

## Geographic Variation among Closely Related, Highly Variable Species with a Wide Distribution Range: the South Andean-Patagonian *Nassauvia* subgenus *Strongyloma* (Asteraceae, Nassauvieae)

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**Abstract**—Morphological variation among the five species of *Nassauvia* subgenus *Strongyloma* was assessed through statistical analyses of morphometric traits in populations throughout the southern Andean-Patagonian region. Uni- and multivariate analyses were used to identify patterns of morphological variation in relation to geography. Additionally, species distribution modeling was implemented to relate these patterns to climatic conditions. No well-defined groups could be recovered through multivariate analyses, although we observed some geographic structure. Latitudinal variation was found in leaves, phyllaries and cypselas, with a cline towards the south, where these structures become shorter and wider. Towards the east, the number of flowers per capitulum decreases, and abaxial corolla lips and cypselas become narrower and shorter. Distribution modeling showed several areas of contact and a large overlap of suitable conditions for more than one species, which is mainly related to the mean temperature of winter. Despite an association between morphological variation with geography and climate, actual geographic distributions of the putative species did not entirely match the clinal pattern of morphology, geography, and climate. Further genetic analyses are still needed to identify the probable processes that led to the complex patterns of observed variation.

**Keywords**—Morphological variation, multivariate analyses, populations, South America, species complex, species distribution modeling.

The study of variation within species that are widely distributed at extensive spatial scales provides an opportunity to observe evolution in progress and understand systematic diversity (Judd et al. 2002; Mascó et al. 2004; Chalcoff et al. 2008). Morphological variation is expected in plants that are widely distributed through different environments because they often respond to direct and indirect environmental factors with changes in phenology, vegetative growth, and reproductive traits. This response gives rise to changes in phenotypic characteristics between populations of the same or related species (Paruelo et al. 1998; Jobbágy et al. 2002) as polymorphisms within populations increase or decrease in frequency along geographic transects (Grant 1989). A taxonomically perplexing case of a polymorphic taxon with wide geographical range is *Nassauvia* Comm. ex Juss. subgenus *Strongyloma* (DC) Cabrera (Asteraceae, Nassauvieae), an early diverging Asteracean group from the South Andean-Patagonian region.

*Nassauvia* is one of the most widely distributed genera in the South Andean-Patagonian region. It comprises 38 species endemic to South America, distributed from southern Bolivia, through the Andes and the Patagonian steppe of Chile and Argentina, to Tierra del Fuego and The Malvinas/Falkland Islands (Cabrera and Willink 1973; Cabrera 1982; Arroyo and Marticorena 1988; Katinas et al. 2009). The genus is divided into two subgenera and four sections, including herbs and small shrubs with imbricate leaves, solitary to aggregate capitula of one to five flowers, bilabiate corollas, style branches crowned by apical papillae, the pappus usually narrowly paleaceous, and gametic chromosome numbers of  $n = 11, 22, \text{ca. } 44$  (Cabrera 1982; Hunziker et al. 1991; Katinas et al. 2009). *Nassauvia* subgen. *Strongyloma* is a well-defined group of small shrubs with a tendency toward heteroblastic development, subulate leaves with a vaginate base accompanied, when brachyblasts are present, by small leaves in rosettes, and with pubescent cypselas. Alpha taxonomy studies discern five species within subgen. *Strongyloma* (Cabrera 1982): *N. axillaris* (Lag. ex Lindl.) D. Don, *N. fuegiana* (Speg.) Cabrera, *N. glomerulosa* (Lag. ex Lindl.) D. Don,

*N. maeviae* Cabrera, and *N. ulicina* (Hook. f.) Macloskie. These species are defined on the basis of the number of flowers per capitulum, type of capitulescence, presence or absence of brachyblasts, and shape and longitude of leaves (Cabrera 1982; Table 1). Variation in these morphological traits does not, however, strictly follow species boundaries. Wide morphological variation within and among these species of this subgenus was observed (Cabrera 1982), suggesting that experimental analyses were needed to refine the species circumscription. Subsequently, a morphological cladistic analysis showed no resolution among these species (Freire et al. 1993). We have observed many plants in the field with differing combinations of the diagnostic morphological characters of these taxa (Table 1). Furthermore, herbarium specimens have been identified differently by various specialists, reinforcing the confusing species boundaries encountered in this group. Thus, interspecific variation in subgen. *Strongyloma* seems to be extensive, in part due to its geographic distribution, which is as wide as the distribution of the entire genus (excluding the Malvinas/Falkland Islands), including diverse climatic conditions and habitats (Paruelo et al. 1998).

A morphological cladistic analysis supported the monophyly of subgen. *Strongyloma* (Freire et al. 1993). However, a more recent molecular phylogenetic study based on the ITS region of nuclear ribosomal DNA, showed that subgen. *Strongyloma* is polyphyletic (Maraner et al. 2012), with *N. axillaris* placed separately from *N. fuegiana*, *N. glomerulosa*, and *N. ulicina* (*N. maeviae* was not included in the analysis). However, Maraner et al. (2012: p. 404) explained that “although *N. axillaris* is placed in section *Mastigophorus* [i.e. subgen. *Nassauvia*] by analyses of ITS data, it groups with other representatives of subgen. *Strongyloma* in a plastid phylogeny (Maraner and Stuessy, unpublished). Indeed, the preponderance of evidence [i.e. several morphological traits], including the inflorescence type, places *N. axillaris* in subgen. *Strongyloma*”. Possible reasons for the discordant placement of *N. axillaris* by the ITS sequences of Maraner et al. (2012) are an error in sample or sequence identity, or the availability of divergent sequence paralogs. Indeed, their ITS sequence of

TABLE 1. Distinguishing traits of the five species traditionally recognized for *Nassauvia* subgen. *Strongyloma*, contrasting the descriptions of Cabrera (1982; left column) and our personal observations (right column).

Species	Cabrera (1982)	Personal observations
<i>N. axillaris</i>	Dimorphic leaves.	Dimorphic leaves.
	Linear-subulate macroblast leaves (10–30 mm long).	Macroblast leaves with narrow, long, triangular blade, crowning a wide sheath (10.4–31.4 mm total length).
	Linear brachyblast leaves (3–10 mm long).	Brachyblast leaves with narrow, long triangular blade, and narrow sheath (2.7–16.0 mm total length).
	Lateral dichasia with 1–3 capitula.	Lateral or terminal solitary capitula, or lateral or terminal dichasia with 2–4 capitula.
	5 flowers per capitulum.	5 flowers per capitulum.
<i>N. fuegiana</i>	Corolla 5 mm long.	Corolla 4.1–7.0 mm long.
	Isomorphic leaves.	Isomorphic leaves to foliar dimorphism little evident.
	Linear-subulate leaves (6–15 mm long).	Macroblast leaves with narrow, long, triangular blade, crowning a wide sheath (6.5–25.7 mm total length).
	Lateral and solitary capitula.	Brachyblast leaves absent or similar to those of <i>N. axillaris</i> (1.8–12.4 mm total length).
	5 (exceptionally fewer) flowers per capitulum.	Lateral or terminal solitary capitula, or lateral or terminal dichasia with 2–4 capitula.
<i>N. glomerulosa</i>	Corolla 5.5 mm long.	3–5 flowers per capitulum.
	Dimorphic leaves.	Corolla 4.4–6.8 mm long.
	Linear-subulate macroblast leaves (5–10 mm long).	Dimorphic leaves.
	Elliptic brachyblast leaves (1 mm long).	Macroblast leaves with narrow, long, triangular blade, crowning a wide sheath (2.3–16.8 mm total length).
	Lateral or terminal capitula, and solitary or in dichasia with 2–3 capitula.	Brachyblast leaves with wide, short, triangular blade, crowning a wide sheath (1.9–10.2 mm total length).
<i>N. maeviae</i>	Lateral or terminal solitary capitula, and solitary or in dichasia with 2–3 capitula.	Lateral or terminal solitary capitula, or lateral dichasia with 2–3 capitula.
	5 flowers per capitulum.	2–5 flowers per capitulum.
	Corolla 5–6 mm long.	Corolla 3.5–6.1 mm long.
	Isomorphic leaves.	Isomorphic leaves to foliar dimorphism little evident.
	Oblong-linear leaves (1–3 mm long).	Macroblast leaves with narrow, short, triangular blade, crowning a wide sheath (2.3–4.3 mm total length).
<i>N. ulicina</i>	Terminal and solitary capitula.	Brachyblast leaves absent or similar to those of <i>N. glomerulosa</i> (2.4–3.0 mm total length).
	3 flowers per capitulum.	Terminal and solitary capitula.
	Corolla 3.2 mm long.	3 flowers per capitulum.
	Dimorphic leaves.	Corolla 4.1–4.4 mm long.
	Linear-subulate macroblast leaves (5–12 mm long).	Dimorphic leaves.
<i>N. axillaris</i>	Linear brachyblast leaves (1–3 mm long).	Macroblast leaves with narrow, long, triangular blade, crowning a wide sheath (3.9–17.1 mm total length).
	Lateral or terminal dichasia with 2–4 capitula.	Brachyblast leaves with narrow, short triangular blade, crowning a wide sheath (1.1–5.2 mm total length).
	1–3 flowers per capitulum.	Lateral or terminal solitary capitula, or lateral or terminal dichasia with 2–4 capitula.
	Corolla 4–4.5 mm long.	2–3 flowers per capitulum.
		Corolla 2.7–5.6 mm long.

*N. axillaris* differs by at least 26 base pairs (4.3%) from 10 *N. axillaris* sequences we have obtained for this species. A re-analysis of the ITS data set of Maraner et al. (2012) with 53 ITS sequences obtained from multiple populations of species of subgen. *Strongyloma* (including the 10 *N. axillaris* sequences), recovers a monophyletic subgen. *Strongyloma* with our sequences of *N. axillaris* placed among other members of subgen. *Strongyloma*, corroborating our expectations based on morphology (tree not shown). A preliminary phylogeographic analysis of subgen. *Strongyloma* based on two plastid molecular markers (Nicola et al. in prep.) further supports the inclusion of *N. axillaris* within subgen. *Strongyloma*.

In this context, the present study intended to improve our understanding of the patterns of morphological variation in *Nassauvia* subgen. *Strongyloma*. More specifically, we were interested to see if: (1) the five recognized species of subgen. *Strongyloma* can be consistently identified using multivariate analyses based on morphological data; (2) the distinctive traits of species belonging to subgen. *Strongyloma* are correlated geographically; and (3) biologically relevant climatic data can help illuminate patterns of morphological variation

in these species. To accomplish these goals, we used uni- and multivariate analyses to statistically identify patterns of morphological variation (Jensen 2003; Henderson 2006 and literature therein) of *Nassauvia* subgen. *Strongyloma*. We also applied statistical analyses to assess relationships between morphological variation and geographic or climatic gradients. Additionally, we used geographic and environmental data and new modeling techniques (Graham et al. 2004; Hijmans et al. 2005; Soberón and Peterson 2005; Elith et al. 2006) to further understand how abiotic factors impact the geographic limits of lineages and species (Graham et al. 2004; Wiens and Graham 2005; Rissler and Apodaca 2007). For that, we performed species distribution modeling as a means to understand how temperature, precipitation, or seasonality might influence the patterns of geographic variation encountered in this subgenus and possible associations with putative species limits.

#### MATERIALS AND METHODS

**Sampling Procedures and Traits Measured**—We sampled 65 localities distributed throughout the range of the five species of *Nassauvia* subgen.

*Strongyloma*, from southern Bolivia (ca. 21° S) to southern Argentina (ca. 53° S), and from western Chile (ca. 74° W) to eastern Argentina (ca. 64° W), mainly in the Patagonian steppe but also in the Andean region, from sea level to 4,250 m above sea level (a. s. l.) (Fig. 1; Appendix 1). Taxonomic identity of each population was established following Cabrera (1982). A total of 172 individuals approximately at the same stage of development were collected: samples of 131 individuals (five to eight plants per locality) were preserved in 70% ethanol, while 37 individuals were sampled from herbarium specimens (from COR, CONC, and SI) to augment the field collected specimens. Four individuals were based on type images (from G, K, and LP). Samples were dissected under a Zeiss 47 50 52–9901 stereomicroscope, and morphometric measurements ( $n = 516$ ) were taken with a calibrated eyepiece micrometer. Herbarium material was hydrated with hot water and detergent, and type images were measured using Image Tool 3.0 (UTHSCSA 2000). A single person obtained three measurements (pseudo-replicates) per plant.

