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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| |  |  |  |  |  |  |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | | species | genetic distance / standard deviation | | | | | | | | | | | | | | *M. sirinhorn* |  | 0.020 | 0.020 | 0.029 | 0.026 | 0.021 | 0.024 | 0.020 | 0.025 | 0.019 | 0.026 | 0.021 | 0.019 | | *M. palmopilosum* | 0.178 |  | 0.018 | 0.025 | 0.024 | 0.020 | 0.018 | 0.015 | 0.023 | 0.014 | 0.024 | 0.015 | 0.014 | | *M. dienbienphuense* | 0.184 | 0.153 |  | 0.028 | 0.026 | 0.013 | 0.018 | 0.015 | 0.023 | 0.015 | 0.024 | 0.017 | 0.015 | | *M. niphanae* | 0.279 | 0.238 | 0.278 |  | 0.025 | 0.027 | 0.027 | 0.026 | 0.023 | 0.024 | 0.026 | 0.026 | 0.026 | | *M. sintangense* | 0.232 | 0.221 | 0.242 | 0.232 |  | 0.028 | 0.025 | 0.024 | 0.019 | 0.024 | 0.025 | 0.024 | 0.024 | | *M. puberimanus* | 0.182 | 0.168 | 0.098 | 0.270 | 0.264 |  | 0.018 | 0.016 | 0.023 | 0.017 | 0.024 | 0.017 | 0.017 | | *M. eriocheirum* | 0.233 | 0.166 | 0.163 | 0.263 | 0.233 | 0.152 |  | 0.015 | 0.024 | 0.017 | 0.026 | 0.019 | 0.017 | | *M. hirsutimanus* | 0.173 | 0.127 | 0.128 | 0.239 | 0.227 | 0.125 | 0.125 |  | 0.022 | 0.013 | 0.025 | 0.016 | 0.014 | | *M. neglectum* | 0.232 | 0.225 | 0.221 | 0.222 | 0.182 | 0.216 | 0.245 | 0.209 |  | 0.022 | 0.022 | 0.024 | 0.024 | | *M. naiyanetri* | 0.169 | 0.124 | 0.142 | 0.235 | 0.222 | 0.150 | 0.157 | 0.117 | 0.219 |  | 0.023 | 0.013 | 0.014 | | *M. rosenbergii* | 0.246 | 0.225 | 0.235 | 0.253 | 0.248 | 0.228 | 0.263 | 0.229 | 0.200 | 0.229 |  | 0.025 | 0.024 | | *M. forcipatum* | 0.181 | 0.122 | 0.138 | 0.249 | 0.221 | 0.135 | 0.178 | 0.132 | 0.239 | 0.101 | 0.241 |  | 0.014 | | *M. malayanum* | 0.183 | 0.127 | 0.137 | 0.258 | 0.245 | 0.151 | 0.166 | 0.122 | 0.249 | 0.130 | 0.242 | 0.131 |  |   Table S3. **The interspecific variation of DNA sequence in COI gene** (the blue text indicates standard deviation) |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
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| Table S1. **The interspecific variation of DNA sequence in 16S rRNA gene** (the blue text indicates standard deviation) |  |  |  |  |  |  |  |  |  |  |  |  |  |
| |  |  |  |  |  |  |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | | *M. sirinhorn* |  | 0.011 | 0.012 | 0.016 | 0.015 | 0.012 | 0.011 | 0.011 | 0.013 | 0.011 | 0.017 | 0.012 | 0.011 | | *M. palmopilosum* | 0.062 |  | 0.009 | 0.015 | 0.016 | 0.010 | 0.010 | 0.009 | 0.013 | 0.007 | 0.014 | 0.007 | 0.008 | | *M. dienbienphuense* | 0.072 | 0.050 |  | 0.014 | 0.017 | 0.007 | 0.009 | 0.008 | 0.014 | 0.010 | 0.015 | 0.010 | 0.009 | | *M. niphanae* | 0.108 | 0.095 | 0.095 |  | 0.017 | 0.016 | 0.014 | 0.013 | 0.012 | 0.014 | 0.017 | 0.014 | 0.014 | | *M. sintangense* | 0.108 | 0.110 | 0.120 | 0.109 |  | 0.017 | 0.016 | 0.016 | 0.013 | 0.016 | 0.019 | 0.017 | 0.017 | | *M. puberimanus* | 0.077 | 0.056 | 0.033 | 0.107 | 0.126 |  | 0.009 | 0.008 | 0.014 | 0.010 | 0.016 | 0.010 | 0.010 | | *M. eriocheirum* | 0.061 | 0.053 | 0.050 | 0.084 | 0.107 | 0.048 |  | 0.006 | 0.011 | 0.010 | 0.015 | 0.010 | 0.008 | | *M. hirsutimanus* | 0.059 | 0.040 | 0.038 | 0.074 | 0.108 | 0.040 | 0.023 |  | 0.011 | 0.008 | 0.014 | 0.009 | 0.008 | | *M. neglectum* | 0.082 | 0.073 | 0.087 | 0.073 | 0.083 | 0.088 | 0.058 | 0.054 |  | 0.012 | 0.014 | 0.012 | 0.012 | | *M. naiyanetri* | 0.066 | 0.032 | 0.062 | 0.090 | 0.113 | 0.063 | 0.053 | 0.044 | 0.071 |  | 0.014 | 0.006 | 0.008 | | *M. rosenbergii* | 0.118 | 0.087 | 0.100 | 0.117 | 0.141 | 0.106 | 0.093 | 0.089 | 0.092 | 0.088 |  | 0.014 | 0.014 | | *M. forcipatum* | 0.074 | 0.030 | 0.054 | 0.094 | 0.125 | 0.056 | 0.052 | 0.041 | 0.069 | 0.024 | 0.090 |  | 0.008 | | *M. malayanum* | 0.071 | 0.047 | 0.061 | 0.100 | 0.121 | 0.068 | 0.050 | 0.045 | 0.073 | 0.045 | 0.095 | 0.043 |  | |  |  |  |  |  |  |  |  |  |  |  |  |  |
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| Table S1. **The interspecific variation of DNA sequence in 18S rRNA gene** (the blue text indicates standard deviation) |  |  |  |  |  |  |  |  |  |  |  |  |  |
| |  |  |  |  |  |  |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | | species | genetic distance | | | | | | | | | | | | | | *M. sirinhorn* |  | 0.001 | 0.002 | 0.002 | 0.005 | 0.001 | 0.002 | 0.001 | 0.004 | 0.001 | 0.004 | 0.001 | 0.001 | | *M. palmopilosum* | 0.002 |  | 0.002 | 0.002 | 0.005 | 0.001 | 0.001 | 0.001 | 0.003 | 0.001 | 0.004 | 0.001 | 0.001 | | *M. dienbienphuense* | 0.011 | 0.011 |  | 0.002 | 0.005 | 0.001 | 0.002 | 0.002 | 0.003 | 0.001 | 0.004 | 0.001 | 0.002 | | *M. niphanae* | 0.005 | 0.003 | 0.014 |  | 0.005 | 0.002 | 0.002 | 0.002 | 0.004 | 0.002 | 0.004 | 0.002 | 0.002 | | *M. sintangense* | 0.024 | 0.022 | 0.032 | 0.021 |  | 0.005 | 0.005 | 0.005 | 0.004 | 0.005 | 0.005 | 0.005 | 0.005 | | *M. puberimanus* | 0.001 | 0.001 | 0.011 | 0.004 | 0.023 |  | 0.002 | 0.001 | 0.003 | 0.000 | 0.004 | 0.000 | 0.001 | | *M. eriocheirum* | 0.004 | 0.002 | 0.013 | 0.005 | 0.021 | 0.003 |  | 0.002 | 0.003 | 0.002 | 0.004 | 0.002 | 0.001 | | *M. hirsutimanus* | 0.003 | 0.003 | 0.012 | 0.006 | 0.024 | 0.002 | 0.004 |  | 0.003 | 0.001 | 0.004 | 0.001 | 0.001 | | *M. neglectum* | 0.012 | 0.012 | 0.020 | 0.013 | 0.018 | 0.011 | 0.012 | 0.012 |  | 0.003 | 0.003 | 0.003 | 0.003 | | *M. naiyanetri* | 0.001 | 0.001 | 0.010 | 0.004 | 0.023 | 0.000 | 0.003 | 0.002 | 0.011 |  | 0.004 | 0.000 | 0.001 | | *M. rosenbergii* | 0.018 | 0.018 | 0.026 | 0.019 | 0.024 | 0.018 | 0.018 | 0.019 | 0.009 | 0.017 |  | 0.004 | 0.004 | | *M. forcipatum* | 0.001 | 0.001 | 0.010 | 0.004 | 0.023 | 0.000 | 0.003 | 0.001 | 0.011 | 0.000 | 0.017 |  | 0.001 | | *M. malayanum* | 0.002 | 0.002 | 0.011 | 0.005 | 0.022 | 0.001 | 0.002 | 0.003 | 0.010 | 0.001 | 0.016 | 0.001 |  | |  |  |  |  |  |  |  |  |  |  |  |  |  |
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Table S1. **The intraspecific variation of DNA sequence in COI gene**

