding by nymphs and imago at the base of the plant causes rapid wilting and drying of the plant (Bottrell and Schoenly 2012; Cheng et al. 2013; Bao and Zhang 2019). In addition, BPH is also a vector of *Rice grassy stunt virus* and *Rice ragged stunt virus* (Bao and Zhang 2019). At high population levels of *N. lugens* can cause significant losses in rice production (Cheng et al. 2013; Zheng et al. 2013; Bao and Zhang 2019).

The BPH cannot tolerate winter in northern Asia, including Japan, Korea, and northern China (He et al. 2012; Fu et al. 2012; Fu et al. 2014). The population originally came from subtropical and tropical areas by flying long distances during the summer (Fu et al. 2014; Hu et al. 2014). BPH infestation in temperate climates originated from annual migrations from tropical Asia and China (He et al. 2012). During autumn, BPH re-migrates (north-tosouth) and BPH populations have been studied in China

and India (Bottrell and Schoenly 2012). Such return migration may help explain how long-distance migration is maintained in the winter.

The intensification of rice production triggered the BPH outbreak in Tropical Asia during the green revolution era in the 1970s and 1980s (Bottrell and Schoenly 2012). Until now, *N. lugens* is the main problem causing rice harvest failure in several countries. Inaccurate identification and prolonged identification of *N. lugens* are obstacles to its field management strategy.

Traditionally, BPH has been identified at the species level by morphological features using anatomical characteristics, namely, wings, front, and external genitalia (Lv et al. 2015). Accurate identification requires extensive expertise and experience and yet sometimes can lead to errors. Morphological identification by an entomologist can reduce the potential for errors. Practical morphological identification is only possible when dealing with small sample sizes and well-preserved specimens. Therefore, it is crucial to utilize a new identification method that is accurate, fast, time-saving, and suitable for large numbers of specimens.

Molecular techniques with high reproducibility and fast results offer an excellent alternative to traditional morphological classification. Several mitochondrial and nuclear genes have been used as genetic markers to

differentiate related species. These include the mitochondrial cytochrome c oxidase subunit 1 (CO1) gene, nuclear 12S-16S-18S ribosomal RNA genes, and ITS1 and ITS2 internal transcription spacers (Brengues et al. 2014; Gomez-Polo et al. 2014; Yu et al. 2014; Wang et al. 2016; Zheng et al. 2021). ITS1 and ITS2 are nonfunctional spacers that separate the 18S-5.8S and 5.8S-28S rRNA genes, respectively (Wang et al. 2016; Zheng et al. 2021). As ITS sequences have low intra-species variation but high variation between species, they are helpful for species classification and phylogenetic analysis for classification and phylogenetic analysis for morphologically similar organisms, both in prokaryotes and eukaryotes (Zheng et al. 2021). Finally, from the molecular identification of the combined mitochondrial COI-COII and ten microsatellite marker loci (Winnie et al. 2020).

The genetic diversity of *N. lugens* has been reported in several countries such as China, South Korea, Pakistan, India, and Malaysia (Jing et al. 2012; Latif et al. 2012; Anant et al. 2021; Zheng et al. 2021). The genetic diversity of *N. lugens* in Indonesia is widely reported in western Indonesia (Java Island) (Winnie et al. 2020; Chaerani et al. 2021). Reports on the genetic diversity of *N. lugens* in eastern Indonesia have not been found. Therefore, this study aims to analyze genetic diversity and determine the intensity of BPH attacks on rice plants in eastern Indonesia, especially Bali.

MATERIALS AND METHODS

Brown Planthopper Sampling from Rice Dwarf Disease Endemic Areas

Samples were taken from nine locations at the rice cultivation center in Bali Province (Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana). The brown planthopper samples taken from rice plants were nymphs and imagos. Nymphs and imagos were used for total DNA extraction. After arriving at the laboratory, the nymphs and imago were stored dry at -20°C.

