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**The FloRes Database: A floral resources
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workflow**

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The FloRes Database: A floral resources trait database for pollinator habitat-assessment generated by a multistep workflow

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Abstract

Background

The decline of pollinating insects in agricultural landscapes proceeds due to intensive land use and the associated loss of habitat and food sources. Those insects depend on the spatial and temporal distribution of nectar and pollen as food resource. Hence, for nature conservation the spatio-temporal assessment of food quantity of habitats is necessary. Therefore, sufficient data of floral plant traits are required.

New information

We present a raw database with the plant traits 1. flowering period, 2. floral-unit density, 3. nectar (nectar volume or sugar content of floral unit), 4. sugar concentration in nectar, 5. pollen mass or volume per floral unit, 6. protein content of pollen and 7. corolla depth. All traits are sampled from literature and online databases. The raw database consists of 843 unspecified (sp.) and specified plant species belong to 488 genera and 102 families with missing information. For utilizing the raw data, we developed a stepwise workflow unifying traits to comparable entities with identical units and aggregating them to an application database, called the FloRes Database (Floral Resources Database). FloRes contains the complete information of traits for 38 taxa and, when corolla depth is excluded, for 70 taxa. The stepwise workflow is implemented in five consecutive scripts written in R, that allow other users easily add information to the raw data and to compute their own application data set. FloRes can be used to evaluate food-resource supply of habitats for pollinators, e.g., to compare seed mixtures of agri-environmental measure, such as flower strips, taking into account flower phenology on a daily basis. Further, calculated for-resource

supply can be used as input for simulation models of pollinator populations, such as the agent-based models BumbleBEEHAVE and SyrFitSources.

Keywords

Pollinators, bumblebees, hoverflies, floral resource, pollen, nectar, corolla, phenology, sugar concentration, protein, habitat assessment

Introduction

The intensive management of land, the associated loss of feeding, shelter and nesting habitats (Beckmann et al. 2019, Carvell et al. 2007, Tilman et al. 2002) and the resulting lack of floral resources in natural and agricultural landscapes in space and time affected pollinators' diversity and abundance (Brown and Paxton 2009, Cardoso et al. 2020, Potts et al. 2010, Williams et al. 2012). Restoring and establishing semi-natural habitats and agri-environmental measures, e.g., hedgerows, meadows or flower strips, can mitigate the decline of pollinating insects through increasing the supply of floral resources (Carvell et al. 2017, Korpela et al. 2013, Pywell et al. 2015).

Pollinators, such as bees and hoverflies, rely on nectar as energy source for movement and vital processes as well as on pollen for reproduction (Haslett 1989, Potts et al. 2003, Westrich 2018). The availability of pollen and nectar must be ensured throughout the season, without temporal gaps in resource availability in order to prevent a decrease of pollinator populations (Roulston and Goodell 2011). Therefore, quantification of the spatio-temporal distribution of floral resources is crucial for assessing the potential of habitats and landscape sections to support pollinators. Many researchers pursue the assessment of habitats for pollinating insects, which requires knowledge about quantity, quality and phenology of floral resources, i.e., nectar and pollen (Potts et al. 2003).

More precisely, the quantification of nectar and pollen supply demands knowledge of:

1. Physiological traits of the flower phenology and flower-unit density
2. The amounts of the floral resources per flower
3. The availability of the floral resources to pollinators determined by the corolla depth

Data on phenology and abundance are comparatively easy to acquire and, therefore, well available, but data on floral resources and corolla depth are scattered. To the best of our knowledge, there is no comprehensive database combining the above-mentioned plant traits in one source to this date. Thus, we compiled a database composed of data about phenology, floral unit density, nectar volumes or sugar amount of floral unit, sugar concentration, pollen per floral unit, protein content of pollen and corolla depth, referred to as the raw database here, based on literature and existing databases of plant traits. Because the raw database does contain very few species with a complete set of traits, we generated a second application database, referred to as FloRes Database (Floral Resources Database), through a multistep workflow. FloRes contains much fewer species

than the raw database, but the included taxa have complete sets of traits. We also publish the multistep workflow written in five consecutive scripts in R (R Core Team 2021) to enable other users to easily add information to the raw database and to compute or enhance the data sets for their own use.