Thirty-one morphological traits were considered in this study (abbreviations given between brackets; Appendix 2). The variables examined were: habit (H; 1 = shrub, 2 = caespitose, and 3 = cushion; Halloy 1990), presence or absence of foliar dimorphism (FD), total macroblast leaf length (MLL), total brachyblast leaf length (BLL), brachyblast leaf width (BLW), brachyblast leaf length/brachyblast leaf width ratio as an estimator of leaf shape (BLS), brachyblast leaf length  $\times$  brachyblast leaf width ratio as an estimator of leaf area (BLA), presence or absence of lateral (LC) or terminal (TC) solitary capitula, and lateral (LD) or terminal dichasia (TD), peduncle length (PL), number of outer phyllaries (NOP), length of outer phyllaries (LOP), width of outer phyllaries (WOP), outer phyllaries length/outer phyllaries width ratio as an estimator of outer phyllaries shape (OPS), outer phyllaries length  $\times$  outer phyllaries width ratio as an estimator of outer phyllaries area (OPA), number of inner phyllaries (NIP), length of inner phyllaries (LIP), width of inner phyllaries (WIP), inner phyllaries length/inner phyllaries width ratio as an estimator of inner phyllaries shape (IPS), inner phyllaries length  $\times$  inner phyllaries width ratio as an estimator of inner phyllaries area (IPA), number of flowers per capitulum (NFC), abaxial lip length (ALL), abaxial lip width (ALW), abaxial lip length/abaxial lip width ratio as an estimator of abaxial lip shape (ALS), abaxial lip length  $\times$  abaxial lip width ratio as an estimator of abaxial lip area (ALA), cypsel length (CL), cypsel width (CW), cypsel length/cypsel width ratio as an estimator of cypsel shape (CS), and cypsel length  $\times$  cypsel width ratio as an estimator of cypsel area (CA). We included morphological characters used by Cabrera (1982) to distinguish subgen. *Strongyloma* species to test their discriminative value (FD, MLL, BLL, BLS, and NFC). We also included a wide selection of vegetative and reproductive characters (selected because of their independence and variability among individuals) to see if additional traits supported the delimitation of species in this subgenus, and to characterize, for the first time, leaf, flower, and fruit variation in this group of plants across its geographic range.

Both brachy- and macroblast leaves of subgen. *Strongyloma* are sessile with a sheathing base. Even though different brachyblast leaf shapes were previously described for species belonging to subgen. *Strongyloma* (Cabrera 1982; ovate in *N. glomerulosa* and linear in the remaining species), this was due to the inclusion of both base and blade in the general outline of *N. glomerulosa* leaves, but not for the other species. Our preliminary observations showed that the blade is always triangular (wide, short to narrow, long) with inwards folded margin when young, expanded at maturity. As brachyblast leaves have uniform shapes, we used the length/width ratio to measure variation of proportions within the same basic shape avoiding the general size effect. The same criterion was applied to phyllaries, abaxial corolla lips, and cypselas. In spite of being a tridimensional structure, we also used length and width as descriptors of cypsel variation because cypselas are not compressed, having a circular transverse section that is uniform across these taxa. Nevertheless, because we are characterizing this tridimensional structure in just two dimensions, we approached our interpretation of variation with caution.

**Morphometric Analyses**—To comply with assumptions of normality and homoscedasticity,  $\log_{10}$  transformation was applied to BLL, BLW, BLS, BLA, OPS, LIP, WIP, IPS, IPA, ALS, ALA, CL, and CS, and square root transformation to MLL, PL, OPA, CL, CW, and CA data, although multivariate procedures are considered to be relatively insensitive to deviations from normality (Tabachnik and Fidell 2001; Henderson 2006). We standardized variables prior to all analyses. In addition, we reduced some data because of multicollinearity among morphological variables using a consensus between principal component analysis (PCA), Spearman's rank correlation coefficients ( $r_s$ ), and variance inflation factors (VIF). Finally, we selected a subset of 18 morphological variables (H,

MLL, BLS, LC, TC, LD, TD, PL, NOP, LOP, OPS, IPS, NFC, ALW, ALS, ALA, CL, and CS) to conduct the statistical analyses. For multivariate analyses referred to populations, a data matrix was prepared with mean values of all variables for each population.

Cluster analysis (CA) of populations was performed using the 18 morphological variables selected above, to gain insights into the natural structure of the observations under study. Hierarchical clustering used the average linkage method, and distances between clusters were calculated using Euclidean distances. The highest value of the cophenetic correlation coefficient was used to select one of several alternative groupings. From the resulting phenograms of the CA, we applied a modified Population Aggregation Analysis (PAA; Davis and Nixon 1992) proposed by Henderson (2004, 2005) for the identification of phylogenetic species. Under this technique species are recognized by unique combinations of qualitative character states and varieties are based on significant mean value differences of quantitative characters. We performed PCA using the quantitative morphological variables to describe the multivariate pattern of the morphological variability among populations and to identify the variables that most contribute to the variability between observations.

Discriminant analysis (DA) of quantitative morphological variables was used to discriminate the five species defined a priori (following Cabrera 1982) in a space where differences between groups are maximized and variation within groups is minimized. DA was also used to assess the relative importance of the variables for discriminating amongst groups. Morphological variables selected by PCA and DA as contributing to the majority of the variation were described by mean, median, quartiles, percentiles, and outliers in box plots to show variability between the five species. All statistical analysis and graphs were carried out in InfoStat 2.0 (Di Rienzo et al. 2011) and implemented in the software package R 2.13 (R Development Core Team 2011).

**Analyses of Climatic and Geographic Patterns of Variation**—We recorded altitude (Alt), and latitudinal (LatS) and longitudinal (LonW) coordinates for localities for *N. axillaris* (43 populations), *N. fuegiana* (19 populations), *N. glomerulosa* (135 populations), and *N. ulicina* (26 populations), covering the entire distribution range of each species using a handheld Geographical Positioning System (GPS) unit. The remaining 36 point localities of *N. fuegiana* and *N. ulicina* obtained from herbarium specimens were geo-referenced using Google Earth 6.0 (<http://www.google.com/earth/index.html>). Given that geographic and taxonomic mistakes can produce a first error source in the models (Feeley and Silman 2010; Newbold 2010), we reviewed carefully the identification of specimens and their associated geographic data. The software based on the maximum-entropy approach for species habitat modeling, Maxent (Phillips et al. 2004), has little sensitivity to sample size, but no algorithm predicts consistently well with small sample sizes ( $n < 30$ ). Therefore, we considered these two predictions as exploratory models (Wisz et al. 2008) that can be compared later according to the quality of the data (Plischoff and Fuentes-Castillo 2011).

Environmental information represented by 19 bioclimatic variables derived from the monthly temperature and rainfall values with a spatial resolution of 2.5 arc-minutes (5 km<sup>2</sup>) were downloaded from the WorldClim 1.4 database (<http://www.worldclim.org/current>; Hijmans et al. 2005). These were: annual mean temperature (Bio1), mean diurnal range (Bio2), isothermality (Bio3), temperature seasonality (Bio4), maximum temperature of warmest period (Bio5), minimum temperature of coldest period (Bio6), temperature annual range (Bio7), mean temperature of wettest quarter (Bio8), mean temperature of driest quarter (Bio9), mean temperature of warmest quarter (Bio10), mean temperature of coldest quarter (Bio11), annual precipitation (Bio12), precipitation of wettest period (Bio13), precipitation of driest period (Bio14), precipitation seasonality (Bio15), precipitation of wettest quarter (Bio16), precipitation of driest quarter (Bio17), precipitation of warmest quarter (Bio18), and precipitation of coldest quarter (Bio19). These environmental variables were extracted for each locality using Diva-Gis 7.3 (Hijmans et al. 2001; Appendix 3).

To avoid over-estimation of climatic data that can lead to misleading results (Elith et al. 2002, 2011; Phillips et al. 2004; Peterson and Nakazawa 2008) we reduced some data because of multicollinearity among climatic variables following a procedure implemented by various authors (e.g. Rissler et al. 2006; Werneck et al. 2011; Sede et al. 2012). We generated 2,000 random points from across Argentina, Bolivia, and Chile using Geo Midpoint (<http://www.geomidpoint.com/random/>), extracted environmental data in Diva-Gis 7.3 (Hijmans et al. 2001), and conducted a series of correlation tests using a Pearson correlation coefficient  $\geq 0.75$  ( $p \leq 0.001$ ). We also implemented PCA and VIF, and determined a consensus between these three multicollinearity tests to identify highly correlated variables. Finally, we selected ten variables that were considered more

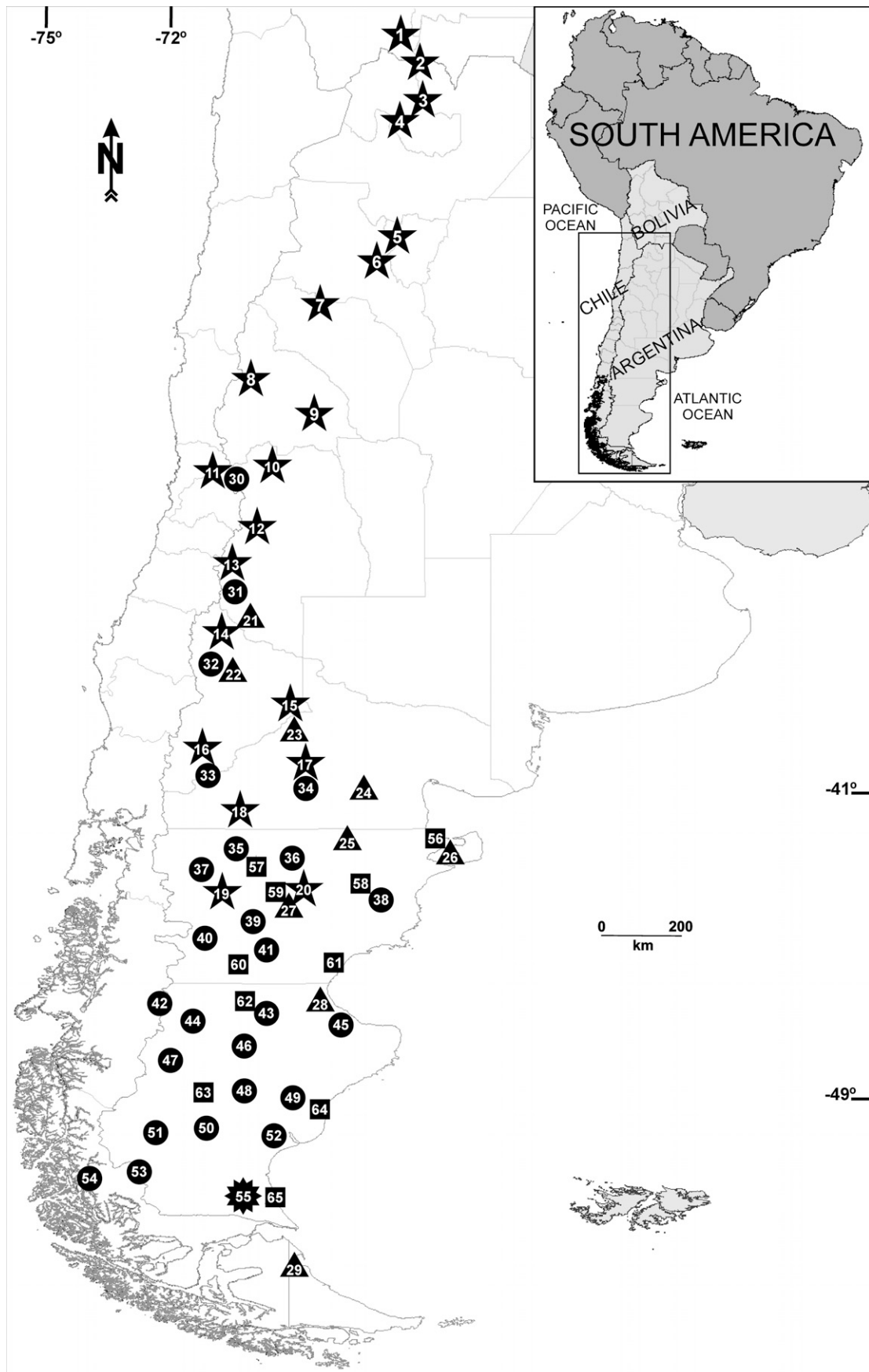


FIG. 1. Location of the 65 populations of *Nassauvia* subgen. *Strongyloma* in the South Andean-Patagonian region. Full locality names are provided in Appendix 1. Symbols indicate the five species according to Cabrera (1982): star *N. axillaris*, triangle *N. fuegiana*, circle *N. glomerulosa*, sun *N. macviae*, and square *N. ulicina*.



TABLE 2. Spearman correlation coefficients ( $r_s$ ) between selected morphological variables, and environmental and geographical data. Significance levels: \*  $p$ , 0.05; \*\*  $p$ , 0.01; \*\*\*  $p$ , 0.001.