Observation of BPH Attack Symptoms and Quantity of BPH Population/rice hills

Observation of symptoms of BPH attack was carried out by observing symptoms of damage to rice plants due to BPH attack. The abundance of the BPH/rice hills population was obtained by counting all nymphs and imagoes obtained. Data on the population per cluster from 20 samples or 20 rice hills at each observation fields were then averaged. For each location, 3 fields of rice cultivation center were taken which were used for observation

BPH Attack Percentage

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The percentage of BPH attacks is calculated using the

following formula:
 $P = \frac{a}{b} \times 100\%$ Note: $P =$ Attack percentage $(\%)$

$$
a =
$$
 Number of rice hills affected by BPH
 $b =$ Number of rice hills observed

Damage Intensity

Determination of scoring on symptoms of rice damage due to BPH attack is based on Table 1. The intensity of damage due to a BPH attack is determined using the formula (Erdiansyah and Damanhuri 2018):

$$
I = \sum_{i=1}^{I} \frac{N i x V i}{N x Z} x 100\%
$$

Note:

- $I =$ Damage intensity Ni = The number of affected rice hills on the score i
- $Vi = Score i$
- $N =$ The number of rice hills observed
- $Z =$ Highest score

Total DNA Extraction from Brown Planthopper

Total DNA extraction of brown planthopper was obtained from one individual imago or one individual nymph based on the modified method of Goodwin et al. (1994). One individual imago was put into a microtube and then added to 100 μl of CTAB (Cethyl Trimethyl Ammonium Bromida) extraction buffer (2% CTAB, 1.4 M NaCl, 100 mM Tris-HCI, 20 mM EDTA (Ethylenediaminetetraacetic acid), and 1% PVP (-40 °C)). Next, 1 μl of proteinase K was added, then the insects were crushed using a micro-pistil, vortexed, and incubated in a water bath of 65°C for 3 minutes. After that, the tube was added with 100 μl CI (chloroform: isoamyl alcohol) in a ratio of 24:1. The tube was then vortexed for 3 minutes and centrifuged at 10,000 rpm for 15 minutes. The supernatant formed was transferred to a new microtube (60 μl) and then added with 3 M NaOAc (pH 5.2), as much as 1/10 of the total volume of the supernatant. Isopropanol was added up to 2/3 of the total volume of the supernatant, then incubated at -20°C for one night. The tube was centrifuged at 10,000 rpm for 10 min, and the supernatant was discarded. The pellets were washed with 100 μl of 80% ethanol (cold) and centrifuged at 8000 rpm for 5 minutes. In the final step, the supernatant was removed, and the pellet was dried for approximately 1 hour. It was then added to a solution of 20 μl TE and stored at -20°C until used.

Amplification of mtCOI Fragments Using the PCR Method

PCR reactants were manufactured with a total volume of 25 μl consisting of 12.5 μl Go Tag Green Master Mix (Promega, US) and 9.5 μl ddH2O. DNA amplification of the mtCOI fragment was carried out using a pair of universal primers mtCOI LCO 1490 (3'primers GGTCAACAAATCATAAAGATATTGG-5') and HCO 2198 (5'-TAAACTTCA GGGTGACCA AAAAATCA-3') (Folmer et al. 1994) each 1 μl, and 1 μl DNA template. PCR reactions were carried out with a Perkin Elmer 480 Thermocycler (Applied Biosystem, US). The PCR reaction was initiated by initial denaturation for 5 min at 94°C. The

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PCR was continued for 35 cycles in the following order: 94°C for 1 minute, 52°C for 35 seconds, 72°C for 1 minute 30 seconds, and a final extension of 72°C for 7 minutes. The PCR results were then analyzed in 1% agarose gel. The DNA fragments of mtCOI were visualized using a UV transilluminator after being immersed in a 2% ethidium bromide solution for 15 minutes and photographed with a digital camera. The result of amplification by PCR technique was in the form of mtCOI DNA fragments with a size of \pm 710 base pairs ($\frac{\text{pbp}}{\text{pbp}}$).

Analysis of DNA Sequence Results

Nucleotide **s**Sequencing DNA fragment purification and mtCOI nucleotide sequencing were performed at PT. 1st Base, Malaysia. The results were then registered in the NCBI gene bank (http://www.ncbi.nlm.nih.gov). Analysis of mtCOI DNA sequence data ChromasPro program was used to combine forward and reverse nucleotide sequences to obtain the mtCOI gene (ChromasPro version 2.01. 2006). The Bioedit program was used to compare mtCOI fragments between samples (Multiple alignments). The phylogenetic relationship was built by comparing the mtCOI sample fragments from the brown planthopper from Indonesia with the mtCOI fragments already stored in the NCBI GenBank (http://www.nchi.nlm.nih.gov) The NCBI GenBank (http://www.ncbi.nlm.nih.gov). criteria for retrieving mtCOI fragments at GenBank were fragments with a nucleotide base length of \pm 710 bp (Boykin et al. 2007) (Table 3; Figure 3). The phylogenetic tree was constructed using the PAUP 4.0b10 program with the maximum parsimony cladistic quantitative method. The cladogram was compiled using the Heuristic method. The cladogram used results from the strick consensus with the statistical bootstrap test to obtain a 100% probability.

