

Read me for data files for MEC-19-1399

File: SagehenPolyergus_IndividualPairs_Relatedness_NestDistances.csv

Type: Comma Separated Values (csv)

Description: Data table showing the relatedness value for each pair of individual ants as determined using KINGROUP software (Konovalov, Manning, & Henshaw, 2004), along with their subpopulation status as determined using STRUCTURE software (Pritchard, Stephens, & Donnelly, 2000), their status as nestmates or not, and the distance between their nests.

Observations: 27,222

Fields: 12

Field descriptions:

Observation: Arbitrary unique number for each observation

Nest1: Name of nest of first individual ant.

Vial1: Name of vial in which first individual ant was stored in in the field preparation for DNA extraction.

Ind1: Name of first individual ant sample. Individual ant names are unique within each vial.

Nest2: Name of nest of second individual ant.

Vial2: Name of vial in which second individual ant was stored in in the field preparation for DNA extraction.

Ind2: Name of second individual ant sample. Individual names are unique within each vial.

NestPair: Unique Name for the pair of nests that each pair of individual ants come from. Order of names is standardized such that alphabetically earlier name is always first. For example, when individuals from Nest 226 and Nest JS048 are compared, the resulting NestPair code is always JS048_226, and never 226_JS048.

Nestmates: Boolean field to indicate if pair of individual ants are from the same nest (TRUE) or not (FALSE).

Subpop: Name of the subpopulation the pair of individual ants belong to, based on STRUCTURE software analysis. Subpop names are 1, 2, or 3.

Relatedness: Estimated pairwise relatedness value as calculated by KINGROUP software for each pair of individual ants. Values range from -1 to 1.

Distance (m): Distance in meters between the two nests inhabited by the pair of individual ants. Note that nestmates have a distance of zero, because they share a nest.

File: SagehenPolyergus_Individuals_Genotypes.csv

Type: Comma Separated Values (csv)

Description: The genotypes of individual ants at 6 microsatellite loci.

Observations: 397

Fields: 13

Field descriptions:

Nest_Vial_Ind: Unique name given to each individual ant whose DNA was sampled. Name is made of individual's nest name, the vial in which it was stored in the field in preparation for DNA extraction, and an individual ant ID which is unique within each vial, all separated by underscores.

Pol1_A ... Pol12_B: These 12 fields give the sizes of the microsatellite alleles observed at each of six loci. Field names are the same as used by Bono (2007), with “_A” or “_B” appended to distinguish first allele from the second allele, for each locus.

File: SagehenPolyergus_Nests_XY_HostSpecies.csv

Type: Comma Separated Values (csv)

Description: The names of, locations of, and host species used by each *Polyergus* nest used in this study. Nest names are consistent across datasheets

Observations: 82

Fields: 4

Field descriptions:

Nest Name: Unique name of each *Polyergus* nest. Nest names are consistent across data files.

X (UTM Zone 10N): The horizontal displacement to the East of the origin of Universal Trans Mercator Zone 10N in meters. Analogous to longitude in a geographic coordinate system.

Y (UTM Zone 10N): The vertical displacement to the North of the origin of Universal Trans Mercator Zone 10N in meters. Analogous to latitude in a geographic coordinate system.

Formica host species: The host species determination for each nest. All host species are in the genus *Formica*. Hosts were determined to as *F. accreta*, *F. argentea*, or *F. subaenescens*. Occasional ambiguous determinations are noted.

References:

- Bono, J. M., Blatrix, R., Antolin, M. F., & Herbers, J. M. (2007). Pirate ants (*Polyergus breviceps*) and sympatric hosts (*Formica occulta* and *Formica* sp. cf. *argentea*): Host specificity and coevolutionary dynamics. *Biological Journal of the Linnean Society*, 91(4), 565–572. doi:10.1111/j.1095-8312.2007.00817.x
- Kononov, D. A., Manning, C., & Henshaw, M. T. (2004). Kingroup: A Program for Pedigree Relationship Reconstruction and Kin Group Assignments Using Genetic Markers. *Molecular Ecology Notes*, 4(4), 779–782. doi:10.1111/j.1471-8286.2004.00796.x
- Pritchard, J. K., Stephens, M., & Donnelly, P. (2000). Inference of population structure using multilocus genotype data. *Genetics*, 155(2), 945–959. doi:10.1111/j.1471-8286.2007.01758.x

File: SagehenPolyergus_Raids

Type: Comma Separated Values (csv)

Description: The dates, raiding nest name, raided nest (or point) name, intraspecific raid status, crossing raid status, and raid distance of raids used in this study. Nest names are consistent across datasheets.

Observations: 863

Fields: 7

Field descriptions:

RaidID: Unique name for each raid.

Raid Date: Calendar date of each raid as DD-MMM-YYYY

Raiding nest: Name of the *Polyergus* nest that initiated the raid.

Raided nest/point: Name of furthest observed point of raid. This is often a host *Formica* species nest, but it is also frequently merely the point at which raiders turned around, or the furthest point we could detect raid activity if a raid was already returning when discovered. Rarely, this nest is also a *Polyergus* nest, and thus may be present in other datasheets in this dataset.

Intraspecific?: Flags the status of a raid as intraspecific (Y) or not (N). Other values are BLANK (no data recorded), or UNKNOWN (no data recorded or unsure if raid was intraspecific or not).

Crosses? (raid # or blank): If this raid crosses another raid, the RaidID of the other raid is given here. Otherwise, the value is "BLANK".

Raid Distance (m): The raid distance in meters.