Thus, with FloRes, we fill a knowledge gap about the floral resources and their provisioning to pollinators according to Hicks et al. (2016). In this way, habitats and food sources, such as semi-natural habitats and agri-environment measures, can be described and assessed for pollinators. Such data can also be useful to compare flowering habitats or seed mixtures (Hicks et al. 2016). Furthermore, the database can be used to generate input data on nectar and pollen supply for simulation models of pollinator populations. In our own research, we applied the FloRes Database to evaluate habitat quality for bumblebees and hoverflies using the agent-based models (ABM) BumbleBEEHAVE with the model BEESCOUT_2.0 (Becher et al. 2018) for bumblebees and SyrFitSources, a yet unpublished ABM, for aphidophagous hoverflies (App, unpublished).

Sampling methods

Sampling description: We collected data for eight floral traits (Table 1) from 34 published articles and their supplementary materials, from two books, reports and dissertations each, and from an online database.

For the raw database some input data of the traits had to be adapted. We calculated the average molar sugar concentration per species from the data of Gilbert (1981) assuming the sugar is pure saccharose. If the values of corolla depth were 0 in the reference of Gilbert (1981) and Becher et al. 2018, the species have open flowers. For species in Becher et al. (2018) which only provide pollen but no nectar, we set corolla depths to NA. If the nectar volume was 0 in Becher et al. (2018), but other references recorded a nectar volume or nectar sugar content > 0 , the values were not transferred in the database.

For the quantitative traits, we gathered, if available, minimum, maximum and mean values. With the traits 'pollen', 'nectar volume', 'sugar per flower' and 'flower' or 'inflorescence density', we recorded the flower unit they referred to, i.e., either per single flower or per inflorescence. The reference flower unit is very important for scaling nectar volume, nectar sugar content and pollen to the same flower unit, enabling merging and aggregation of trait data from different sources. Furthermore, the nomenclature of species varied in the literature. So, we equalized the species names in our database in column 'species' in our database, but we also included the names used in the original publications to facilitate joins and backtrackings with the data source (column 'species_name_reference' in our database).

Data preparation and multistep workflow

We compiled the FloRes Database so as to include as many species/ taxa with a complete set of traits as possible through a multistep workflow in R 4.1.0 (R Core Team 2021) using five consecutive scripts:

1. We converted flowers and inflorescences per square meter as well nectar and pollen per flower or inflorescence to the level floral units using formula 1 and 2 (Script: 1_Inflorescences.R). This step requires the dataset "AgriLand_FlowerDensity_perspecies.csv" of Baude et al. (2015).
2. We converted trait values to the same physical units for each trait and calculated missing trait values from other traits using equations 3 to 5 and 7 to 9 (Script: 2_units.R).
3. We took the means (except for flowers per square metre where we used the maximum) of multiple trait entries for each species (Script: 3_Aggregate_species.R).
4. We either unified synonymous species names or grouped species on a reasonable taxonomic level (taxon) for the next step to combine and aggregate the plant species. Further, we deleted those with few entries (Script: 4_Selecting_taxa.R). The grouping of species are given in the required auxiliary file 'Taxa_to_aggregate.csv' and can be edited.
5. We calculated the means of the traits of the synonymous species and repeated, now with the more complete dataset, the derivation of traits from other traits using equations 4 and 6 (Script: 5_Aggregation_selected_taxa.R).

The first and second script were used to convert the data to equal units, whereas scripts three to five were used to aggregate and combine the trait data on the most suitable taxonomic level, preferably on species level (column 'taxon' in our database). However, we could frequently aggregate only on genus level.

Conversions of units

- **Floral units per area**

For assessing the quantity of floral resources on habitat scale, the quantity of pollen or nectar (sugar) per standardized area is needed. In the raw data, the floral reference unit, either single flower or inflorescence, sometimes varied between flower-unit density, nectar and pollen data. For simplification the terms raceme, panicle, corymb, globular raceme, umbel or catkin in the database of Baude et al. (2015) were defined by us as inflorescences for reference floral unit. So, in order to facilitate calculations of nectar or pollen per square meter, we used the entity of the floral units (Carvalho et al. 2008). According to Carvalho et al. (2008), a floral unit is defined from the perspective of the insects as the number of flowers that can be visited without flying, ranging from a single flower up to thousands. Thus, single flowers could be summed up to inflorescences or inflorescences down to single flowers. Therefore, we transformed abundances of single flowers f_a [m^{-2}] into abundances of floral units fu_A [m^{-2}] through division by the number of open flowers per inflorescence f_i using the information from Baude et al. 2015 (equation 1).