	MLL	BLS	PL	NOP	LOP	OPS	IPS	NFC	ALW	ALS	ALA	CL	CS	Alt	LatS	LonW
Bio1	0.19	0.25*	0.05	-0.18	-0.08	0.24*	0.32**	-0.35**	-0.16	0.11	-0.11	-0.10	0.23	-0.34**	0.15	0.47***
Bio3	0.59***	0.38**	-0.07	-0.12	0.10	0.30*	0.32**	0.33**	0.12	0.09	0.16	-0.19	0.10	0.72***	0.82***	0.15
Bio7	0.68***	0.50***	0.18	-0.01	0.07	0.35**	0.40**	0.23	0.15	0.06	0.24*	-0.05	0.12	0.56***	0.76***	0.32**
Bio8	0.23	0.18	-0.22	-0.26*	-0.19	0.14	0.18	-0.24	-0.28*	0.16	-0.26*	-0.34**	0.27*	-0.08	0.20	0.59***
Bio9	0.09	0.18	0.28*	0.00	0.07	0.13	0.40***	-0.22	0.15	-0.04	0.22	0.26*	0.05	-0.29*	0.04	-0.04
Bio11	0.15	0.20	-0.02	-0.22	-0.07	0.21	0.27*	-0.35**	-0.18	0.12	-0.14	-0.11	0.25*	-0.40***	0.10	0.46***
Bio12	-0.01	-0.02	0.02	0.02	0.22	0.05	0.06	0.21	0.24	-0.05	0.25*	0.12	0.00	0.14	0.12	-0.37**
Bio15	0.43***	0.28*	-0.01	-0.06	0.15	0.21	0.15	0.28*	0.05	0.02	0.10	-0.24*	-0.09	0.65***	0.69***	0.00
Bio18	0.07	-0.06	-0.33**	-0.06	0.02	-0.03	-0.08	0.09	-0.15	0.13	-0.18	-0.25*	0.13	0.13	0.12	0.27*
Bio19	-0.17	-0.05	0.27*	0.10	0.22	-0.02	0.07	0.06	0.38**	-0.20	0.39**	0.39**	-0.07	-0.18	-0.20	-0.62***
Alt	0.50***	0.24	0.02	0.11	0.12	0.11	-0.01	0.54***	0.14	0.03	0.19	-0.16	-0.19			
LatS	0.73***	0.45***	0.01	-0.13	0.09	0.39**	0.37**	0.30**	0.06	0.12	0.15	-0.22	0.06			
LonW	0.29*	0.26*	-0.21	-0.23	-0.05	0.33**	0.26*	-0.25*	-0.32**	0.15	-0.33**	-0.39**	0.30*			

biologically meaningful and directly relevant to these species. These were: Bio1, Bio3, Bio7, Bio8, Bio9, Bio11, Bio12, Bio15, Bio18, and Bio19. Multicollinearity tests were performed in InfoStat 2.0 (Di Rienzo et al. 2011) and implemented in the software package R 2.13 (R Development Core Team 2011).

We first measured the degree of association between the morphological variables with the environmental and geographic data selected above for each of the 63 populations individually (Table 2). We then modeled the present potential geographic distribution of each species of *Nassauvia* subgen. *Strongyloma* using known point locality information and the environmental data selected in Diva-Gis 7.3 (Hijmans et al. 2001) and Maxent 3.3.3, with the maximum entropy machine-learning algorithm (Phillips et al. 2004). A model for *N. maeviae* could not be achieved due to extremely low number of known localities (only one with certainty). Nonetheless, we considered point locality information and relevant trends of this species.

The bioclimatic layers were trimmed to the areas surrounding each species and then projected over a larger region that included latitude 17°41' S to 55°49' S and longitude 57°31' W to 75°43' W for all species in Diva-Gis. Projections in Maxent were run using the following settings for all models: 10 replicates with auto features, response curves, jackknife tests, logistic output format, random seed, random test percentage = 10, replicate run type = crossvalidate, regularization multiplier = 1, maximum iterations = 1,000, convergence threshold = 0.00001, and maximum number of background points = 10,000 following a similar procedure described by Fontanella et al. (2012) and Sede et al. (2012). To determine the threshold value for each projection, we used the minimum training value averaged over the 10 runs. Variable importance was determined comparing percent contribution values and jackknife plots.

## RESULTS

**Cluster Analysis**—Considerable heterogeneity exists across the entire dataset used in the cluster analysis (CA, Fig. 2). Populations of *N. axillaris* tend to group together, although most stepparian populations within this species are well separated from a separate cluster of mostly Andean populations. Andean populations of *N. axillaris* are closer to *N. glomerulosa* populations than stepparian populations of *N. axillaris*. Populations of *N. glomerulosa* were grouped together in one large cluster, with the exception of the southernmost population from Chile, which was grouped with populations of *N. ulicina*. Furthermore, populations of *N. ulicina* remained grouped in one cluster, with the exception of a population located in northern Santa Cruz Province, which was grouped with stepparian populations of *N. axillaris*. Lastly, populations of *N. fuegiana* were distributed throughout the different clusters defined above, and the sample of *N. maeviae* was grouped with populations of *N. ulicina*. Population Aggregation Analysis failed to recover any major cluster characterized by a unique combination of qualitative character states, or with significant differences in mean values of quantitative traits.

**Principal Component Analysis**—In the principal component analysis (PCA), the first three principal components (PC) accounted for 70% of the variation across populations (Fig. 3). The first PC expressed mainly variation in macroblast leaf length (MLL; eigenvector = +0.32), brachyblast leaf length (BLL; +0.37), outer phyllaries shape (OPS; +0.41), inner phyllaries shape (IPS; +0.35), and cypselas shape (CS; +0.39), generally contrasting longer leaves and longer and narrower phyllaries and cypselas in populations at the right extreme of the scatter plot with shorter leaves and shorter and wider phyllaries and cypselas in populations at the left extreme of the resulting scatter plot (Fig. 3A). The second PC expressed mainly variation in abaxial corolla lip area (ALA; +0.51), abaxial corolla lip width (ALW; +0.43), and cypselas length (CL; +0.42), with larger areas of abaxial corolla lips, wider abaxial corolla lips, and longer cypselas at the upper extreme of the scatter plot; and smaller areas of abaxial corolla lips, narrower abaxial corolla lips, and shorter cypselas at the lower extreme of the resulting scatter plot (Fig. 3A). The third PC expressed mainly variation in abaxial corolla lip shape (ALS; +0.59), number of flowers per capitulum (NFC; +0.48), and ALW (-0.46), contrasting populations with longer and narrower abaxial corolla lips and higher number of flowers per capitulum at the upper extreme of the scatter plot; and populations with shorter and wider abaxial corolla lips and lower number of flowers per capitulum at the lower extreme of the resulting scatter plot (Fig. 3B). We observed relatively undifferentiated data clouds consistent with the unclear clustering revealed in the CA, and a mixture of populations relative to the five species traditionally recognized by Cabrera (1982).

**Discriminant Analysis**—In the discriminant analysis (DA), the first two canonical axes accounted for 95% of the overall variation among populations (Fig. 4). Because the third canonical axis explained less than 4% of the variation, only results from the first two axes were reported. Prediction ellipses with 95% confidence for the five groups defined a priori overlapped in the plane and their centroids lie close to one another along each of the first two axes. Cross-validation obtained from the discriminant function gave an average error rate of 5%, meaning that one sample of *N. axillaris* should be clustered with *N. fuegiana*, one sample of *N. glomerulosa* should be grouped with *N. maeviae*, and one sample of *N. ulicina* should be clustered with *N. maeviae*. Although the average error rate was low, when we successively included more populations in the analysis, the overlap of the ellipses was

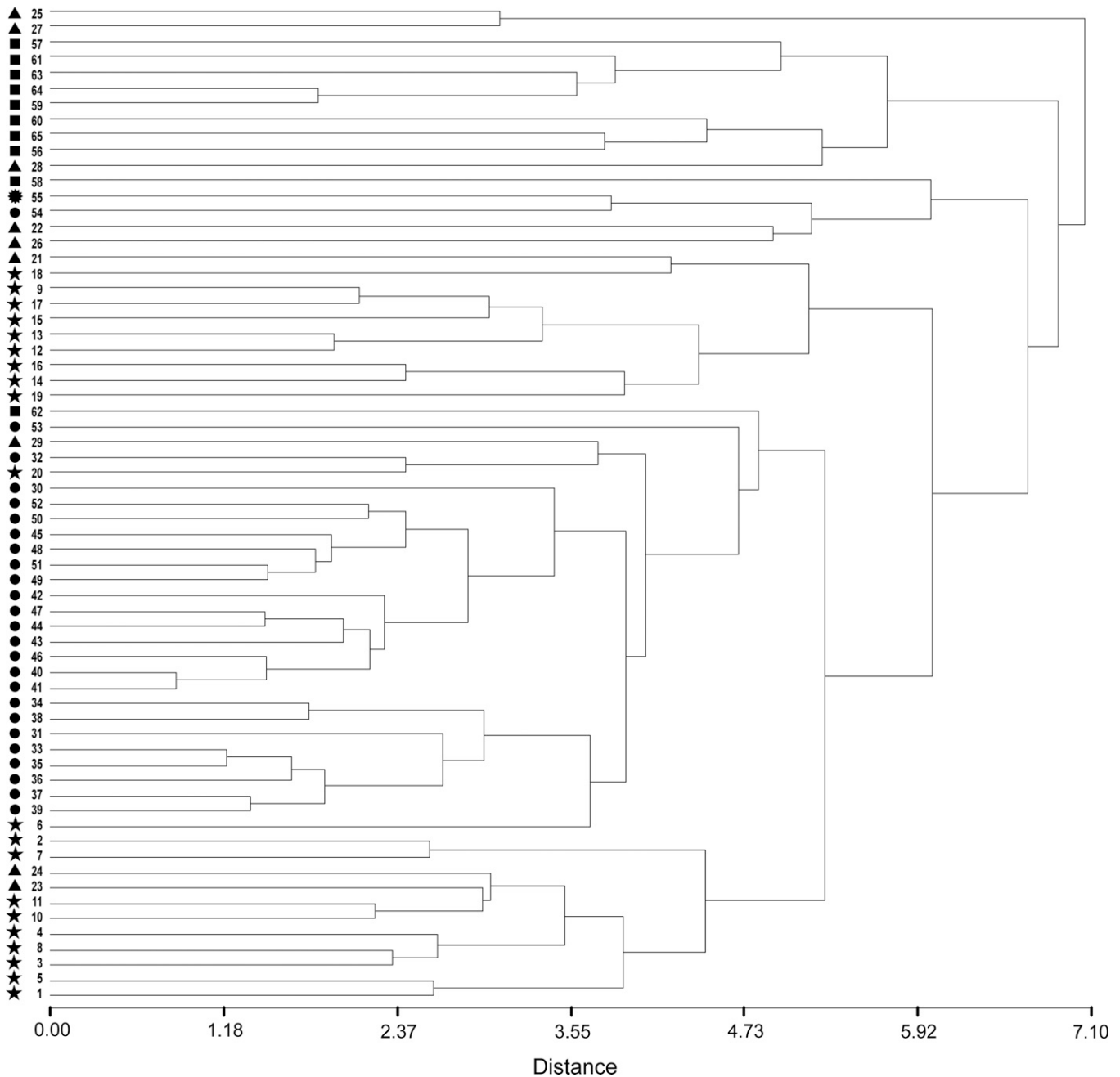


FIG. 2. Resulting phenogram of cluster analysis (CA) of the 65 populations of *Nassauvia* subgen. *Strongyloma* studied based on 18 morphological variables. Full locality names are provided in Appendix 1. Symbols indicate the five species according to Cabrera (1982): star *N. axillaris*, triangle *N. fuegiana*, circle *N. glomerulosa*, sun *N. maeviae*, and square *N. ulicina*.

correspondingly greater. Populations of *N. axillaris* are well differentiated from populations of *N. maeviae*–*N. ulicina* on the first axis, based on differences in ALW (wider abaxial corolla lips in populations at the right extreme of the scatter plot) and ALA (larger areas of abaxial corolla lips in populations at the left extreme of the resulting scatter plot). Differences in ALW (wider abaxial corolla lips in populations at the upper extreme of the scatter plot) and ALA (larger areas of abaxial corolla lips in populations at the lower extreme of the resulting scatter plot) allowed discriminating the observations between the *N. glomerulosa* group and the *N. ulicina* group on the second axis. Populations of *N. axillaris* remained clearly separated from populations of *N. glomerulosa* and *N. ulicina*. Populations of *N. glomerulosa* remained separated from pop-

ulations of *N. ulicina*, with the exception of two populations of *N. glomerulosa*; one from eastern Chubut Province and other from the center of Río Negro Province. Finally, we observed that populations of *N. fuegiana* were distributed through the groups of populations of *N. axillaris* and *N. ulicina*, and the population of *N. maeviae* was grouped with populations of *N. ulicina*. These results were consistent with the resulting phenogram obtained from the CA and with the resulting scatter plot of the PCA.

