



# Dataset of wing venation measurements for *Apis mellifera caucasica*, *A. mellifera carnica* and *A. mellifera mellifera* (Hymenoptera: Apidae), their hybrids and backcrosses

Paweł Węgrzynowicz<sup>‡</sup>, Aleksandra Łoś<sup>‡,§</sup>

<sup>‡</sup> Research Institute of Horticulture, Skierniewice, Poland

<sup>§</sup> Institute of Nature Conservation, Polish Academy of Sciences, Kraków, Poland

Corresponding author: Aleksandra Łoś ([los-aleksandra@o2.pl](mailto:los-aleksandra@o2.pl))

Academic editor: Laurence Packer

Received: 28 Apr 2020 | Accepted: 24 Jul 2020 | Published: 05 Aug 2020

Citation: Węgrzynowicz P, Łoś A (2020) Dataset of wing venation measurements for *Apis mellifera caucasica*, *A. mellifera carnica* and *A. mellifera mellifera* (Hymenoptera: Apidae), their hybrids and backcrosses. Biodiversity Data Journal 8: e53724. <https://doi.org/10.3897/BDJ.8.e53724>

## Abstract

### Background

Wing venation is used as a tool in honeybee (*Apis mellifera* L., 1758) subspecies identification. The presented dataset concerns nineteen landmarks located at honeybee worker's forewing vein junctions. Landmarks of *Apis mellifera caucasica* Pollmann, 1889, *A. mellifera carnica* Pollmann, 1879 and *A. mellifera mellifera* Linnaeus, 1758, their hybrids and backcrosses were measured. In total, data from 9590 wings were collected. The dataset could be used in geometric morphometric analysis, studies of degree of inheritance of morphological features and, after further development and supplementation with other local subspecies and hybrids, can contribute to in-depth evolutionary research on honeybees.

## New information

Baseline dataset for wing venation of hybrids and backcrosses of *A. mellifera carnica*, *A. mellifera caucasica* and *A. mellifera mellifera*.

## Keywords

morphometric analysis, geometric morphometry, honeybee, subspecies

## Introduction

Wing venation is commonly analysed as an important characteristic of insect species (e.g. Owen 2012, Perrard et al. 2014, Rossa et al. 2016, Breitzkreuz et al. 2017, Loh et al. 2017, Jacquelin et al. 2018). In honeybees (*Apis mellifera*), the measurement of wing venation is used for subspecies determination (Tofilski 2008, Gerula et al. 2009, Tofilski 2010, Francoy et al. 2012, Santana et al. 2014, da Silva et al. 2015, Węgrzynowicz et al. 2019, Gerula et al. 2009, Santana et al. 2014, Tofilski 2008, Węgrzynowicz et al. 2019). Due to a significant correlation between morphometric and molecular methods, the measurements and analysis of wing veins are a cost-effective and reliable identification measure (Miguel et al. 2011, Oleksa and Tofilski 2015, Henriques et al. 2020, Oleksa and Tofilski 2015). Geometric morphometrics, based upon nineteen landmarks located at honeybee worker's forewing vein junctions, has been used in Poland since 2008 as a tool for assessing subspecies identity (Tofilski 2008, Gerula et al. 2009). Creating databases that not only include representatives of various subspecies, but also data from hybrids and backcrosses, seems to be particularly valuable. This Data Paper provides raw metadata freely available for further exploration, which can be correlated, for example, with the reference samples for the subspecies from the Morphometric Bee Data Bank in Oberursel, Germany. It may also be used to assess inheritance of morphological features.

## Sampling methods

**Sampling description:** The original colonies of subspecies came from long-term breeding. *Apis mellifera carnica* and *A. mellifera caucasica* come from colonies maintained within a selection carried out by the Research Institute of Horticulture. *A. mellifera mellifera* was supplied from a conservation breeding programme supervised by the National Animal Husbandry Center ([https://www.kchz.agro.pl/wykaz-ksiegi-1\\_03\\_2019\\_1/](https://www.kchz.agro.pl/wykaz-ksiegi-1_03_2019_1/)). These subspecies are commonly maintained in Poland. Methodology described by Węgrzynowicz et al. (2019) was used in order to obtain the parental generation of bees from *A. mellifera carnica*, *A. mellifera caucasica* and *A. mellifera mellifera* subspecies, their hybrids and backcrosses. Two hundred queens with 24 different genotypes have been obtained, representing all possible hybrid and backcrosses combinations of *Apis mellifera carnica*, *A. mellifera caucasica* and *A. mellifera mellifera* subspecies. To conduct morphometric analyses, worker bee samples were taken shortly after emergence directly from incubated

