

Study on DNA barcoding of *Riptortus* (Hemiptera: Alydidae) in China

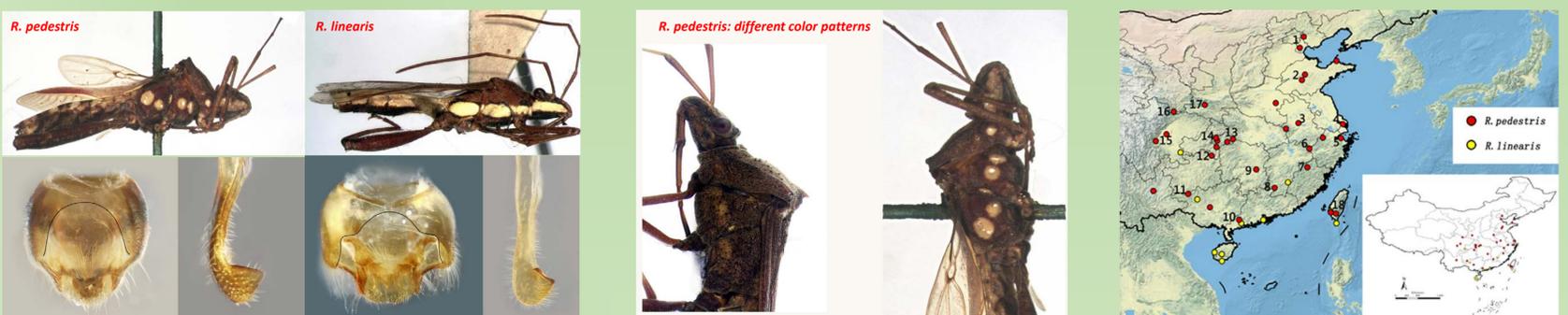
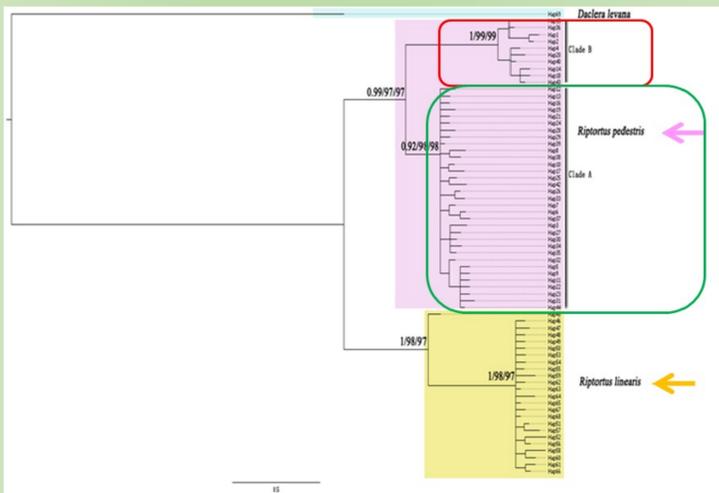
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**Abstract:**

Riptortus Stål is a small genus of Hemiptera: Heteroptera: Alydidae: Alydinae, which consists of 27 species in the world. *Riptortus pedestris* and *Riptortus linearis* are two widely distributed species in China. In this study, a total of 144 samples of *Riptortus pedestris* and *Riptortus linearis* were sequenced. We used the sequence of COI and Cyt b to analyze the genetic intra- and interspecific relationships between the two species. As a result, there was a significant interspecific genetic gap among the two species and the distance between the species is much larger than that within species. The genetic analysis within each species shows that there was no significant subdivision between geographic populations of *Riptortus linearis*, while the populations of *Riptortus pedestris* are split into two clades and the distance between the two clades is not as significant as that of two different species. Evidence from morphological and geographical distribution suggested that the geographical barrier may not be the main cause of *Riptortus pedestris* as genetic differentiation.