**Descriptive Statistics and Correlation Coefficients**—Variation within the five species traditionally recognized by Cabrera (1982) based on the 65 populations examined and the ten quantitative characters (MLL, BLS, OPS, IPS, NFC, ALW, ALS, ALA, CL, and CS) selected by PCA and DA as most

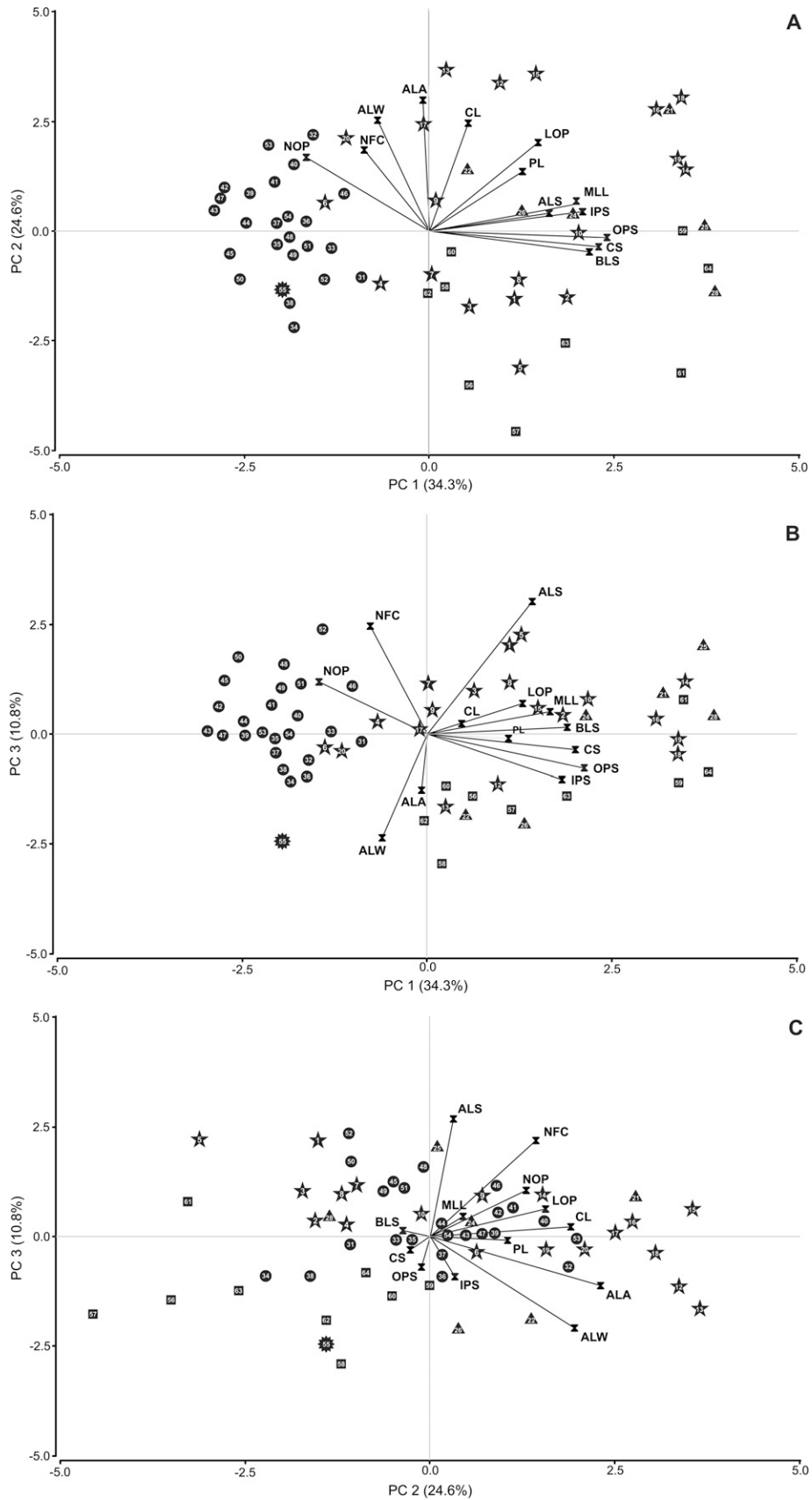


FIG. 3. Scatter plots of the first three principal components of the principal component analysis (PCA) of the 65 populations of *Nassauvia* subgen. *Strongyloma* studied based on 13 quantitative morphological variables. The eigenvalues associated with each PC are provided in parentheses. Full names of populations are provided in Appendix 1 and acronyms for the different morphological variables are in Materials and Methods. Arrows show the contribution of each variable to the PCs. Symbols indicate the five species according to Cabrera (1982): star *N. axillarlis*, triangle *N. fuegiana*, circle *N. glomerulosa*, sun *N. maeviae*, and square *N. ulicina*. A. PC1 versus PC2. B. PC1 versus PC3. C. PC2 versus PC3.

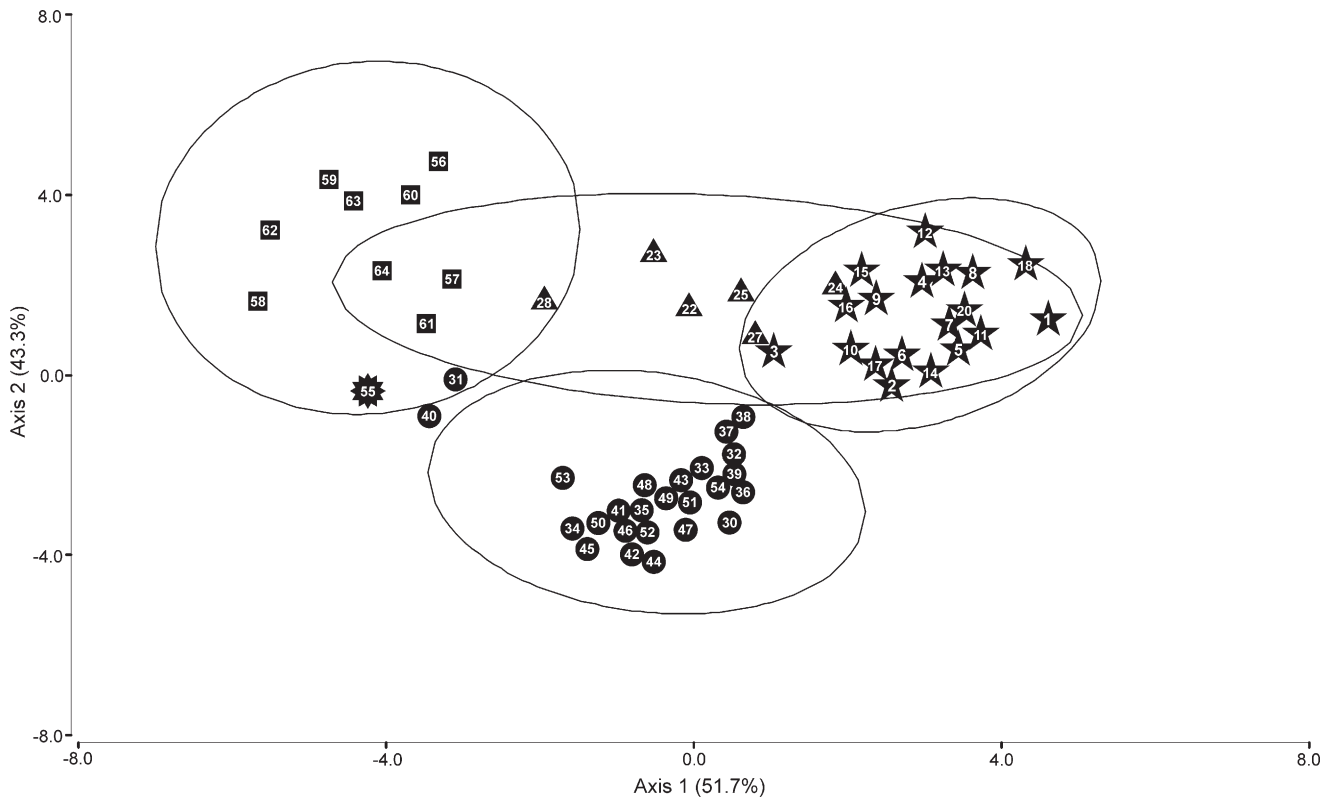


FIG. 4. Representation of multivariate observations into five groups defined a priori according to the five species recognized by Cabrera (1982) in the discriminant space formed by the first two canonical axes of the discriminant analysis (DA) using the 65 populations of *Nassauvia* subgen. *Strongyloma* studied and 13 quantitative morphological variables. The eigenvalues associated with each axis are provided in parentheses. Outlines correspond to ellipses of prediction. Symbols indicate the five species according to Cabrera (1982): star *N. axillaris*, triangle *N. fuegiana*, circle *N. glomerulosa*, sun *N. maeviae*, and square *N. ulicina*.

informative, reveals ranges of variation in each character that overlap to such an extent that none of them can be used individually to reliably delimit species in this subgenus (Fig. 5). In general, leaf traits showed higher coefficients of variation (52.7–130.6%) than floral traits (13.8–70.5%; Appendix 2).

Like other statistical values, correlation values do not explain causality; we therefore only report significant values with apparent biological meaning for some of the selected variables. MLL was significantly and positively correlated with isothermality (Bio3;  $r_s = +0.59$ ,  $p < 0.001$ ), the temperature annual range (Bio7;  $r_s = +0.68$ ,  $p < 0.001$ ), and the precipitation seasonality (Bio15;  $r_s = +0.43$ ,  $p < 0.001$ ). BLS was also significantly and positively correlated with Bio3 ( $r_s = +0.38$ ,  $p < 0.01$ ), Bio7 ( $r_s = +0.50$ ,  $p < 0.001$ ), and Bio15 ( $r_s = +0.28$ ,  $p < 0.05$ ). OPS and IPS were significantly and positively correlated with the annual mean temperature (Bio1;  $r_s = +0.24$ ,  $p < 0.05$  and  $r_s = +0.32$ ,  $p < 0.01$  respectively), Bio3 ( $r_s = +0.30$ ,  $p < 0.05$  and  $r_s = +0.32$ ,  $p < 0.01$  respectively), and Bio7 ( $r_s = +0.35$ ,  $p < 0.01$  and  $r_s = +0.40$ ,  $p < 0.01$  respectively). NFC was significantly and positively correlated with Bio3 ( $r_s = +0.33$ ,  $p < 0.01$ ) and Bio15 ( $r_s = +0.28$ ,  $p < 0.05$ ), and negatively correlated with Bio1 ( $r_s = -0.35$ ,  $p < 0.01$ ) and the mean temperature of the coldest quarter (Bio11;  $r_s = -0.35$ ,  $p < 0.01$ ). ALW, ALA, and CL were significantly and negatively correlated with the mean temperature of the wettest quarter (Bio8;  $r_s = -0.28$ ,  $p < 0.05$ ;  $r_s = -0.26$ ,  $p < 0.05$  and  $r_s = -0.34$ ,  $p < 0.01$  respectively) and positively correlated with the precipitation of the coldest quarter (Bio19;  $r_s = +0.38$ ,  $p < 0.01$ ;  $r_s = +0.39$ ,  $p < 0.01$  and  $r_s = +0.39$ ,  $p < 0.01$  respectively; Table 2). In the principal component analysis, the first PC showed a weak correlation with South latitude (LatS;

$r_s = +0.44$ ,  $p < 0.001$ ), West longitude (LonW;  $r_s = +0.34$ ,  $p < 0.01$ ), Bio3 ( $r_s = +0.31$ ,  $p < 0.05$ ), and Bio7 ( $r_s = +0.39$ ,  $p < 0.01$ ). The second PC showed a weak correlation with LonW ( $r_s = -0.43$ ,  $p < 0.001$ ), Bio8 ( $r_s = -0.41$ ,  $p < 0.01$ ), Bio11 ( $r_s = -0.28$ ,  $p < 0.05$ ), and Bio19 ( $r_s = +0.43$ ,  $p < 0.001$ ). The third PC showed a weak correlation with the mean temperature of the driest quarter (Bio 9;  $r_s = -0.30$ ,  $p < 0.05$ ) and Bio19 ( $r_s = -0.30$ ,  $p < 0.05$ ; results not shown in Table 2).

In general, plants with longer and narrower leaves, phyllaries, and cypselas were associated with a wider annual temperature range, as registered in northern Patagonia. Variation moved clinally towards the south, where those structures were shorter and wider, and annual temperature range was narrower. Plants with greater number of flowers per capitulum (five or, less commonly, four), longer cypselas, and wider abaxial corolla lips with larger area were associated with lower temperatures and higher precipitation of winter, as occurs in western Patagonia. Towards the east, the number of flowers per capitulum was lower (three or, less commonly, one or two), cypselas were shorter, and abaxial corolla lips were narrower with a smaller area, while registered temperature in winter was higher and precipitation was lower. As values mentioned above were relatively low and the correlations were relatively weak in all cases, the results should be interpreted cautiously. Groups of populations resulting from the multivariate analyses were not clearly related to any geographical and/or ecological range.