$$fu_A = f_A / f_I \quad (1)$$

- **Pollen and nectar per floral unit**

Floral resources R_f , i.e., pollen or nectar, were multiplied with the number of open flowers per floral unit f_i (Baude et al. 2015) to get the floral resource R_{fu} per floral unit:

$$R_{fu} = P_f \cdot f_i \quad (2)$$

For open flowers per inflorescence of *Helianthus annuus*, we used data from Minckley et al. (1994), because *H. annuus* was not recorded in Baude et al. (2015)

For floral units per area, we used the maximum value, not the mean, when there were multiple values per species assuming that the maximum represented 100 % cover of the plant species. This allows to scale the floral resource per square meter in a given habitat more precisely when cover percentages of plant species are available.

- **Nectar volume, nectar sugar content and sugar concentration of nectar**

Mostly, nectar was measured as secretion of liquid per flower and day [volume flower⁻¹ d⁻¹] (e.g., Becher et al. 2016, Bosch et al. 1997, Hedtke 2000, Horn 2017) or as the sugar content per flower and day [mass flower⁻¹ d⁻¹] (e.g., Baude et al. 2016, Crane et al. 1984, Hicks et al. 2016, Maurizio and Schaper 1994). We orientated us by this convention and calculated both the volume [ml floral unit⁻¹ d⁻¹] and sugar content per flower [mg floral unit⁻¹ d⁻¹]. For the conversion of nectar volume to sugar content and vice versa, we used the equations 3 to 6.

To receive sugar in mass per flower m_z [mg], we multiplied nectar volume V_{nec} [ml] by the density of saccharose ρ_z [1570 mg ml⁻¹] and by the sugar concentration c_{perc} [%]:

$$m_z = \rho_z V_{nec} \frac{c_{perc}}{100} \quad (3)$$

When only molar concentration of sugar c_{mol} [mol l⁻¹] was given, we used the following equation with molar mass of saccharose M_z [342,300 mg mol⁻¹]:

$$m_z = V_{nec} M_z \frac{c_{mol}}{1000} \quad (4)$$

To calculate V_{nec} [ml] from sugar content per floral unit m_z [mg] we used

$$V_{nec} = \frac{m_z}{\rho_z \cdot c_{perc}} 100 \quad (5)$$

When c_{perc} was not given, we used c_{mol} to calculate V_{nec}

$$V_{nec} = \frac{m_z}{M_z c_{mol}} 1000 \quad (6)$$

For our application, we needed the sugar concentration in molar concentration, so we transformed c_{perc} to molar concentration following:

$$c_{mol} = c_{perc} \frac{\rho_z}{M_z} 10 \quad (7)$$

- **Mass of pollen per floral unit and pollen protein content**

Also for pollen, the physical units differed due to extraction methods. Mostly, the mass of pollen was given and the values only needed to be scaled to mg, if given in g or μg . However, sometimes it was given as estimated volume of pollen grains (Hicks et al. 2016). Therefore, we used

$$m_p = V_p * \rho_p \quad (8)$$

to calculate pollen mass m_p [mg] from the pollen volume V_p [ml] and the pollen density ρ_p [mg ml⁻¹]. Because for most species the density of fresh pollen ρ_p is not known, we used

$$\rho_p = \rho_{prot} P_{prot} + \frac{(1 - P_{prot})}{3} (\rho_{starch} + \rho_{fat} + \rho_{water}) \quad (9)$$

with mean densities of protein ρ_{prot} [1300 mg ml⁻¹] (Chick and Martin 1913), of starch ρ_{starch} [1440 mg ml⁻¹] (Marousis and Saravacos 1990), fat ρ_{fat} [900 mg ml²] (Deutsches Institut für Normung e.V. 2002) and water ρ_{water} [1000 mg ml⁻¹] and with the proportion of protein of the pollen P_{prot} [-]. When P_{prot} was not given for a plant species, we estimated it through mean protein content of the genus, as the protein contents are relatively similar among the species of a genus (Roulston et al. 2000). When the protein amount could not be estimated for a genus, it was estimated as the mean of all species in the database.