combs. Bees were stored in plastic containers filled with 96% ethyl alcohol at room temperature for 4 to 5 months. After this period, each worker bee had its right wing removed. The wings were mounted in a glass photographic frame and scanned with a Nikon Coolscan 500 ED scanner (image resolution 2400 dpi, greyscale). Wing images were analysed with DrawWing software (freely available at: <http://drawwing.org/node/2>) to determine the coordinates of nineteen landmark features (Suppl. material 1). The dataset (Suppl. material 2, Suppl. material 3) contains parameter measurements for individually analysed honeybee wings.

## Geographic coverage

**Description:** The Institute of Horticulture, Apiculture Division in Puławy, Poland. Altitude above sea level: 137 m.

**Coordinates:** 51.246 Latitude; 21.581 Longitude.

## Taxonomic coverage

**Description:** Wing venation is a suite of characteristics that allows the identification of subspecies. Locally-sustained bees of *A. m. caucasica*, *A. m. carnica* and *A. m. mellifera* with stabilised wing parameters were used to create hybrid and backcrossed workers and all were included in our baseline dataset.

## Temporal coverage

**Data range:** 2013-5-20 - 2015-9-15.

**Notes:** Beekeeping seasons in Poland.

## Usage rights

**Use license:** Creative Commons Public Domain Waiver (CC-Zero)

## Data resources

**Data package title:** Dataset of wing venation measurements

**Number of data sets:** 2

**Data set name:** Wing\_venation\_dataset

Column label	Column description
No.	serial number
Queen/Colony ID	Queen/Colony ID
Maternal origin ID	Maternal origin ID
Fatherly origin ID	Paternalorigin ID
GENOTYPE	GENOTYPE - short name which is described in the "Genotype_description" set
WINGS ID	WINGS ID - individual ID given to each sample from a combination of: "No.", "Queen/Colony ID", "Maternal origin ID", "Fatherly origin ID", "GENOTYPE"
x0, y0 - x18, y18	Parameter coordinates (in separate columns)

**Data set name:** Genotype\_description

Column label	Column description
GENOTYPE	GENOTYPE
Number of measured wings	Number of measured wings
Colonies amount	Colonies amount
Abbreviation description	Abbreviation description [P0, P1 - parental generations, F1 - hybrid generation, BC - backcrosses generation; lowercase letters represent the subspecies: first letter: parental-queen, second letter: paternal-drone (m - <i>A. m. mellifera</i> , k - <i>A. m. carnica</i> , c - <i>A. m. caucasica</i> )]

## Acknowledgements

We would like to thank the entire scientific and technical team of the Apiculture Division (Research Institute of Horticulture, Skierniewice, Poland) for help in breeding works, as well as for all directions and support. The reviewers and editors have given us extremely valuable guidance and significantly improved the quality of our paper for which we are extremely grateful.

## Author contributions

PW designed and implemented a research project that enabled data collection, conducted measurements, prepared the dataset and supervised writing of the manuscript. AŁ conceived the research, prepared the dataset for publication and helped write the

manuscript. Both authors agree with the final version of the manuscript and declare no conflict of interest.