|  |  |  |
| --- | --- | --- |
| Species | Genetic distance | Standard deviation |
| *M. sirinhorn* | 0.004 | 0.003 |
| *M. palmopilosum* | 0.028 | 0.005 |
| *M. dienbienphuense* | 0.026 | 0.005 |
| *M. niphanae* | n/c | n/c |
| *M. sintangense* | n/c | n/c |
| *M. puberimanus* | 0.011 | 0.003 |
| *M. eriocheirum* | 0.040 | 0.006 |
| *M. hirsutimanus* | 0.011 | 0.003 |
| *M. neglectum* | n/c | n/c |
| *M. naiyanetri* | 0.046 | 0.006 |
| *M. rosenbergii* | n/c | n/c |
| *M. forcipatum* | 0.005 | 0.002 |
| *M. malayanum* | 0.084 | 0.011 |

Table S1. **The intraspecific variation of DNA sequence in 16S rRNA gene**

|  |  |  |
| --- | --- | --- |
| Species | Genetic distance | Standard deviation |
| *M. sirinhorn* | 0.002 | 0.002 |
| *M. palmopilosum* | 0.004 | 0.002 |
| *M. dienbienphuense* | 0.010 | 0.003 |
| *M. niphanae* | n/c | n/c |
| *M. sintangense* | n/c | n/c |
| *M. puberimanus* | 0.010 | 0.003 |
| *M. eriocheirum* | 0.005 | 0.002 |
| *M. hirsutimanus* | 0.002 | 0.001 |
| *M. neglectum* | n/c | n/c |
| *M. naiyanetri* | 0.012 | 0.003 |
| *M. rosenbergii* | n/c | n/c |
| *M. forcipatum* | 0 | 0 |
| *M. malayanum* | 0.035 | 0.007 |

Table S1. **The intraspecific variation of DNA sequence in 16S rRNA gene**

|  |  |  |
| --- | --- | --- |
| Species | Genetic distance | Standard deviation |
| *M. sirinhorn* | 0.000 | 0.000 |
| *M. palmopilosum* | 0.000 | 0.000 |
| *M. dienbienphuense* | 0.021 | 0.003 |
| *M. niphanae* | n/c | n/c |
| *M. sintangense* | n/c | n/c |
| *M. puberimanus* | 0.001 | 0.001 |
| *M. eriocheirum* | 0.002 | 0.001 |
| *M. hirsutimanus* | 0.002 | 0.001 |
| *M. neglectum* | n/c | n/c |
| *M. naiyanetri* | 0.000 | 0.000 |
| *M. rosenbergii* | n/c | n/c |
| *M. forcipatum* | 0.000 | 0.000 |
| *M. malayanum* | 0.000 | 0.000 |