Aggregation of data and FloRes Database

After equalizing floral, physical and chemical units (Script: 2_units.R), we aggregated the traits using the mean of multiple entries per taxon, except for the case of floral units per area, where we used the maximum value to receive an approximate density of floral units at 100 % coverage of the species (script: 3_Aggregate_species.R). Subsequently, we checked the species for completeness of traits and grouped closely related taxa with incomplete, but complementary trait information in a table (Taxa_to_aggregate.csv) for further aggregation on genus level or a reasonable higher taxonomic level. We use this table to add the information of which plant species should be aggregated in the script 4_Selecting_taxa.R. Finally, we aggregated the traits a second time by the selected taxon (species, genus or higher level). In cases where values for molar sugar concentration were still lacking after step 5, we inserted the average value of 40% of sugar concentration as an estimate for wildflowers, as given in Westrich (2018).

After the final aggregation, we got three different output tables for the FloRes Database. "5_FloRes_raw" contains the mean values of all taxa for which at least some trait data were available. "5_FloRes_complete_trait" is the dataset of taxa without any gaps "5_Selected_taxa_no_corolla" contains taxa where all traits except for corolla depths were complete. Those datasets can finally be used to calculate the amount of nectar and pollen

of habitats within any defined time period, given that the plant species of the habitats are included in the database.

Geographic coverage

Description: The database is a collection of data from the Northern Hemisphere, focus on Central Europe.

Coordinates: ; .

Usage licence

Usage licence: Creative Commons Public Domain Waiver (CC-Zero)

Data resources

Data package title: The FloRes Database: A floral resources trait database for pollinator habitat-assessment generated by a multistep workflow

Resource link: https://datadryad.org/stash/share/pYjuf_kRaA0N9Lw25svZa_rnQ_mENIlyQAC2rkXicEI

Number of data sets: 2

Data set name: Data.zip

Download URL: https://datadryad.org/stash/share/pYjuf_kRaA0N9Lw25svZa_rnQ_mENIlyQAC2rkXicEI

Data format: .csv

Description: The raw data, all intermediate and auxiliary datasets and the finally FloRes Database are published in the Dryad repository.

In the raw database the same traits are covered, but the units and the dependent flower units are given in extra columns ending on the “_unit” and “_regarding_flowering_unit”. Further, the literature citation is given in the column ending with “_references”.

Column label	Column description
Phenology	Flower life span and flowering start and end given as day of the year [d]
Flower unit density	The number of single flowers or inflorescences per square meter [m ²]
Nectar volume	The nectar volume per single flower or inflorescences [ml]

Sugar concentration in nectar	The concentration of sugar in nectar in mol per litre [mol l ⁻¹] or percentage [%]. Sugar is assumed to be pure saccharose.
Sugar per flower	The absolute sugar content of nectar per single flower or inflorescences [mg]
Pollen	The pollen per single flower or inflorescences [mg or ml]
Protein content of pollen	The amount of protein in pollen [%]
Corolla depth	The depth of the corolla tube [mm]

Data set name: multistep_workflow_scripts.zip

Download

URL: https://datadryad.org/stash/share/pYjuf_kRaA0N9Lw25svZa_rnQ_mENIlyQAC2rkXicEI.

Data format: .R

Data format version: R.-4.1.0

Description: All scripts used for generating the FloRes Database from the raw data.

Column label	Column description
none	none

Additional information

Data Statistics

Raw database

The raw database counted a total of 843 specified and unspecified plant species. Synonyms of species names were not counted as the same species. These species belonged to 448 genera and 102 families.

Most of the collected species had either data for one or few traits (Fig. 1). Only few species had entries of four to seven traits of interest. Only 27 had a complete set of traits of interest.

To explore the quality of the raw database, the percentage of the species with one or more entries per trait were plotted (Fig. 2). Flowering period had the fewest species with lacking entries. Yet, less than 40% of species were provided with data for each of the other traits. Hence, most of the species were insufficiently provided with trait data. Therefore, it was necessary to combine and aggregate species on a reasonable taxonomic level for a comprehensive habitat assessment.