**Species Distribution Modeling**—Species distribution models show the minimum presence threshold for the five named entities that constitute *Nassauvia* subgen. *Strongyloma*



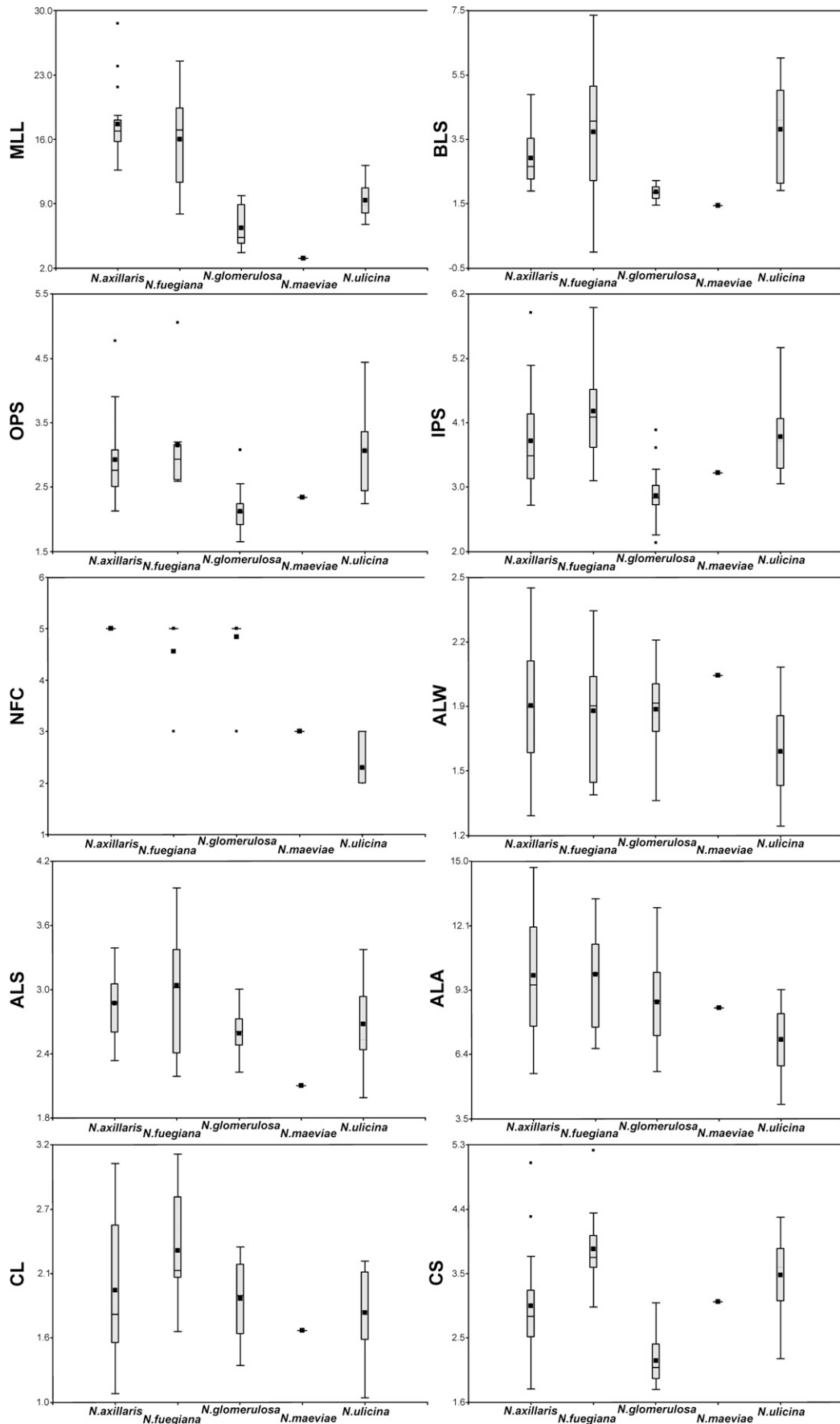


FIG. 5. Box-plots describing the variation of quantitative characters in *Nassauvia* subgen. *Strongyloma* according to the five species traditionally recognized by Cabrera (1982). Acronyms for the different morphological variables are in Materials and Methods.

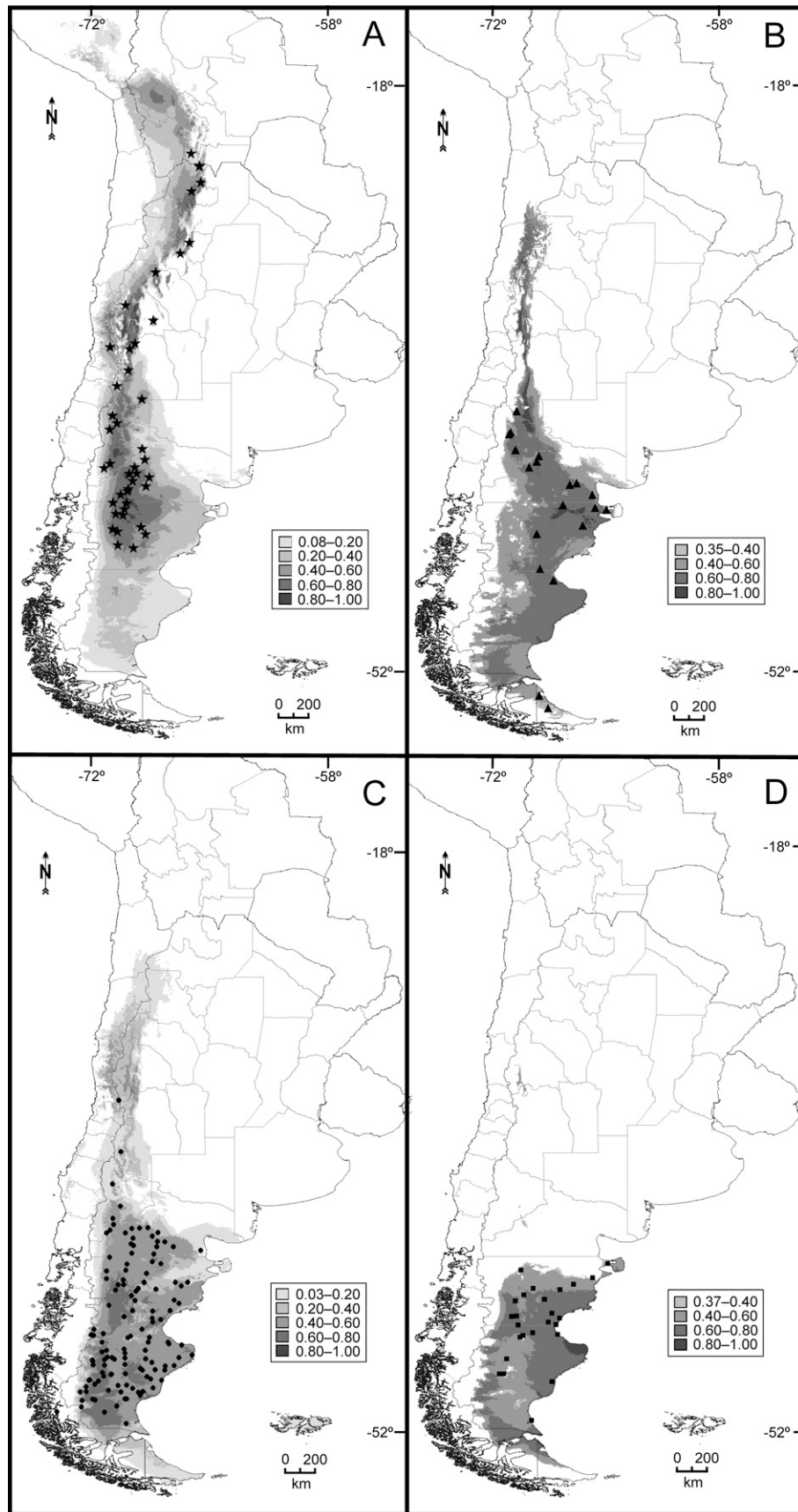


FIG. 6. Predictive distribution models for the species that traditionally constitute *Nassauvia* subgenus *Strongyloma* showing habitat suitability in southern South America. Darker colors indicate regions with a higher probability of species occurrence; lowest values correspond to the minimum training presence logistic threshold. Symbols refer to point localities on which the models are based: A. *N. axillaris*, B. *N. fuegiana*, C. *N. glomerulosa*, and D. *N. ulicina*. *N. maeviae* was not analyzed.

(Fig. 6). The mean values of the area under the curve (AUC) of the receiver-operating characteristic (ROC) were 99.5% ( $\pm 4\%$ ), 99.6% ( $\pm 2\%$ ), 99.2 ( $\pm 2\%$ ), and 99.7% ( $\pm 1\%$ ) for *N. axillaris*, *N. fuegiana*, *N. glomerulosa*, and *N. ulicina*, respectively.

For *N. axillaris*, some overprediction between projected and realized distribution areas was found, mainly in northwestern Bolivia, southwestern Perú, and Santa Cruz Province in Argentina, where this species has never been observed. Although the highest percent contribution (pc) was from variable Bio3 (pc = 43.1%) and the largest permutation importance (pi) was from Bio1 (pi = 45.2%), Jackknife tests showed Bio11 to have the most useful information when used in isolation (pc = 0.9%; pi = 30.7%) and Bio7 to have the most information than other variables (pc = 4.8%; pi = 5.9%). In addition, some overprediction was found for the distribution model of *N. fuegiana*, mainly in the Andes of western Argentina and eastern Chile, and in Santa Cruz Province in Argentina, where the species has never been collected. The environmental variable with the most useful information by itself and not present in the other variables was Bio11 (pc = 4.1%; pi = 84.3%). The projection of the distribution model for *N. glomerulosa* was a fairly good representation of the extant geographical distribution of this species, although some discordances with the known distribution were found, particularly in the Andes of western Argentina and eastern Chile, in the Islas Malvinas/Falkland Islands, and in Tierra del Fuego Province in Argentina. Nevertheless, it has been recorded in the latter. Jackknife tests showed Bio11 to have the most useful information when used in isolation (pc = 12.2%; pi = 1.6%) and Bio18 to have the most unique information (pc = 32.2%; pi = 27.9%). For *N. ulicina*, the distribution model showed great similarity with the current distribution of the species. Jackknife tests showed Bio11 to have the most useful information when used in isolation (pc = 1.1%; pi = 56%) and Bio7 to have the most unique information (pc = 6.6%; pi = 19.3%).

Considering relevant trends, suitable conditions for *N. axillaris* occurred mostly in the Andes of Argentina, Bolivia, and Chile from 18° S to 45° S. Appropriate environments for *N. fuegiana* were in the Andes of Argentina from 31° S to 38° S and also in the steppe, in northeastern Chubut Province, in Argentina. For *N. glomerulosa*, suitable habitats occur in Chubut and Santa Cruz, mainly in the southwestern parts of these two provinces. *N. maeviae* was recorded only for its type locality in the southeastern of Santa Cruz Province, in Argentina, in the surroundings of Laguna La Leona. Some specimens cited for southern Chile have been misidentified and actually correspond to what is traditionally recognized as the cushioned form of *N. glomerulosa*. Appropriate environments for *N. ulicina* were principally in northeastern Santa Cruz Province.

#### DISCUSSION

Our data did not allow an overall and clear separation of the species of *Nassauvia* subgen. *Strongyloma* due to overlapping ranges of morphological variation. Although some structure was detected in our data, there was no single character set allowing a clear discrimination of the species, according to the initial determinations following Cabrera (1982). Traits traditionally used to distinguish the five species that constitute subgen. *Strongyloma* (FD, MLL, BLL, BLS, and NFC) account for most of the sample variation, but they do not have significant morphological discontinuities along the large distribution range of the group. In addition, abaxial

corolla lip width and area also contribute substantially to the total sample variation, but, like the traditional distinguishing features noted above, they also lack discontinuities that would make these features useful diagnostically. Our results indicate that variation in morphological traits in subgen. *Strongyloma* is clinal, and it is possible that a larger sampling might further emphasize the continuity of character variation.

