

Resolving taxonomic ambiguity and cryptic speciation of *Hypotrigena* species through Morphometrics and DNA barcoding

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Abstract

Stingless bees are important pollinators of plants contributing significantly to biodiversity and food security. The use of morphological features in the identification of stingless bees in the genus *Hypotrigena* is extremely difficult due to many similarities among species resulting in taxonomic ambiguity. Here, we apply both traditional morphometrics and DNA barcoding as complementary tools for the identification of three *Hypotrigena* species: *Hypotrigena gribodoi*, *H. ruspolii* and *H. araujoii*.

Results: Our results show that morphometrics separates *H. gribodoi* and *H. ruspolii* from *H. araujoii*, however there is an overlap between *H. gribodoi* and *H. ruspolii*. On the other hand, DNA barcoding separates the three species reliably and consistently. However, there is lower genetic divergence between *H. araujoii* and *H. gribodoi* from Kakamega (1.4%) than between *H. gribodoi* collected from Kakamega and *H. gribodoi* from Mwingi (4.3%). The high intraspecific distance in *H. gribodoi* strongly suggests cryptic speciation within this species.

Significance: The combined use of morphometrics and molecular taxonomic approaches (DNA barcoding) provides a convenient, robust, and reliable way to identify *Hypotrigena* species. The high intraspecific divergence highlights the need for a thorough revision of *H. gribodoi* species.

Study Objectives

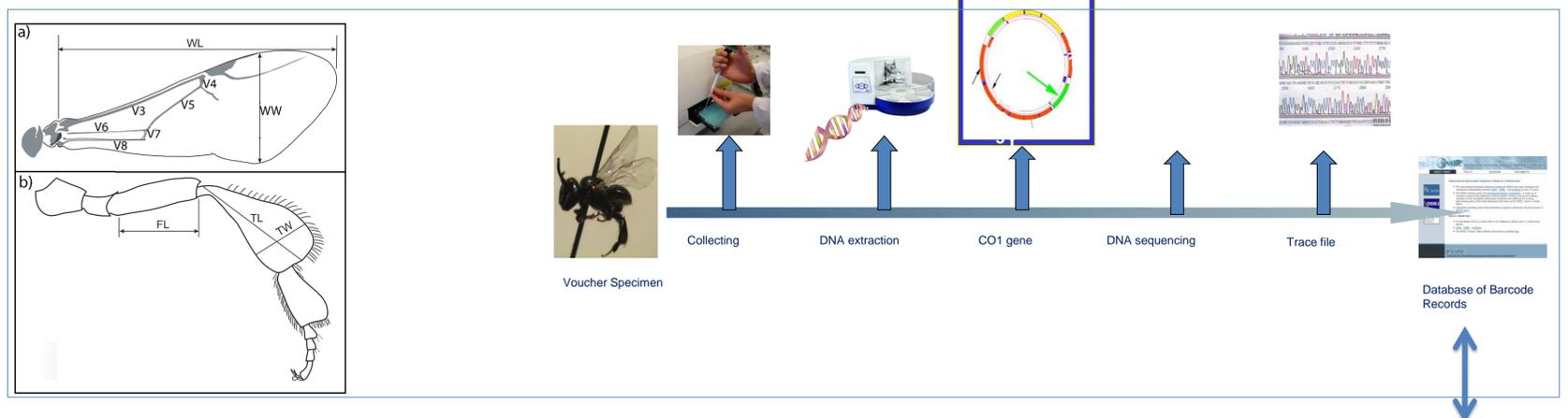
Overall objective

To contribute to taxonomic knowledge of stingless bees for conservation of biodiversity and improvement of their domestication

