

1 **Supplemental Data**

2 **Long-term surveillance defines spatial and temporal patterns**
3 **implicating *Culex tarsalis* as the primary vector of West Nile virus**

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Supplemental Information

Supplemental Tables

Table S1. Summary of combined WNV+ pools for *Culex* species in Iowa, 2002-2016.

Supplemental Figures

Figure S1. Identification of *Culex pipiens* group blood meals by species.

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Species	# Specimens tested	# Pools tested	# pools WNV+	MIR
<i>Cx. erraticus</i>	4585	283	6	1.31
<i>Cx. pipiens</i> group	129763	4888	241	1.86
<i>Cx. tarsalis</i>	22863	731	46	2.01

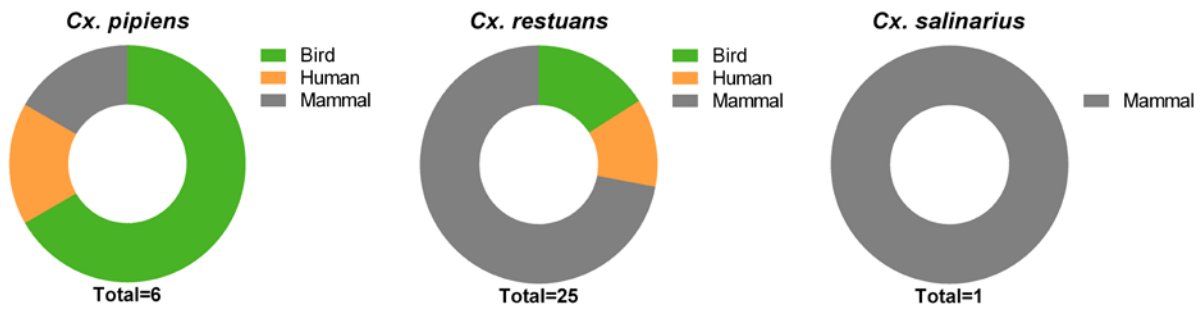
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30 **Table S1. Summary of combined WNV+ pools for *Culex* species in Iowa, 2002-2016.**

31 Mosquito number, pools tested, and WNV+ pools for each *Culex* species in Iowa.

32 Minimum infection rate (MIR) was calculated as a bias-corrected maximum likelihood
33 estimate.

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35 **Figure S1. Identification of *Culex pipiens* group blood meals by species.**
 36 *Culex pipiens* group mosquito samples in which the blood meal source was identified
 37 were further speciated to confirm if the sample was *Cx. pipiens*, *Cx. restuans*, or *Cx.*
 38 *salinarius*. The percentage of blood meals taken respectively from birds, humans, and
 39 non-human mammals are displayed for each mosquito species. The total number (n) of
 40 identified blood meals is displayed below.
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