Despite some association between morphological variation with geography and climate, the actual geographic distribution of the samples identified to species following Cabrera (1982) does not entirely match that clinal pattern of morphology, geography, and climate. Diagnostic traits of *N. axillaris* (longest and narrowest leaves, phyllaries, and cypselas, 5-flowered capitula, and widest abaxial corolla lips with largest area) are frequently found in populations from northwestern Patagonia, but some populations of *N. axillaris* also occur in central southern Chubut. On the opposite end of the range, in southeastern Patagonia, we found *N. maeviae* with the shortest and widest leaves, phyllaries, and cypselas, 3-flowered capitula, and narrowest abaxial corolla lips with smallest area. Diagnostic traits of *N. ulicina* are frequently found in populations from central eastern Patagonia, but some populations occur both in the northeast (morphologically close to *N. fuegiana*) and the southeast (morphologically close to *N. maeviae*). Although both diagnostic traits of *N. glomerulosa* and *N. fuegiana* occur throughout Patagonia, traits of *N. glomerulosa* are highly frequent while traits of *N. fuegiana* appear in a few scattered populations.

In considering these results, we examined the nomenclatural types for each of the five putative species. These type specimens appear to be morphologically different from each other and certainly suggest the presence of five distinct species. However, it is interesting to note that the type localities of *N. fuegiana*, *N. maeviae*, and *N. ulicina* are located at the southernmost end of the geographical distribution of the subgenus. These three sites are located fairly close together, although the biological communities and soils are somewhat different. The type locality of *N. fuegiana* is located in northern Tierra del Fuego Province, where humid grasslands of *Festuca gracillima* dominate this great continental island (Cabrera and Willink 1973; León et al. 1998). *N. maeviae* is found with certainty only in its type locality, in a very particular area in the southeast of Santa Cruz Province with chalky and stony soil in a community dominated by *Frankenia microphylla* and *Lepidophyllum cupressiforme*, although these edaphic communities with hygrophilous vegetation are present across the Patagonian steppe, in some low-lying parts of the grasslands or coastal areas (Cabrera and Willink 1973). The type locality of *N. ulicina* is located in southeastern Santa Cruz Province, where xeric grasslands of *Festuca pallenscens* dominate the Gallegos River Basin (Cabrera and Willink 1973; León et al. 1998). On the other hand, the two remaining type localities, for *N. axillaris* and *N. glomerulosa*, are very close together, in the Cordillera of the Andes in central Chile, but the labels of the specimens are not very detailed. This area corresponds to the northwestern end of the geographical distribution of *N. glomerulosa*, and to a midpoint within the distribution of *N. axillaris*. Thus, except for *N. axillaris*, the type localities for each putative species are located almost at the extremes of the geographical distribution of the subgenus. These extreme locations also have marked differences in altitude (Appendix 1), soil types, and plant communities. Our results demonstrate clinal variation in vegetative and

reproductive characters within subgen. *Strongyloma*, such that the morphological differences originally observed in the type specimens of the putative species of subgen. *Strongyloma* may be more related to the environmental and latitudinal differences of the type locations rather than reflecting well-established taxonomic boundaries.

Based on our sampling and species distribution modeling, suitable geographic and climatic areas for each species are greater than previously considered (Fig. 6); adequate conditions for each species overlap considerably. Species distribution modeling identifies the mean temperature of the coldest quarter as the environmental variable that most influences the geographical distribution of this group of plants. This variable is biologically significant because it is associated with the beginning of the growing period, with the growing period delayed as the mean temperature of winter decreases (Paruelo et al. 1998; Jobbágy et al. 2002). Temperature appears to be the primary control of phenology in Patagonia with a NW–SE distribution of the isotherms, while solar radiation and photoperiod present a latitudinal cline (Paruelo et al. 1998). Several areas exist with suitable environmental conditions for these species that largely overlap, and syntopy of two or three of these species in several areas of Patagonia has been documented. There are multiple areas of contact in the southern Andean-Patagonian region, namely: (i) some areas located in southern Mendoza, in north-central Neuquén, in west-central Río Negro, and in the center of Chubut where *N. axillaris*, *N. glomerulosa*, and often *N. fuegiana* coexist; (ii) the center of Chubut where *N. axillaris*, *N. fuegiana*, and *N. ulicina* coexist; (iii) the center of Chubut where *N. glomerulosa* and *N. ulicina* coexist; and (iv) eastern Chubut and northeastern Santa Cruz where *N. fuegiana* and *N. glomerulosa*, *N. fuegiana* and *N. ulicina*, or *N. glomerulosa* and *N. ulicina* coexist. It is of special interest that many individuals with intermediate morphological characteristics were encountered in southern Mendoza Province and in the center of Chubut Province, suggesting that these are particularly dynamic areas for evolution and possible gene exchange among this group of plants.

*Nassauvia* subgen. *Strongyloma* is taxonomically problematic, with considerable and complex morphological variation. This subgenus cannot be clearly divided into well-defined groups. Based on the results presented here, we conclude that *Nassauvia* subgen. *Strongyloma* should be considered a large, highly polymorphic species complex composed of a set of five entities, distributed over a large geographical area, with clinal morphological variation. Ecological and morphological differences among the members of the species complex from extreme locations have led to their classification as distinct taxonomic species. Some evidence, such as the intermediacy observed in statistical analyzes graphs and overlap of suitable areas of species distributions suggest the possibility of gene exchange between populations of different named entities. The biological structure of subgen. *Strongyloma* may be the result of incipient speciation or the consequence of hybridization in contact areas of distribution. However, further analyses are still needed to test those hypotheses, especially using molecular and chromosomal techniques at population level, to test horizontal gene transfer, incomplete lineage sorting, and the delimitation of genetically cohesive groups.

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- APPENDIX 1. Specimens examined. Entries are in the order of species and authors (last identification according to Cabrera, 1982), population code number (in bold), country (in capital letters), province, locality, geographic coordinates and altitude (between square brackets), collector and number (in italics; if not: s. n. = sine numero - without number), and herbarium acronym (between parentheses; *TI* = type image and *T* = type).
- N. axillaris** (Lag. ex Lindl.) D. Don. 1; BOLIVIA. Potosí: Tupiza [21°28' S, 65°43' W, 2,970 m], *Fiebrig* 3114 (SI). 2; ARGENTINA. Salta: Santa Victoria [22°12' S, 65°13' W, 4,250 m], *Zuloaga* 10678 (SI). 3; Jujuy: Pucará [23°10' S, 65°09' W, 3,500 m], *Kiesling* 3653 (SI). 4; Abra de Lipán [23°41' S, 65°41' W, 4,200 m], *Zuloaga* 3559 (SI). 5; Tucumán: Ojo de Agua [26°42' S, 65°48' W, 2,900 m], *Gómez-Sosa* 236 (SI). 6; Catamarca: Mina Capitán [27°22' S, 66°20' W, 3,740 m], *Zuloaga* 11934 (SI). 7; La Rioja: Famatina [28°27' S, 67°49' W, 3,000 m], *Hunziker* 1877 (SI). 8; San Juan: Agua Negra [30°23' S, 69°35' W, 3,000 m], *Cabrera* 30130 (SI). 9; San Juan: Pie de Palo [31°17' S, 67°57' W, 3,130 m], *Kiesling* 6292 (SI). 10; Mendoza: Quebrada del Toro [32°38' S, 69°02' W, 1,580 m], *Nicora* 4441 (SI). 11; CHILE. Valparaíso: Andes [32°51' S, 70°29' W, 1,000 m], s. n. (K, *TI*). 12; ARGENTINA. Mendoza: Refugio Cruz de Piedra [34°14' S, 69°25' W, 2,622 m], *Zavala* 57 (SI). 13; Las Leñas Amarillas [35°09' S, 70°04' W, 2,203 m], *Cabrera* 33389 (SI). 14; Neuquén: Vegas del Pelán [36°54' S, 70°20' W, 1,750 m], *Boelcke* 11107 (SI). 15; Primeros Pinos [38°52' S, 68°35' W, 518 m], *Cabrera* 32869 (SI). 16; Junín de los Andes [40°00' S, 70°50' W, 670 m], *Merrill King* 9385 (SI). 17; Río Negro: Sierra de Queupuníyeu [40°32' S, 68°11' W, 1,156 m], *Nicola* 109 (SI). 18; Ojo de Agua [41°33' S, 69°52' W, 1,115 m], *Burkart* 19763 (SI). 19; Chubut: Estancia Quichaura [43°35' S, 70°20' W, 910 m], *Soriano* 2429 (SI). 20; Los Altos [43°53' S, 68°25' W, 364 m], *Cabrera* 33293 (SI).
- N. fuegiana** (Speg.) Cabrera. 21; ARGENTINA. Mendoza: Ranquil de Lirkay [36°39' S, 69°47' W, 1,161 m], *Ruiz Leal* 21922 (SI). 22; Neuquén: Churriaca [37°54' S, 70°08' W, 1,390 m], *Ruiz Leal* 18019 (SI). 23; Río Negro: Ruta Provincial 74 [39°18' S, 68°28' W, 637 m], *Cosacov* s. n. (SI). 24; Meseta de Somuncurá [40°58' S, 66°40' W, 618 m], *Zanotti* 23 (SI). 25; Chubut: Telsen [42°09' S, 67°05' W, 613 m], *Arroyo* 465 (SI). 26; Isla de los Pájaros [42°25' S, 64°31' W, 7 m], *Daciuk* 60 (SI). 27; Paso de Indios [43°50' S, 68°35' W, 250 m], *Nicola* 76 (SI). 28; Santa Cruz: Caleta Olivia [46°34' S, 67°38' W, 300 m], *Donat* s. n. c (SI). 29; Tierra del Fuego: Golfo de San Sebastián [53°18' S, 68°27' W, 15 m], s. n. (LP, *TI*).
- N. glomerulosa** (Lag. ex Lindl.) D. Don. 30; CHILE. Valparaíso: Cordillera del Portillo [32°50' S, 70°08' W, 2,870 m], *Née* s. n. (G, *TI*). 31; ARGENTINA. Mendoza: Bardas Blancas [35°50' S, 70°00' W, 1,540 m], *Zuloaga* 12419 (SI). 32; Neuquén: El Huecú [37°43' S, 70°30' W, 1,483 m], *Nicola* 127 (SI). 33; Collón Curá [40°25' S, 70°39' W, 604 m], *Sérsic* 4122 (CORD). 34; Río Negro: Los Menucos [40°46' S, 68°11' W, 874 m], *Zanotti* 35 (SI). 35; Chubut: ColánConhué [42°45' S, 69°43' W, 584 m], *Nicola* 8 (SI). 36; Laguna Fría [42°56' S, 68°31' W, 1,025 m], *Nicola* 5 (SI). 37; Los Rífleros [43°15' S, 70°52' W, 676 m], *Nicola* 17 (SI). 38; Dique Florentino Ameghino [43°41' S, 66°29' W, 260 m], *Nicola* 62 (SI). 39; Estancia Cañadón Grande [44°15' S, 69°24' W, 900 m], *Nicola* 33 (SI). 40; Alto Río Senguer [44°48' S, 70°42' W, 643 m], *Nicola* 28 (SI). 41; Sierra del Castillo [45°07' S, 69°20' W, 854 m], *Nicola* 29 (SI). 42; CHILE. Aysén: Chile Chico [46°32' S, 71°45' W, 300 m], *García* 4191 (CONC). 43; ARGENTINA. Santa Cruz: Las Heras [46°36' S, 69°27' W, 343 m], *Biganzoli* 2345 (SI). 44; Puesto Lebrún [46°58' S, 71°06' W, 1,353 m], *Paiaro* s. n. (SI). 45; Fitz Roy [46°58' S, 67°16' W, 242 m], *Biganzoli* 2343 (SI). 46; Estancia Piedra Grande [47°36' S, 69°46' W, 775 m], *Paiaro* s. n. (SI). 47; Estancia Cerro Beltza [48°00' S, 71°41' W, 912 m], *Paiaro* s. n. (SI). 48; Gobernador Gregores [48°48' S, 69°45' W, 331 m], *Zanotti* 66 (SI). 49; Estancia Cerro Perdido [48°58' S, 68°29' W, 241 m], *Zanotti* 64 (SI). 50; Cerro Mank Aike [49°46' S, 70°44' W, 807 m], *Paiaro* s. n. (SI). 51; Hotel La Leona [49°51' S, 72°02' W, 294 m], *Zanotti* 93 (SI). 52; Luis Piedra Buena [49°54' S, 69°00' W, 108 m], *Zanotti* 70 (SI). 53; CHILE. Magallanes: Sierra de los Baguales [50°44' S, 72°20' W, 700 m], *Arroyo* 841140 (CONC). 54; Torres del Paine [51°02' S, 73°45' W, 200 m], *Domínguez* 297 (CONC).
- N. maeviae** Cabrera. 55; ARGENTINA. Santa Cruz: Laguna La Leona [51°31' S, 69°47' W, 63 m], *Correa* s. n. (SI, *T*).
- N. ulicina** (Hook. f.) Macloskie. 56; ARGENTINA. Chubut: Isla de los Pájaros [42°25' S, 64°31' W, 7 m], *Daciuk* 61 (SI). 57; Paso del Sapo [42°48' S, 69°34' W, 387 m], *Zanotti* 59 (SI). 58; Las Chapas [43°38' S, 66°31' W, 261 m], *Botta* 436 (SI). 59; Paso de Indios [43°52' S, 68°51' W, 285 m], *Arroyo* 64 (SI). 60; Río Senguer [45°28' S, 69°50' W, 421 m], *Nicola* 170 (SI). 61; Bahía Solano [45°35' S, 67°19' W, 190 m], *de Marco* 207 (SI). 62; Santa Cruz: Las Heras [46°36' S, 69°27' W, 343 m], *Biganzoli* 2347 (SI). 63; Gobernador Gregores [48°50' S, 70°49' W, 430 m], *Ruiz Leal* 24214 (SI). 64; Puerto San Julián [49°17' S, 67°47' W, 40 m], *Dusén* 5328 (SI). 65; Cabo Buen Tiempo [51°32' S, 68°57' W, 60 m], *Capt. King* s. n. (K, *TI*).

