Mosquitoes sampled from CO2 traps (DP1.10043.001)

Measurement

Mass, taxonomic identification, and sex of mosquitoes collected in CO2 traps.

Collection methodology

Traps consist of fans attached to insulated coolers filled with dry ice and hung from a Shepard's hook. A small hole in the cooler ensures that as the dry ice sublimates, the CO2 escapes. This is the lure for mosquitoes. The fan distributes the CO2 around the catch cup located under the cooler. Traps are set for day and night collection. The catch cup is tied off and stored on dry ice while the insulated cooler is refilled with dry ice. Mosquitoes are then stored in the -80°C freezer and obvious bycatch is removed. Samples are sent to the external laboratory in falcon tubes with tissue paper as padding to protect specimens.

For information about disturbances, land management activities, and other incidents that may impact data at NEON sites, see the Site management and event reporting (DP1.10111.001) data product.

Data package contents

mos_trapping: Mosquito trapping data from field operations
mos_barcoding: Mosquito barcoding sample data from external labs
mos_archivepooling: Mosquito archival information from external labs
mos_expertTaxonomistIDRaw: Mosquito identifications by expert taxonomists - raw
mos_subsampling: Generation of mosquito samples for barcoding, archiving and pathogen testing
mos_expertTaxonomistIDProcessed: Mosquito identifications by expert taxonomists - desynonomized
mos_sorting: Mosquito sorting data from external labs
mos_identificationHistory: Mosquito identification history for records where identifications have changed
variables: Description and units for each column of data in data tables
readme: Data product description, issue log, and other metadata about the data product
validation: Description of data validation applied at the points of collection and ingest

Data quality

In the mos_trapping table, the fanStatus, catchCupStatus, and dryIceStatus fields record any problems with the trapping apparatus noted at the time of sample collection. The sampleCondition field notes any issues with the sample itself, and is present in the mos_trapping, mos_sorting, and mos_expertTaxonomistID..

tables, tracking whether the condition of the sample changes as it travels through different facilities and analyses. In the mos_sorting table, differences between repeat measurements are noted for count, genus, and species; see variables file for details.

Please note that quality checks are comprehensive but not exhaustive; therefore, unknown data quality issues may exist. Users are advised to evaluate quality of the data as relevant to the scientific research question being addressed, perform data review and post-processing prior to analysis, and use the data quality information and issue logs included in download packages to aid interpretation.

Standard calculations

For wrapper functions to download data from the API, and functions to merge tabular data files across sites and months, NEON provides the neonUtilities package in R and the neonutilities package in Python. See the Download and Explore NEON Data tutorial for introductory instructions in both programming languages.

During the identification process any trap that appears to contain more than 200 mosquitoes is subsampled such that only a random subset of ~200 mosquitoes are identified. The laboratory reports the weight of the total sample, the subsample, and then the weight of all bycatch removed from the subsample. The individualCount reported for subsampled traps should be corrected for the proportion of the sample analyzed. To make this correction individualCount should be multiplied by totalWeight/subsampleWeight to estimate the full number of mosquitoes present in the trapped sample.

Table joining

Table 1	Table 2	Join by field(s)
mos_trapping	mos_sorting	sampleID
mos_sorting	mos_subsampling	Requires intermediate table: join via mos_expertTaxonomistID table (either Processed or Raw)
mos_trapping	mos_subsampling	Requires intermediate table: join via mos_sorting table and mos_expertTaxonomistID table (either Processed or Raw)
mos_sorting	mos_expertTaxonomistIDProcessed	subsampleID
mos_sorting	mos_expertTaxonomistIDRaw	subsampleID

Table 1	Table 2	Join by field(s)
mos_expertTaxonomistIDProcessed	mos_archivepooling	Requires intermediate table: join via mos_subsampling table
mos_expertTaxonomistIDRaw	mos_archivepooling	Requires intermediate table: join via mos_subsampling table
mos_archivepooling	mos_barcoding	Full join not recommended: tables not related
mos_archivepooling	mos_sorting	Requires intermediate table: join via mos_sorting table and mos_expertTaxonomistID table (either Processed or Raw) and mos_subsampling table
mos_archivepooling	mos_subsampling	archiveID
mos_archivepooling	mos_trapping	Requires intermediate table: join via mos_sorting and mos_expertTaxonomistID table (either Processed or Raw) and mos_subsampling tables
mos_barcoding	mos_expertTaxonomistIDProcessed	Not fully automatable: multiple individualIDs pooled into each individualIDList
mos_barcoding	mos_expertTaxonomistIDRaw	Not fully automatable: multiple individualIDs pooled into each individualIDList
mos_barcoding	mos_sorting	Not fully automatable: multiple individualIDs pooled into each individualIDList
mos_barcoding	mos_subsampling	Not fully automatable: multiple individualIDs pooled into each individualIDList
mos_barcoding	mos_trapping	Not fully automatable: multiple individualIDs pooled into each individualIDList

Table 1	Table 2	Join by field(s)
mos_expertTaxonomistIDProcessed	mos_expertTaxonomistIDRaw	subsampleID,scientificName, sex
mos_expertTaxonomistIDProcessed	mos_subsampling	subsampleID,scientificName, sex
mos_expertTaxonomistIDProcessed	mos_trapping	Requires intermediate table: join via mos_sorting table
mos_expertTaxonomistIDRaw	mos_subsampling	subsampleID,scientificName, sex
mos_expertTaxonomistIDRaw	mos_trapping	Requires intermediate table: join via mos_sorting table
mos_identificationHistory	Any other table	Full join not recommended: Previous identifications of the same individual can be linked by identificationHistoryID in the mos_expertTaxonomistID table (either Processed or Raw)

Documentation

📄 **Standard Operating Procedures and Protocols for Mosquito Taxonomic Identification**
Kansas_Bio_Survey_SOP_10182016 | 180 KiB | PDF

📄 **TOS Science Design for Mosquito Abundance, Diversity, and Phenology**
NEON.DOC.000910vC | 532 KiB | PDF

📄 **TOS Science Design for Vectors and Pathogens**
NEON.DOC.000911vC | 1.9 MiB | PDF

📄 **TOS Protocol and Procedure: MOS – Mosquito Sampling**
NEON.DOC.014049vN | 3.3 MiB | PDF

📄 **NEON User Guide to Mosquitos Sampled From CO2 Traps (DP1.10043.001) and Mosquito-borne Pathogen Status (DP1.10041.001)**
NEON_mosquito_userGuide_vF | 343.9 KiB | PDF

📄 **Vector Disease Control International Denver Surveillance Laboratory Standard Operating Procedures [NEON Sample Processing Version, 2020]**
VDCI_Mosquito_Identification_2020 | 701.4 KiB | PDF

For more information on data product documentation, see:
https://data.neonscience.org/data-products/DP1.10043.001

Citation

To cite data from Mosquitoes sampled from CO2 traps (DP1.10043.001), see citation here:
https://data.neonscience.org/data-products/DP1.10043.001
For general guidance in citing NEON data and documentation, see the citation guidelines page:
https://www.neonscience.org/data-samples/guidelines-policies/citing

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NEON welcomes discussion with data users! Reach out with any questions or concerns about NEON data:
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