FloRes Database

After aggregating and combining the traits of the same species or closely related taxa, 42 taxa with a complete set of traits remained in the FloRes Database. Those taxa belonged to 38 genera and 17 families. When excluding corolla depth, the numbers rose up to 70 taxa from 63 genera and 22 families.

All traits varied strongly among the taxa (Fig. 3). Most remarkable was the huge span of the floral units per square meter and of nectar and pollen per floral unit, ranging across three to five orders of magnitude. Correlations among traits were mostly weak or moderate (Fig. 4). However, there was a strong positive correlation ($r = 0.77$) between nectar volume and sugar per floral unit ($t = 7.86$, $df = 40$, $p\text{-value} = 1.234e-09$), which is in line with the moderate variation in sugar concentration (Fig. 3). Further, there was a positive correlation ($r = 0.54$) between pollen and sugar per floral units ($t = 4.2137$, $df = 40$, $p\text{-value} = 1.389e-04$), which could be explained by larger floral units spending more sugar and pollen. Correlations were calculated with Pearson's correlation coefficient using R. Significance levels of correlations are as well calculated with R.

Limitations and uncertainties

We did not collect own data in the field or laboratory, but we gathered trait values from different sources. Thus, we often did not know if the density of floral units referred to 100 % cover of the plant species in its habitat. When not specified, we assumed highest given density as 100% cover. Additionally, the habitats where the flower units per area were counted were mostly unknown. Therefore, an accurate estimation of nectar and pollen supply on habitat levels is hampered. Also, the volume of nectar per flower varies per day and also within the day. The diurnal rhythm was not considered. Further, the sugar content in nectar depends on the temperature and moisture of soil and air (Westrich 2018). Hence, the complete database can only give a rough estimation of floral resources. Frequently, pollen is given in grains or volume and without exact measurements of pollen densities. Therefore, the values of pollen mass derived from volume are rough estimates. Also, the nectar volume and sugar content per floral unit were derived from mass, where necessary, assuming molar mass and density of saccharose, although nectar is often a mixture of glucose, fructose and saccharose (Percival 1961).

Applications

The FloRes Database facilitates to describe and assess habitats and food sources such as semi-natural habitats and agri-environment measures, e.g., flower strips for pollinators at local and landscape level. We used table "5_Selected_taxa_no_corolla" as input file for the floral resources of habitats in BumbleBEEHAVE and SyrFitSources to assess the landscape quality for pollinators. However, before we could apply the data as a base for model input of nectar and pollen amount, we had to fill in missing values of the corolla depths through educated guesses for each target species, enlarging the number of usable taxa of plants from 38 up to 70. For our specific models, the units of the traits needed to be converted, or column names had to be changed.

Another application of the database may be to evaluate existing seed mixtures for flower strips or other agri-environmental measure, or to design new ones, that ensure continuity in floral resource availability throughout the year, similar as it was done in Hicks et al. (2016). Finally, the described workflow and the published scripts allow us and other users to easily expand and improve the database by simply adding new lines to the raw database. This will facilitate a steady improvement of pollinator habitat assessments.

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Author contributions

FBB and MA share the first authorship. The conception of both databases and the multistep workflow is from FBB and MA. FBB researched for the data of floral resource and compiled it into the raw database. MA contributed the R scripts and calculations for the multistep workflow. FBB, MA and JT contributed to writing and editing of the final manuscript. All authors have read and agreed to the published version of the manuscript.

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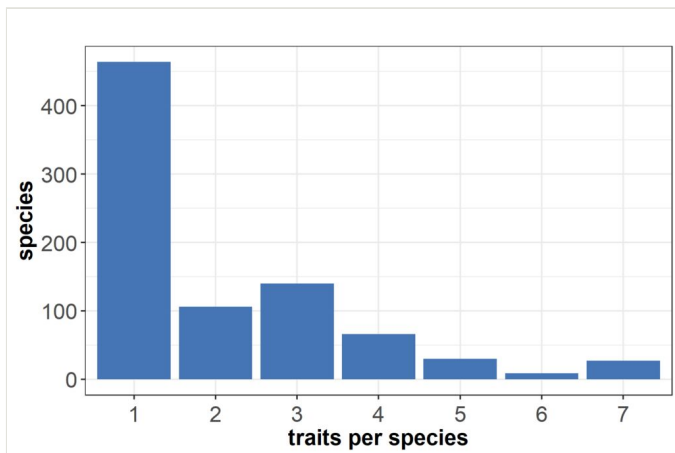


Figure 1.