APPENDIX 2. Mean values (SD) of the 31 morphological traits measured for the 65 populations of *Nassauvia* subgen. *Strongyloma* studied. See Appendix 1 for the full names of population codes and Materials and Methods for full names of trait acronyms. Mean and CV are the average values (SD) and coefficient of variation of population means for each one of the species (n. c. = not correspond; CV does not correspond for categorical variables). Total means and total CVs for the entire data set are also shown.

Code	H	FD	MLL	BLL	BLW	BLS	BLA	LC	TC	LD	TD
1	1	1	17.6 (1.7)	4.6 (1.5)	2.4 (0.2)	1.9 (0.7)	11.1 (3.4)	1	0	0	0
2	1	1	16.4 (5.1)	6.5 (0.5)	1.6 (0.4)	4.1 (0.9)	10.7 (2.7)	1	1	0	0
3	1	1	18.6 (4.0)	3.4 (0.8)	1.4 (0.6)	2.6 (0.8)	5.2 (2.9)	1	0	1	0
4	1	1	16.2 (3.2)	5.7 (0.8)	2.5 (0.5)	2.4 (0.9)	13.8 (1.3)	1	0	1	0
5	1	1	17.2 (1.3)	6.1 (1.5)	1.7 (0.2)	3.6 (0.6)	10.2 (3.2)	1	0	0	0
6	2	1	16.9 (3.3)	7.9 (1.1)	2.9 (0.5)	2.7 (0.4)	23.6 (6.7)	1	0	1	0
7	1	1	16.2 (3.7)	5.5 (0.3)	2.6 (0.5)	2.2 (0.5)	14.2 (2.4)	1	1	0	0
8	1	1	28.6 (2.9)	5.2 (0.8)	2.2 (0.5)	2.4 (0.3)	11.4 (4.0)	1	0	1	0
9	1	1	14.7 (2.1)	5.4 (0.3)	2.1 (0.1)	2.6 (0.2)	11.6 (0.6)	1	0	1	0
10	1	1	24.0 (3.6)	7.3 (1.8)	1.7 (0.6)	4.9 (2.7)	11.9 (5.1)	1	0	1	0
11	1	1	15.7 (3.0)	4.3 (0.6)	1.0 (0.1)	4.1 (0.4)	4.4 (0.9)	1	0	1	0
12	2	1	21.6 (2.4)	12.1 (2.3)	4.5 (1.0)	2.8 (0.8)	55.5 (18.9)	1	0	1	0
13	2	1	13.7 (3.0)	4.7 (0.5)	1.9 (0.2)	2.5 (0.2)	8.9 (1.9)	1	0	1	0
14	1	1	18.1 (3.0)	4.7 (0.1)	1.3 (0.3)	3.8 (0.7)	6.1 (1.4)	1	0	1	0
15	1	1	16.7 (1.6)	4.4 (0.2)	2.0 (0.2)	2.2 (0.3)	8.5 (1.0)	1	0	1	0
16	1	1	17.5 (0.4)	4.7 (0.2)	1.7 (0.3)	2.8 (0.4)	8.0 (1.5)	1	0	1	0
17	1	1	15.2 (1.5)	4.7 (0.6)	2.5 (0.6)	2.0 (0.4)	11.9 (3.8)	1	0	1	0
18	1	1	16.9 (0.4)	5.0 (1.3)	1.6 (0.4)	3.1 (0.1)	8.3 (3.9)	1	0	1	1
19	1	1	12.7 (1.8)	3.9 (0.6)	1.9 (0.1)	2.0 (0.2)	7.6 (1.6)	1	0	0	0
20	1	1	12.7 (1.8)	3.9 (0.6)	1.9 (0.1)	2.0 (0.2)	7.6 (1.6)	1	0	0	0
<i>N. axillaris</i> mean	1	1	17.6	5.7	2.1	2.9	12.9	1	0	1	0
<i>N. axillaris</i> CV	n. c.	n. c.	20.3	33.8	35.8	28.4	84.4	n. c.	n. c.	n. c.	n. c.
21	1	1	23.0 (0.8)	8.2 (0.9)	1.4 (0.2)	5.6 (0.2)	11.3 (3.0)	0	0	1	1
22	1	1	14.1 (1.7)	5.4 (0.6)	1.3 (0.2)	4.1 (0.3)	7.3 (1.6)	0	1	0	0
23	1	1	19.4 (1.2)	6.5 (1.0)	3.0 (0.5)	2.2 (0.1)	19.7 (6.1)	1	0	0	0
24	1	1	17.9 (1.9)	7.6 (0.2)	1.5 (0.2)	5.2 (0.5)	11.4 (1.7)	1	0	0	0
25	1	1	17.0 (0.9)	8.1 (0.9)	1.1 (0.2)	7.4 (1.6)	9.1 (1.5)	1	1	0	0
26	2	1	9.1 (1.1)	2.1 (0.4)	2.0 (0.3)	1.1 (0.3)	4.1 (0.7)	0	1	0	0
27	1	1	24.5 (1.5)	10.2 (2.6)	2.0 (0.3)	5.0 (1.0)	21.0 (7.7)	1	1	0	0
28	2	1	7.9 (1.9)	2.8 (0.0)	0.9 (0.1)	3.1 (0.5)	2.6 (0.3)	0	0	1	1
29	2	0	11.3 (2.3)	0.0 (0.0)	0.0 (0.0)	0.0 (0.0)	0.0 (0.0)	1	0	0	0
<i>N. fuegiana</i> mean	1	1	16.0	5.7	1.5	3.7	9.6	1	0	0	0
<i>N. fuegiana</i> CV	n. c.	n. c.	36.8	59.3	55.7	62.9	74.9	n. c.	n. c.	n. c.	n. c.
30	2	1	5.4 (0.2)	1.0 (0.0)	0.5 (0.1)	1.8 (0.1)	0.5 (0.1)	1	0	0	0
31	2	1	9.8 (1.8)	1.6 (0.4)	0.8 (0.2)	2.1 (0.6)	1.2 (0.4)	1	0	0	0
32	2	1	9.2 (1.4)	1.8 (0.3)	0.9 (0.2)	2.0 (0.6)	1.7 (0.4)	1	0	0	0
33	1	1	9.6 (2.7)	1.5 (0.4)	0.8 (0.2)	2.0 (0.3)	1.2 (0.6)	1	0	0	0
34	1	1	7.2 (1.6)	1.5 (0.3)	0.7 (0.1)	2.2 (0.3)	1.0 (0.2)	1	0	0	0
35	1	1	9.6 (1.2)	1.4 (0.2)	0.7 (0.1)	2.0 (0.4)	1.1 (0.3)	1	0	0	0
36	1	1	9.4 (1.9)	1.5 (0.2)	0.7 (0.1)	2.2 (0.4)	1.1 (0.3)	1	0	0	0
37	1	1	9.9 (1.1)	1.4 (0.1)	0.6 (0.0)	2.2 (0.2)	0.9 (0.41)	1	0	0	0
38	1	1	8.9 (1.5)	1.4 (0.2)	0.7 (0.1)	2.0 (0.3)	1.0 (0.3)	1	0	0	0
39	1	1	7.7 (1.0)	1.6 (0.1)	0.8 (0.1)	2.1 (0.4)	1.2 (0.3)	1	0	0	0
40	3	1	4.7 (0.6)	1.7 (0.2)	0.9 (0.1)	1.8 (0.2)	1.6 (0.4)	1	0	0	0
41	3	1	4.4 (1.0)	1.9 (0.2)	0.9 (0.1)	2.2 (0.4)	1.7 (0.2)	1	0	0	0
42	3	1	4.5 (0.2)	1.8 (0.2)	1.2 (0.1)	1.6 (0.2)	2.1 (0.3)	1	0	0	0
43	2	1	4.7 (1.3)	1.4 (0.2)	0.9 (0.1)	1.7 (0.3)	1.2 (0.2)	1	0	0	0
44	3	1	4.8 (0.2)	1.9 (0.2)	1.0 (0.1)	1.9 (0.3)	2.0 (0.3)	1	0	0	0
45	2	1	3.7 (0.6)	1.4 (0.2)	1.0 (0.1)	1.5 (0.2)	1.4 (0.3)	1	0	0	0
46	3	1	6.6 (0.7)	1.7 (0.2)	0.9 (0.2)	1.8 (0.4)	1.6 (0.3)	1	0	0	0
47	3	1	5.0 (0.9)	1.7 (0.3)	1.1 (0.2)	1.6 (0.2)	1.9 (0.6)	1	0	0	0
48	3	1	4.6 (0.7)	1.5 (0.2)	1.0 (0.2)	1.5 (0.2)	1.5 (0.3)	1	0	0	0
49	2	1	4.3 (0.9)	1.4 (0.1)	0.8 (0.1)	1.8 (0.3)	1.2 (0.2)	1	0	0	0
50	3	1	4.9 (1.1)	1.5 (0.2)	1.0 (0.2)	1.6 (0.3)	1.5 (0.4)	1	0	0	0
51	2	1	5.8 (0.4)	1.7 (0.1)	1.0 (0.1)	1.8 (0.3)	1.6 (0.2)	1	0	0	0
52	2	1	5.8 (0.5)	1.6 (0.2)	0.9 (0.1)	1.8 (0.2)	1.4 (0.2)	1	0	0	0
53	3	1	4.6 (0.1)	2.1 (0.2)	1.5 (0.1)	1.5 (0.2)	3.0 (0.1)	1	0	1	0
54	3	1	4.2 (0.4)	2.0 (0.1)	1.1 (0.2)	1.8 (0.2)	2.3 (0.4)	0	1	0	0
<i>N. glomerulosa</i> mean	2	1	6.4	1.6	0.9	1.9	1.5	1	0	0	0
<i>N. glomerulosa</i> CV	n. c.	n. c.	34.2	15.0	22.1	12.6	35.5	n. c.	n. c.	n. c.	n. c.
55	3	1	3.1 (1.1)	2.7 (0.3)	1.9 (0.2)	1.4 (0.1)	5.1 (1.0)	0	1	0	0
<i>N. maeviae</i> mean	3	1	3.1	2.7	1.9	1.4	5.1	0	1	0	0
<i>N. maeviae</i> CV	n. c.	n. c.	0.0	0.0	0.0	0.0	0.0	n. c.	n. c.	n. c.	n. c.
56	2	1	7.0 (3.2)	2.1 (0.5)	0.8 (0.3)	2.7 (0.6)	1.8 (0.9)	1	0	1	1
57	2	1	11.7 (3.2)	3.2 (0.7)	0.6 (0.1)	5.5 (1.8)	1.9 (0.6)	0	0	1	0
58	2	1	8.0 (1.8)	1.8 (0.1)	0.8 (0.1)	2.1 (0.1)	1.5 (0.3)	1	1	1	1

(Continued)

## APPENDIX 2. (Continued).

Code	H	FD	MLL	BLL	BLW	BLS	BLA	LC	TC	LD	TD
59	2	1	13.2 (4.9)	4.0 (1.1)	1.0 (0.2)	4.1 (0.3)	4.0 (2.0)	0	0	1	0
60	2	1	7.9 (2.6)	2.7 (0.3)	1.5 (0.3)	1.9 (0.3)	4.0 (1.0)	0	0	1	1
61	2	1	10.6 (3.1)	3.3 (0.1)	0.6 (0.1)	6.0 (0.8)	1.8 (0.2)	0	0	1	0
62	2	1	8.3 (2.2)	2.0 (0.4)	0.9 (0.2)	2.1 (0.4)	1.9 (0.6)	1	0	1	0
63	2	1	10.7 (4.5)	4.5 (0.5)	1.0 (0.1)	4.6 (0.9)	4.5 (0.4)	0	0	1	0
64	2	1	9.3 (3.9)	3.0 (0.3)	0.6 (0.2)	5.0 (1.6)	1.9 (0.8)	0	0	1	0
65	2	1	6.8 (0.2)	2.2 (0.3)	0.5 (0.1)	4.1 (0.4)	1.2 (0.4)	1	0	1	1
<i>N. ulicina</i> mean	2	1	9.4	2.9	0.8	3.8	2.5	0	0	1	0
<i>N. ulicina</i> CV	n. c.	n. c.	22.7	31.1	33.2	39.7	48.8	n. c.	n. c.	n. c.	n. c.
Total mean	2	1	8.9	3.6	1.3	2.7	6.2	1	0	0	0
Total CV	n. c.	n. c.	52.7	68.6	56.0	50.2	130.6	n. c.	n. c.	n. c.	n. c.