Keywords: DNA barcoding, *Riptortus*, genetic diversity, geographic population

Backgrounds**Results****COI Genetic Diversity**

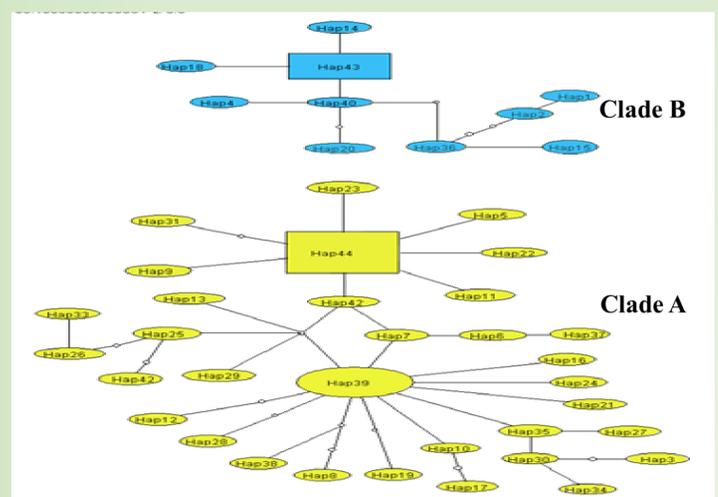
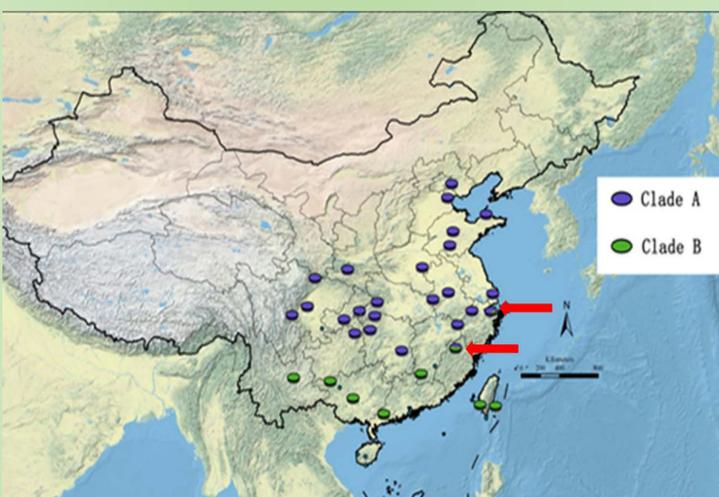
| | Haplotypes NO. h | Haplotypes diversity, Hd | Nucleotide diversity, π | Segregating site, S | Average number of difference, K |
|---------------------|------------------|--------------------------|-----------------------------|---------------------|---------------------------------|
| <i>R. pedestris</i> | 43 | 0.881 | 0.01278 | 60 | 9.444 |
| <i>R. linearis</i> | 24 | 0.904 | 0.00438 | 39 | 3.234 |

Cytb Genetic Diversity

| | Haplotypes NO. h | Haplotypes diversity, Hd | Nucleotide diversity, π | Segregating site, S | Average number of difference, K |
|---------------------|------------------|--------------------------|-----------------------------|---------------------|---------------------------------|
| <i>R. pedestris</i> | 57 | 1.000 | 0.01661 | 78 | 12.573 |
| <i>R. linearis</i> | 37 | 1.000 | 0.01282 | 68 | 9.707 |

Intra- and Interspecies Genetic Distance (K2P)

| | Intraspecies | | | | Interspecies |
|--------------|---------------------|--------------------|--|---|--------------|
| | <i>R. pedestris</i> | <i>R. linearis</i> | Average Distance (<i>R. pedestris</i>) | Average Distance (<i>R. linearis</i>) | |
| COI | 0.001-0.033 | 0.001-0.028 | 0.013 | 0.007 | 0.063 |
| Cyt b | 0.001-0.041 | 0.001-0.024 | 0.017 | 0.013 | 0.083 |

**Conclusion**

- Riptortus pedestris* and *Riptortus linearis* are two different species and also prove that the shape of the pronotal spot can be used as a stable trait of the classification between *Riptortus pedestris* and *Riptortus linearis*.
- There was no significant subdivision between geographic populations of *Riptortus linearis*.
- The populations of *Riptortus pedestris* are split into two clades and the distance between the two clades (0.26) is not as significant as that of two different species.
- The evidence from morphology does not support the division of *Riptortus pedestris* into two species.

Reference

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