Number of species in the raw database which had at least one entry per trait. The traits comprised phenology, floral unit density per area, corolla depth, nectar volume per floral unit, sugar concentration in nectar, pollen per floral unit and protein content of pollen.

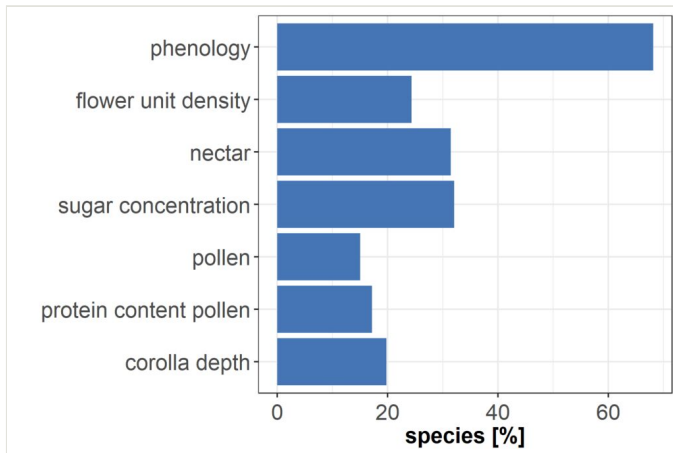


Figure 2.
Percent of species with one or more entries per trait.

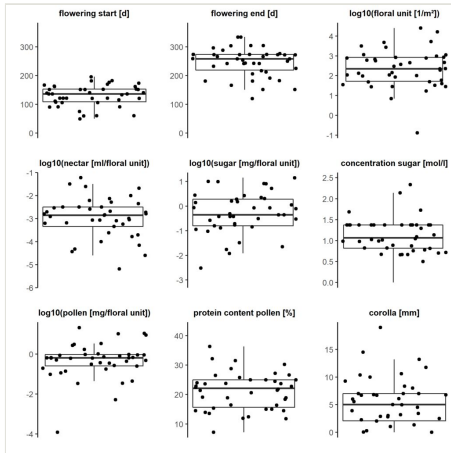


Figure 3.
Distribution of floral-trait values.

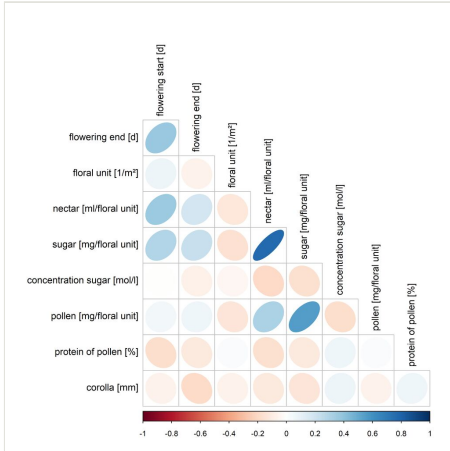


Figure 4.
Correlations between the species' traits.

Table 1.

Traits in raw and FloRes database

Trait	Coded in database	Description	Units raw database	Units FloRes database
Physiological traits				
Phenology	flowering flowering_start flowering_end	Flower life span and flowering start and end given as day of the year	d	d
Flower unit density	flowers_m2	The number of single flowers or inflorescences per square meter [m ²]	n/m ²	n/m ²
Floral resources				
Nectar volume ^c	nectar_volume	The nectar volume per single flower or inflorescences	μl, ml, l/m ²	ml
Sugar concentration in nectar ^a	sugar_conc	The concentration of sugar in nectar in mol per litre and percentage	mol l ⁻¹ , %	mol l ⁻¹ , %
Sugar per flower	nectar_sugar_cont	The absolute sugar content of nectar per single flower or inflorescences	μg, mg	mg
Pollen	pollen	The pollen per single flower or inflorescences	μg, mg, g/m ² , μl,	mg
Protein content of pollen	protein	The amount of protein in pollen	%, g/100g dry mass	%
Resource availability				
Corolla depth ^b	corolla	The depth of the corolla tube	mm	mm