RESULTS AND DISCUSSION

The brown planthopper causes direct and indirect damage to rice plants. Direct damage was in the form of stunted and uneven growth of rice plants (Figure 1A and 1B), yellow plants (Figure 1C), and hopperburn caused by fluid in rice plant cells sucked by BPH nymphs, brachiptera (Fig. short wings), and macroptera (long wings) (Figures 1E and 1F). Indirect damage was caused by BPH, which acts as a vector of *Rice grassy stunt virus* and *Rice ragged stunt virus*, causing stunted rice plants (Figure 1D). Besides Bali or other parts of Indonesia, BPH attacks on rice crops were also reported in China, where hopperburn affected 60% of all examined crops (Hu et al. 2014). Transmission of the stunt virus by the brown planthoppers occurs persistently (Horgan et al. 2015). Virus infection causes damage to plants because viruses use plant proteins for replication, resulting in loss of crop production (Listihani et al. 2020; Damayanti et al. 2022; Listihani et al. 2022; Pandawani et al. 2022; Selangga and Listihani 2022; Selangga et al. 2022). Therefore, infection with RGSV and RRSV in rice plants causes rice to lack nutrients to the point of stunting.

A percentage of BPH attacks of more than 50% was found in Gianyar, Bangli, Jembrana, and Badung Regencies (Table 2). The BPH population was primarily found in Ciherang and IR-64 varieties of rice in the Badung Regency, with 43.67 BPH per rice hills (Table 2). Baehaki (2012) added that the economic threshold could be measured through the number or population of pests and planting age. BPH is said to have reached the economic threshold when the population of this pest was found in the field, as many as nine BPH per rice hill when the rice age was less than 40 DAP or 18 BPH when the rice was more than 40 DAP (Baehaki 2012). In general, rice varieties grown in all observation locations in Bali were BPH susceptible varieties, such as Ciherang, IR-64, Inpari 32, and Situbagendit.

The dynamics of BPH development in the field can be influenced by several factors, including host plant factors and natural enemies (Ferrater et al. 2015; Horgan et al. 2015; Kobayashi 2016). The host plant factors that affect the BPH population are related to the age of the rice plant. When the observations were made, the rice plants were still in the vegetative phase, aged 4-6 WAP. According to Jing et al. (2014), naturally, BPH usually comes to young rice fields, and insects usually come in the first two weeks after planting. Thus, the brown planthopper in rice cultivation might be the first generation of planthoppers that have not yet reproduced because one BPH life cycle takes between 3-4 weeks (IRRI 2009).

BPH observations in Denpasar, Tabanan, Karangasem, and Klungkung eities districts were dominated by macroptera imago (Table 2). According to Horgan et al. (2017), the planthopper that first came to the plantation was the macroptera planthopper as a winged immigrant planthopper. Meanwhile, in Badung, Gianyar, Buleleng, Bangli, and Jembrana districtsregencies, nymphsal BPH was dominated by BPH, and several individuals were in the imago phase of brachiptera and macroptera. The dominance of the nymph phase caused the population of BPH in Badung, Gianyar, Buleleng, Bangli, and Jembrana districts to be the highest when compared to the districtscities of Denpasar, Tabanan, Karangasem, and Klungkung. The presence of the brachiptera planthopper might be contributed to the increase in the nymph population (Baehaki 2012). Rapid population growth usually occurs in groups with many young individuals (Horgan et al. 2015; Triwidodo and Listihani 2020).

The average intensity of BPH attack on Ciherang and IR-64 varieties of rice was higher than in other varieties. In the Ciherang and IR-64 varieties of rice, the average value of the highest attack intensity was 30% (Figure 2). It is because farmers grow rice varieties Ciherang and IR-64 from year to year without any replacement of other varieties. Furthermore, rice varieties Ciherang and IR-64 became very susceptible to BPH attacks. In addition, BPH is a pest that begins to attack rice plants from a young age, even when the rice is still in the nursery.

