

Mosquito Wing Measurements Separate Potential West Nile Vectors: A Morphometric Study of Three *Culex* Species

By: Paige Robinson, Charlie Sither, and Brian Byrd

Abstract

Culex interrogator (Dyar and Knab), Culex restuans (Theobald), and Culex quinquefasciatus (Say) are three morphologically similar species with syntopic distributions. Culex restuans and Cx. quinquefasciatus are known West Nile vectors, while Cx. interrogator has not been reported to transmit this virus. Recent range expansions of Cx. interrogator has increased the need to identify morphological characters that can differentiate between these three similar mosquito species. Accurate identification is crucial to aid with West Nile virus surveillance efforts and potentially prevent misappropriation of resources or unnecessary interventions (e.g. pesticide application). The four morphological characteristics used in this study include the length and width of the whole wing, the length of the R2 cell, and the length of the R2+3 vein. We evaluated both intraindividual and interindividual differences in the three species. In conjunction with prior research (Shin et al., 2016) these characters are useful for accurate discrimination of Cx. interrogator from Cx. restuans and Cx. quinquefasciatus. Preliminary results suggest that wing length or an index can be used to distinguish Cx. interrogator from Cx. restuans and Cx. quinquefasciatus. An index comparing the ratios of wing measurements can separate 92% (n=25, 95% CI: 74.0-99.0%) of the Cx. restuans and Cx. quinquefasciatus. However, some wing character measurements overlap between species and investigators may need to rely on either different morphometric measurements or molecular methods to confirm results. When taken together, these measurements accurately identify 94.9% (n=39, 95% CI: 82.7%-99.4%) of the three species. The current species identification is based on morphology alone (non-wing characters), and will be confirmed by a species-specific rDNA PCR assay which produces amplicon size polymorphisms visible by gel electrophoresis (in progress).

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Mosquito Wing Measurements Separate Potential West Nile Vectors: A Morphometric Study of Three *Culex* species

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Fig. 2. To determine if there are intraindividual differences within a single specimen, we compared the wing length (a), wing width (b), R2 cell length (c), and R2-s wing vein length between the left and right wings in 39 individual specimens. Paired comparisons (Mann-Whitney test) failed to reject the null hypothesis that there are differences between each wing (P > 0.05) for each series of measurements.

ABSTRACT: Culex interrogator (Dyar and Knab), Culex restuans (Theobald), and Culex quinquefasciatus (Sav) are three morphologically similar species with syntopic distributions. Culex restuans and Cx. guinguefasciatus are known West Nile vectors (Fig 1a.), while Cx. interrogator has not been reported to transmit this virus. Recent range expansions of Cx. interrogator has increased the need to identify morphological characters that can differentiate between these three similar mosquito species. Accurate identification is crucial to aid with West Nile virus surveillance efforts and potentially prevent misappropriation of resources or unnecessary interventions (e.g. pesticide application). The four morphological characteristics (Fig. 1b) used in this study include the length and width of the whole wing, the length of the R_2 cell, and the length of the R₂₊₃ vein. We evaluated both intraindividual (Fig. 2) and interindividual differences in the three species. In conjunction with prior research (Shin et al., 2016) these characters are useful for accurate discrimination of Cx. interrogator from Cx. restuans and Cx. quinquefasciatus (Figs. 3 and 4). Preliminary results suggest that wing length (Fig. 3a) or an index (Fig. 4a) can be used to distinguish Cx. interrogator from Cx. restuans and Cx. quinquefasciatus. An index comparing the ratios of wing measurements (Fig. 4b) can separate 92% (n=25, 95% CI: 74.0-99.0%) of the Cx. restuans and Cx. guinguefasciatus. However, some wing character measurements overlap between species and investigators may need to rely on either different morphometric measurements or molecular methods to confirm results. When taken together, these measurements accurately identify 94.9% (n=39, 95% CI: 82.7%-99.4%) of the three species. The current species identification is based on morphology alone (non-wing characters), and will be confirmed by a species-specific rDNA PCR assay which produces amplicon size polymorphisms visible by gel electrophoresis (in progress).





Fig. 4. Indices accurately distinguish Cx. Interrogator (Species 'A') from Cx. quinquefasciatus (Species 'B') and Cx. restuans (Species 'C'): a) The wing width, wing length, R2 cell and R2s lengths, when multiplied X 10, will distinguish Culax interrogator (Species 'A') from the other two species. This index, when < 5, distinguishes all Cx. Interrogator from the other species. D/Luke restuans (Species 'C') can commonly be distinguished (index ≥ 13) from Cx. quinquefasciatus (Species 'B'), but not always (green dots above dashed line). This index (Wing Length/Wing Width) X [R2 cell Length/R2s; Vein Length]) accurately distinguished 23 of 25 (92%) of the two species.

Conclusions/Future Directions

Conclusions: In this study we found: 1) No appreciable intraindividual variation (**Fig. 2**) in mosquito wing measurements, suggesting we can use either wing for measurements, 2) A single index (**Fig. 4a**) is useful to distinguish Cx. *Intergator* from Cx. *restuans* and Cx. *quinquefasciatus*, and 3) the two WNV vectors can be distinguished 92% (n=25, 95% CI: 74.0-99.0) of the time using a single index (**Fig. 4b**). Taken together, we can accurately identify 94.9% (n=39, 95% CI: 82.7%-93.4%) of the three species.

Future Directions: Our mosquitoes were originally identified using classical morphological characters often disturbed or removed during collection. Thus, our current species identification is based on morphology alone (non-wing characters), and will be confirmed by a species-specific rDNA PCR assay (in progress). We also plan to include additional speciments bincrease our sample size and population diversity.

Selected References

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