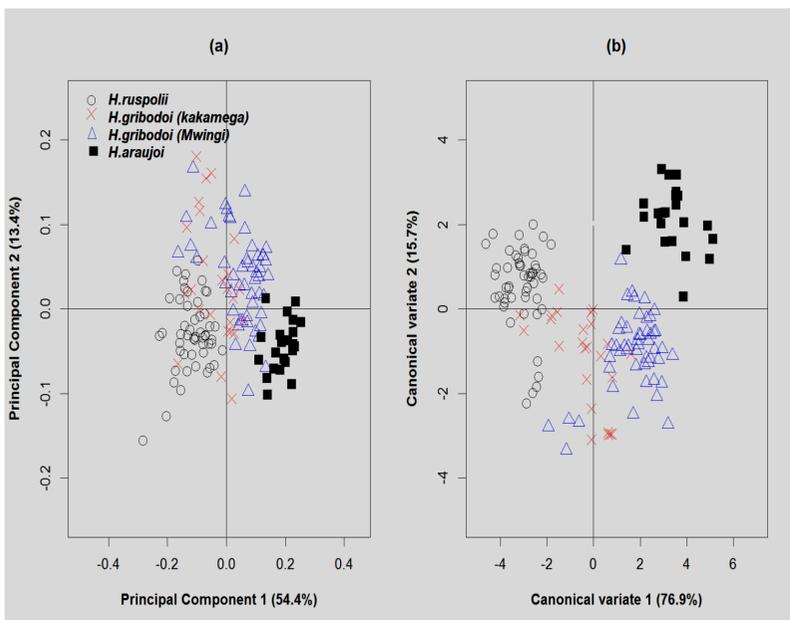
Specific Objectives

To characterize *Hypotrigena* species ;*H. gribodoi*, *H. araujoii*, and *H. ruspolii* using morphological and molecular tools

Methodology



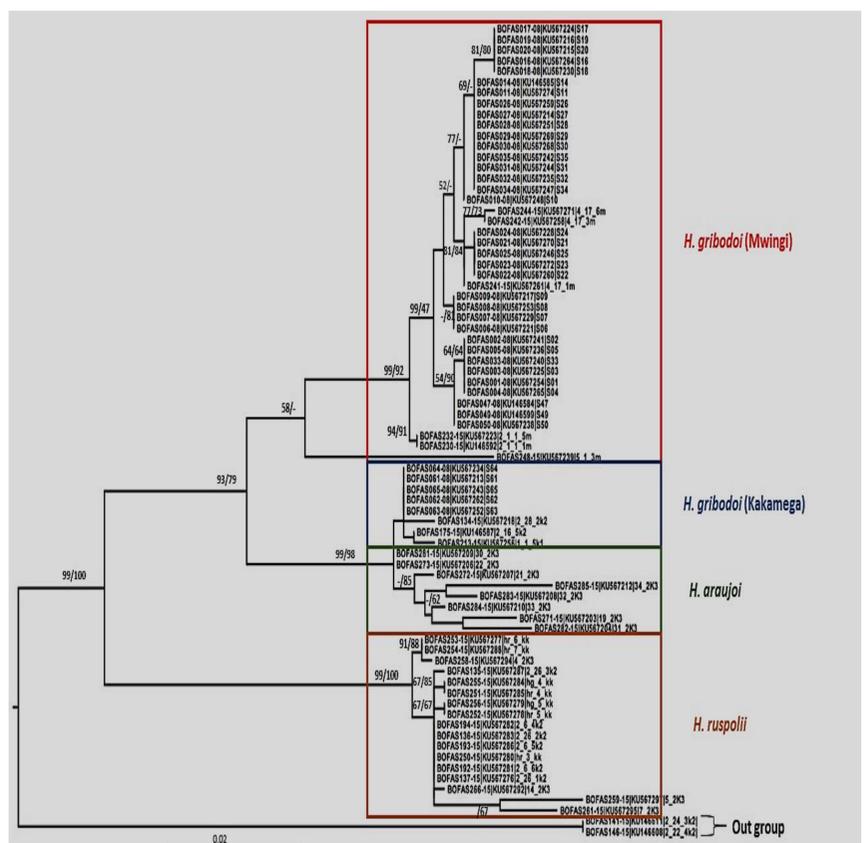
Results



Multivariate analyses of the wing morphometric measurements

PCA: partial separation of *H. araujoii* from *H. gribodoi* and *H. ruspolii*

CVA: *H. araujoii* and *H. ruspolii* separate completely. An overlap between *H. ruspolii* and *H. gribodoi* from Kakamega



RaxML phylogram, bootstrap values for both Neighbor-joining (NJ) and Maximum Likelihood (ML) analyses are displayed above the nodes (NJ/ML).

	<i>H. araujoii</i>	<i>H. gribodoi_kk</i>	<i>H. gribodoi_mwi</i>	<i>H. ruspolii</i>
<i>H. gribodoi_kk</i>		0.015		
<i>H. gribodoi_mwi</i>		0.061	0.047	
<i>H. ruspolii</i>	0.103	0.088	0.087	

Between groups Genetic distance- Note the low interspecific distance between *H. araujoii* and *H. gribodoi* from Kakamega compared to *H. gribodoi* in Mwingi

References

Eardley, 2004. *African Plant Protection*. vol. 10, no. 2, 63-96.

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