According to Vu et al. (2014), fluctuations in BPH pest attacks are more influenced by the growth phase of the rice plant that is the host in the field. BPH pests are often found when rice plants are in the vegetative and generative stages (Bottrell and Schoenly 2012). Horgan et al. (2017) added that BPH pests could damage rice plants at all stages of

growth and act as vectors for grass and dwarf viruses. BPH attack was higher when rice was in the vegetative phase than in the generative phase (Horgan et al. 2015). It happens because the pests attack the young rice stalks. Considering the type of mouth of BPH, which is included in the suction, BPH can suck the liquid from the rice stems and cause the plant leaves to turn yellow (Anant et al. 2021). According to Choi et al. (2019) and Sutrawati et al. (2021), during the vegetative phase, food availability in the form of nitrogen is abundant in rice plants. Rice plants need nitrogen to form plant organs. Food is one of the factors that affect the life of insects. Horgan (2018) continued that the N element absorbed by plants also serves as a source of nutrition for BPH. If food is available with good quality (suitable for pests), then the insect pest population will increase, and vice versa (Horgan 2018; Triwidodo and Listihani 2020).

The mtCOI DNA band was successfully amplified from the total DNA extraction of one imago or nymph of BPH. The mtCOI fragment that was successfully amplified corresponds to a size of ± 710 bp in all samples from nine districts in Bali, namely Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana (Figure 3). Nucleotide and amino acid sequence analysis showed high homology with *N. lugens* sequences in the database at GenBank, 94.2 – 99.7% and 95.8 - 100%, respectively (Table 3). *N. lugens* sequences from Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana showed the highest nucleotide, and amino acid homology with *N. lugens* isolate FSD-034 from Pakistan (MK301229) biotype Y, respectively. 99.5 -99.74% and 100% (Table 3). The results of the molecular detection of *N. lugens* using the PCR method in Bali, Indonesia, are the first reports of the molecular character of *N. lugens* in Indonesia.

Samples from Indonesia formed a group with *N. lugens* biotype Y fragment mtCOI from Pakistan, India, South Korea, and China (Figure 4). This study found *N. lugens* biotype Y in rice plants for the first time in Indonesia. The Indonesian sample did not form separate groups according to the proximity of the district locations but formed a polytomy cladogram (Figure 4). This polytomy cladogram shows that the *N. lugens* between regencies (Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana) were observed to have the same ancestry. These results indicate high locomotion ability with genetic mixing between *N. lugens* in Bali isolates. Similar conditions were also demonstrated in *N. lugens* among Asian isolates using mitochondrial sequences showing genetic mixing. It can also be correlated with the theory of long-distance migration of *N. lugens*, which migrates from the tropics (northern Vietnam) in April-May to temperate regions (China, Korea, and Japan) in June-July as shown based on meteorological studies (Otuka et al. 2008). The population of *N. lugens* is a long-distance migratory flight from the tropics to temperate Asia before modern pesticides are widely used in tropical rice. Due to the infrequent use of insecticides prior to the 1960s in the tropics, factors other than insecticides may

have triggered long-wing movements to form *N. lugens* populations (Bottrell and Schoenly 2012).

In previous studies in Indonesia, BPH biotypes 1, 2, 3, and 4 have been found. Kobayashi et al. (2014) reported that the brown planthopper is a highly adaptive insect because it can form new biotypes. In early 1975 the IR-26 rice variety from IRRI Philippines was introduced. The IR-26 variety was unique because it contained a Bph1 resistant gene to anticipate fluctuations in the brown planthopper population. However, in 1976 there was a great population explosion in several rice production centers due to changes in the brown planthopper population from biotype 1 to biotype 2. As an anticipatory measure against brown planthopper biotype 2, in 1980, the IR-42 rice variety (containing the bph2 resistant gene) was introduced from IRRI Philippines. Unfortunately, in 1981 there was another explosion in the brown planthopper population in Simalungun, North Sumatra, and several other areas due to changes in the brown planthopper population from biotype 2 to biotype 3. To deal with the brown planthopper biotype 3, rice variety IR-56 was introduced (containing the gene bph3 resistance) in 1983 and IR-64 (containing the bph1+ resistance gene) in 1986. The introduction process continues. In 1991, the IR-74 variety (containing the bph3 resistant gene) was introduced. In 2006, the resistance gene IR-64 was broken because the brown planthopper population changed to biotype 4 (Baehaki 2012). The stability of the biotype zero brown planthoppers persisted for 41 years before becoming brown planthopper biotype 1. The change of brown planthopper biotype $\hat{1}$ to biotype 2 only took 4 years, and the change of biotype 2 brown planthopper to biotype 3 within 5 years. Until 2005, the brown planthopper biotype 3 was still dominated by biotype 3, and in 2006 the biotype 4 brown planthopper began to develop. The long existence of the biotype 3 brown planthopper was caused by the development of the IR-64 (bph1+) variety over a long period. IR-64 is a resistant variety (durable resistance) that can withstand changes in brown planthoppers to a more virulent biotype.