## References

- Breitzkreuz LV, Winterton S, Engel M (2017) Wing tracheation in Chrysopidae and other Neuropterida (Insecta): A resolution of the confusion about vein fusion. *American Museum Novitates* 3890 (3890): 1-44. <https://doi.org/10.1206/3890.1>
- da Silva FL, Grassi Sella ML, Francoy TM, Costa AHR (2015) Evaluating classification and feature selection techniques for honeybee subspecies identification using wing images. *Computers and Electronics in Agriculture* 114: 68-77. <https://doi.org/10.1016/j.compag.2015.03.012>
- Francoy TM, Gonçalves LS, De Jong D (2012) Rapid morphological changes in populations of hybrids between Africanized and European honey bees. *Genetics and Molecular Research* 11 (3): 3349-3356. <https://doi.org/10.4238/2012.september.17.5>
- Gerula D, Tofilski A, Węgrzynowicz P, Skowronek W (2009) Computer-assisted discrimination of honeybee subspecies used for breeding in Poland. *Journal of Apicultural Science* 52 (2): 105-114.
- Henriques D, Chávez-Galarza J, Teixeira JSG, Ferreira H, Neves CJ, Francoy T, Pinto MA (2020) Wing geometric morphometrics of workers and drones and single nucleotide polymorphisms provide similar genetic structure in the Iberian honey bee (*Apis mellifera iberiensis*). *Insects* 11 (2). <https://doi.org/10.3390/insects11020089>
- Jacquelin L, Desutter-Grandcolas L, Chintauan-Marquier I, Boistel R, Zheng D, Prokop J, Nel A (2018) New insights on basiventral sclerites using 3D tools and homology of wing veins in Odonatoptera (Insecta). *Scientific Reports* 8 (1). <https://doi.org/10.1038/s41598-017-18615-0>
- Loh SYM, Ogawa Y, Kawana S, Tamura K, Lee HK (2017) Semi-automated quantitative *Drosophila* wings measurements. *BMC Bioinformatics* 18 (1). <https://doi.org/10.1186/s12859-017-1720-y>
- Miguel I, Baylac M, Iriondo M, Manzano C, Garnery L, Estonba A (2011) Both geometric morphometric and microsatellite data consistently support the differentiation of the *Apis mellifera* M evolutionary branch. *Apidologie* 42 (2): 150-161. <https://doi.org/10.1051/apido/2010048>
- Oleksa A, Tofilski A (2015) Wing geometric morphometrics and microsatellite analysis provide similar discrimination of honey bee subspecies. *Apidologie* 46 (1): 49-60. <https://doi.org/10.1007/s13592-014-0300-7>
- Owen ER (2012) Applications of morphometrics to the Hymenoptera, particularly bumble bees (*Bombus*, Apidae). *Morphometrics* <https://doi.org/10.5772/34745>
- Perrard A, Baylac M, Carpenter JM, Villemant C (2014) Evolution of wing shape in hornets: why is the wing venation efficient for species identification? *Journal of Evolutionary Biology* 27 (12): 2665-2675. <https://doi.org/10.1111/jeb.12523>
- Rossa R, Goczał J, Tofilski A (2016) Within- and between-species variation of wing venation in genus *Monochamus* (Coleoptera: Cerambycidae). *Journal of Insect Science* 16 (1). <https://doi.org/10.1093/jisesa/iev153>
- Santana F, Costa AR, Truzzi F, Silva F, Santos S, Francoy T, Saraiva A (2014) A reference process for automating bee species identification based on wing images and

digital image processing. *Ecological Informatics* 24: 248-260. <https://doi.org/10.1016/j.ecoinf.2013.12.001>

- Tofilski A (2008) Using geometric morphometrics and standard morphometry to discriminate three honeybee subspecies. *Apidologie* 39 (5): 558-563. <https://doi.org/10.1051/apido:2008037>
- Tofilski A (2010) Automatic measurement of honeybee wings. *Systematics Association Special Volumes* 277-288. <https://doi.org/10.1201/9781420008074.ch17>
- Węgrzynowicz P, Gerula D, Tofilski A, Panasiuk B, Bierkowska M (2019) Maternal inheritance in hybrids of three honey bee subspecies. *Journal of Apicultural Science* 63 (1): 131-138. <https://doi.org/10.2478/jas-2019-0010>

## Supplementary materials

### Suppl. material 1: Image of the x and y coordinates obtained with the DrawWing software for 19 vein connections on the right wing of worker honey bee [doi](#)

**Authors:** Paweł Węgrzynowicz

**Data type:** Image

[Download file](#) (2.32 MB)

### Suppl. material 2: Dataset of wing venation measurements - abbreviations descriptions [doi](#)

**Authors:** Paweł Węgrzynowicz

**Data type:** txt

**Brief description:** Descriptions of the abbreviated names of the genotypes used in the dataset of wing venation measurements.

[Download file](#) (3.07 kb)

### Suppl. material 3: Dataset of wing venation measurements [doi](#)

**Authors:** Paweł Węgrzynowicz

**Data type:** txt

**Brief description:** The database contains the x and y coordinates obtained with DrawWing software for 19 vein junctions on the right wing of worker honeybees (38 coordinates for each wing). The analysed wings originate from offspring of 200 queens with 24 different genotypes representing all possible hybrid and backcrosses combinations of *Apis mellifera carnica*, *A. mellifera caucasica* and *A. mellifera mellifera* subspecies. Results from a total of 9590 wings are presented in the dataset.

[Download file](#) (1.77 MB)