The continuous cultivation of IR-64 rice varieties by farmers in Bali led to the emergence of a new biotype BPH, namely Y. Insects of biotype Y originated from biotype 1 by eating YHY15 resistant varieties for more than two years for 33 generations (Jing et al. 2012). Rice varieties YHY15 carry the Bph15 resistance gene (Jing et al. 2012).

This study shows great potential in the population of *N. lugens* to adapt to previously resistant rice varieties. This study reported that rice varieties Situbagendit and Inpari 32, previously resistant to BPH, were susceptible to BPH. This research can provide information to farmers not to continuously plant susceptible varieties, which could cause BPH epidemics in the field, as well as the emergence of new, more virulent BPH biotypes. Thus a new control strategy based on a forecasting system can be developed for the regional management of this insect.

In conclusion, *N. lugens* that attacks rice plants in Bali (Badung, Gianyar, Klungkung, Bangli, Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana) belongs to biotype Y. Symptoms of damage to rice plants are most severe in Badung Regency. Apart from Ciherang and IR-64

varieties, Situbagendit and Inpari 32 varieties are susceptible to BPH attack.

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Table 1. The damage score of rice plants due to BPH attack

Score	Appearance	Description
Ω	Healthy	No planthopper was found in any rice hill.
	Very light damage	The rice hills occupied by the planthoppers did not show dead midribs, few exuviae, and the rice stalks had not yet overgrown with <i>Colletotrichum dematium</i> and Cladosporium fungi that followed the brown planthopper attack.
	Slightly damaged	The rice hills occupied by the planthoppers have shown dead midribs, many exuviae, and the rice stems are overgrown with <i>Colletotrichum dematium</i> and Cladosporium fungi that follow the brown planthopper attack.
	Heavily damaged	Rice hills inhabited by planthoppers showed damage marked by many dead midribs, many exuviae, stunted and black-looking tillers, and overgrown with <i>Colletotrichum dematium</i> and Cladosporium fungi.
	Partially dead	Some of the stems in the rice hill die, or the rice hill withers due to planthoppers attack.
9	Hopperburn	Rice hills die from hopperburn

Sumber: Baehaki (2012)

Table 2. Population and symptoms of BPH attack on rice plants in Bali

Note: DAP= day after planting

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Table 3. Nucleotide (nt) and amino acid (aa) homology of *N. lugens* in rice from Bali, Indonesia, compared with *N. lugens* from other countries in GenBank

Notes: nt (nucleotide), aa (amino acid), IDN (Indonesia), PAK (Pakistan), IND (India), KOR (South Korea), CHN (China), *N. bakeri* and *Sogatella furcifera* from China was used as outgroups
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Figure 1. Symptoms of BPH attack on rice plants in Bali: A. rice plant growth is stunted; B. uneven plant growth (spots); C. yellow
plant; D. dwarf rice plants; E. plants die like burning (hopperburn); F. BPH brachiptera

Observation locations in 9 Regency in Bali

Figure 2. The attack intensity of *N. lugens* on rice in Bali Province

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Figure 3. DNA amplification of *N. lugens* in rice plants in Bali using primers LCO 1490/HCO 2198. 1. Denpasar City, 2. Bagung, 3.
Gianyar, 4. Tabanan, 5. Buleleng, 6. Karangasemt, 7. Klungkung, 8. Bangli, 9. Jembrana, a

Figure 4. The cladogram of the mtCOI fragment of N. lugens from eastern Indonesia, Bali (Badung, Gianyar, Klungkung, Bangli,
Karangasem, Tabanan, Denpasar City, Buleleng, and Jembrana) was compared with mtCOI fragments fro that had been deposited on the NCBI website. *N. bakeri and Sogatella furcifera fr*om China were used as outgroups. The numbers on the
branching cladograms represent bootstrap values with 100% probability. IDN (Indonesia),

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