Code	PL	NOP	LOP	WOP	OPS	OPA	NIP	LIP	WIP	IPS	IPA
1	0.8 (0.3)	3 (1)	4.1 (0.4)	1.3 (0.0)	3.1 (0.3)	5.5 (0.7)	5 (0)	4.8 (0.1)	1.4 (0.2)	3.5 (0.5)	6.7 (1.1)
2	0.5 (0.0)	2 (0)	3.9 (0.5)	1.1 (0.1)	3.5 (0.1)	4.5 (1.0)	5 (0)	4.8 (0.2)	1.4 (0.3)	3.6 (0.7)	6.6 (1.5)
3	0.5 (0.1)	3 (1)	3.3 (0.3)	1.3 (0.2)	2.7 (0.5)	4.2 (0.9)	5 (0)	4.9 (0.1)	1.4 (0.1)	3.6 (0.2)	6.8 (0.6)
4	1.3 (0.0)	3 (0)	3.9 (0.1)	1.6 (0.1)	2.4 (0.1)	6.2 (0.2)	5 (0)	4.6 (0.1)	1.5 (0.1)	3.0 (0.1)	7.0 (0.5)
5	0.4 (0.1)	2 (0)	3.9 (0.2)	1.6 (0.2)	2.5 (0.3)	6.3 (0.5)	5 (0)	5.7 (0.5)	1.6 (0.2)	3.5 (0.7)	9.2 (0.5)
6	2.9 (0.5)	5 (1)	4.0 (0.4)	1.6 (0.2)	2.4 (0.2)	6.6 (1.2)	5 (0)	5.0 (0.5)	1.7 (0.3)	3.0 (0.4)	8.7 (2.2)
7	0.5 (0.0)	3 (1)	4.4 (0.2)	1.7 (0.2)	2.5 (0.2)	7.6 (1.1)	5 (0)	5.3 (0.5)	1.9 (0.4)	2.8 (0.4)	10.1 (2.8)
8	1.8 (0.5)	2 (1)	3.3 (0.2)	1.2 (0.3)	2.8 (0.9)	4.0 (0.9)	5 (0)	4.8 (0.5)	1.4 (0.1)	3.5 (0.5)	6.6 (0.6)
9	2.9 (0.0)	4 (1)	4.4 (0.2)	1.8 (0.0)	2.4 (0.1)	8.1 (0.4)	5 (0)	5.4 (0.5)	1.7 (0.3)	3.2 (0.3)	9.2 (2.4)
10	4.1 (0.1)	2 (1)	3.7 (0.4)	1.4 (0.4)	2.8 (0.7)	5.2 (1.8)	5 (0)	5.8 (0.4)	1.7 (0.2)	3.5 (0.1)	9.7 (1.7)
11	3.8 (0.0)	3 (0)	3.5 (0.5)	1.2 (0.0)	2.8 (0.5)	4.4 (0.6)	5 (0)	5.4 (0.8)	1.1 (0.0)	5.0 (0.8)	5.7 (0.7)
12	5.4 (2.1)	4 (0)	4.6 (0.6)	1.7 (0.2)	2.7 (0.3)	7.9 (1.8)	5 (0)	6.6 (0.8)	1.8 (0.3)	3.8 (0.6)	11.7 (2.4)
13	5.5 (0.0)	5 (1)	4.7 (0.4)	1.8 (0.2)	2.6 (0.1)	8.3 (1.5)	5 (0)	7.3 (0.7)	1.6 (0.5)	4.8 (1.3)	11.8 (4.3)
14	3.1 (1.0)	3 (1)	5.9 (0.5)	1.7 (0.1)	3.4 (0.1)	10.4 (1.5)	5 (0)	7.1 (0.4)	1.8 (0.1)	4.0 (0.4)	12.9 (0.9)
15	3.2 (0.5)	5 (1)	5.4 (0.5)	1.8 (0.3)	3.0 (0.4)	9.8 (2.4)	5 (0)	8.6 (0.3)	2.0 (0.2)	4.4 (0.6)	17.3 (1.6)
16	4.4 (1.4)	4 (1)	5.3 (0.6)	1.6 (0.1)	3.2 (0.5)	8.6 (1.1)	5 (0)	7.6 (0.4)	1.7 (0.1)	4.4 (0.5)	13.2 (0.5)
17	4.0 (0.6)	5 (0)	4.6 (0.6)	1.8 (0.2)	2.6 (0.3)	8.3 (1.7)	5 (0)	6.1 (0.7)	1.8 (0.2)	3.5 (0.3)	10.9 (2.3)
18	4.4 (1.6)	3 (0)	5.3 (0.3)	1.4 (0.2)	3.9 (0.4)	7.3 (1.3)	5 (0)	8.5 (0.9)	1.5 (0.1)	5.9 (0.9)	12.4 (1.2)
19	0.9 (0.0)	4 (1)	4.5 (0.7)	2.1 (0.3)	2.1 (0.2)	9.6 (2.7)	5 (0)	7.1 (0.5)	2.6 (0.2)	2.8 (0.2)	18.4 (2.9)
20	0.9 (0.0)	4 (1)	4.5 (0.7)	2.1 (0.3)	2.1 (0.2)	9.6 (2.7)	5 (0)	7.1 (0.5)	2.6 (0.2)	2.8 (0.2)	18.4 (2.9)
<i>N. axillaris</i> mean	2.9	3	4.4	1.5	2.9	6.9	5	6.1	1.6	3.8	10.2
<i>N. axillaris</i> CV	67.6	31	16.5	18.2	20.7	29.0	0	20.8	18.9	21.0	34.0
21	8.0 (2.8)	4 (0)	4.7 (1.1)	1.7 (0.1)	2.8 (0.7)	7.9 (1.8)	5 (0)	7.3 (0.4)	1.8 (0.1)	4.0 (0.4)	13.2 (0.6)
22	0.5 (0.0)	2 (1)	4.3 (0.6)	1.7 (0.1)	2.6 (0.5)	7.3 (0.9)	5 (0)	5.5 (0.4)	1.5 (0.1)	3.7 (0.2)	8.1 (1.0)
23	3.4 (0.2)	2 (0)	3.6 (0.6)	1.3 (0.3)	2.7 (0.5)	4.9 (1.6)	5 (0)	5.7 (0.5)	1.4 (0.1)	4.2 (0.2)	7.8 (1.4)
24	4.7 (0.4)	4 (0)	3.7 (0.1)	1.2 (0.1)	3.2 (0.3)	4.4 (0.6)	5 (0)	6.0 (0.6)	1.7 (0.2)	3.5 (0.7)	10.5 (1.4)
25	2.0 (0.0)	3 (1)	4.2 (0.2)	1.6 (0.0)	2.6 (0.1)	6.9 (0.3)	5 (0)	6.8 (0.3)	1.3 (0.1)	5.1 (0.5)	8.9 (0.2)
26	0.5 (0.0)	2 (1)	4.3 (0.4)	1.4 (0.2)	3.2 (0.1)	6.0 (1.4)	5 (1)	6.0 (0.2)	1.0 (0.1)	6.0 (0.6)	6.0 (0.6)
27	6.0 (0.4)	?	?	?	?	?	5 (0)	9.4 (0.9)	2.0 (0.2)	4.6 (0.7)	19.0 (1.8)
28	9.0 (0.0)	2 (1)	4.4 (0.6)	0.9 (0.1)	5.1 (1.0)	3.9 (0.4)	3 (0)	5.6 (0.1)	1.4 (0.3)	4.2 (0.9)	7.7 (1.3)
29	?	3 (0)	3.9 (0.0)	1.2 (0.0)	3.1 (0.0)	4.8 (0.0)	5 (0)	5.1 (0.0)	1.6 (0.0)	3.1 (0.0)	8.3 (0.0)
<i>N. fuegiana</i> mean	4.3	3	4.2	1.4	3.2	5.8	5	6.4	1.5	4.3	10.0
<i>N. fuegiana</i> CV	76.2	32	9.1	20.5	25.6	25.7	14	20.5	20.4	20.4	40.0
30	?	3 (0)	4.4 (0.0)	1.4 (0.0)	3.1 (0.0)	6.4 (0.0)	5 (0)	5.1 (0.0)	1.8 (0.0)	2.8 (0.0)	9.0 (0.0)
31	1.6 (0.1)	3 (0)	3.6 (0.5)	1.5 (0.1)	2.4 (0.4)	5.2 (0.6)	5 (0)	5.2 (0.5)	1.3 (0.1)	4.0 (0.6)	6.7 (0.1)
32	2.3 (0.1)	5 (1)	4.2 (0.5)	1.9 (0.2)	2.2 (0.2)	7.9 (1.6)	5 (0)	6.0 (0.7)	2.0 (0.2)	3.0 (0.3)	12.1 (2.6)
33	2.0 (0.6)	4 (1)	3.0 (0.4)	1.3 (0.2)	2.4 (0.4)	3.9 (1.0)	5 (0)	5.1 (0.6)	1.4 (0.2)	3.7 (0.5)	7.2 (1.5)
34	1.5 (0.2)	4 (1)	2.9 (0.4)	1.3 (0.2)	2.3 (0.5)	3.6 (0.6)	3 (0)	4.6 (0.4)	1.5 (0.3)	3.2 (0.7)	7.0 (1.9)
35	2.0 (0.5)	4 (0)	3.2 (0.4)	1.6 (0.2)	2.1 (0.3)	5.0 (1.2)	5 (0)	5.0 (0.6)	1.6 (0.2)	3.1 (0.4)	8.2 (1.6)
36	1.9 (0.4)	4 (0)	3.6 (0.5)	1.4 (0.1)	2.6 (0.3)	5.2 (1.1)	5 (0)	4.9 (0.6)	1.5 (0.1)	3.3 (0.3)	7.4 (1.4)
37	2.3 (0.5)	5 (1)	3.1 (0.5)	1.5 (0.2)	2.1 (0.3)	4.7 (1.3)	5 (0)	5.1 (0.5)	1.6 (0.2)	3.1 (0.3)	8.5 (1.3)
38	1.6 (0.5)	4 (0)	2.8 (0.5)	1.5 (0.2)	1.9 (0.4)	4.2 (1.0)	3 (0)	4.8 (0.5)	1.7 (0.1)	2.8 (0.2)	8.3 (1.2)
39	2.2 (0.2)	6 (0)	3.6 (0.5)	1.6 (0.2)	2.2 (0.2)	5.9 (1.5)	5 (0)	5.4 (0.3)	1.8 (0.2)	3.0 (0.3)	9.9 (1.1)
40	2.7 (0.7)	5 (1)	4.4 (0.4)	2.1 (0.4)	2.1 (0.4)	9.2 (1.8)	5 (0)	6.4 (0.3)	2.3 (0.3)	2.8 (0.3)	15.1 (2.2)
41	2.8 (1.0)	5 (0)	4.3 (0.4)	2.2 (0.2)	1.9 (0.2)	9.4 (1.3)	5 (0)	5.9 (0.5)	2.2 (0.2)	2.7 (0.3)	13.4 (1.7)
42	0.9 (0.1)	4 (0)	4.0 (0.4)	2.1 (0.0)	2.0 (0.2)	8.3 (0.7)	5 (0)	7.0 (0.1)	2.9 (0.3)	2.4 (0.3)	20.6 (1.9)
43	2.3 (0.4)	5 (1)	3.7 (0.4)	1.9 (0.3)	2.0 (0.3)	7.0 (1.7)	5 (0)	5.5 (0.6)	2.0 (0.2)	2.8 (0.4)	11.0 (2.0)
44	2.0 (0.6)	4 (1)	3.4 (0.5)	1.9 (0.3)	1.8 (0.2)	6.7 (1.9)	5 (0)	5.9 (0.6)	2.2 (0.3)	2.7 (0.4)	13.3 (2.1)
45	1.9 (0.4)	6 (0)	3.9 (0.6)	1.9 (0.3)	2.1 (0.5)	7.4 (1.6)	5 (0)	5.2 (0.9)	1.7 (0.2)	3.1 (0.8)	8.9 (1.3)
46	3.4 (1.2)	5 (0)	4.3 (0.5)	2.1 (0.2)	2.1 (0.2)	9.1 (1.7)	5 (0)	6.4 (0.4)	2.2 (0.3)	2.9 (0.3)	14.3 (2.2)
47	1.5 (0.6)	5 (0)	3.7 (0.3)	2.1 (0.2)	1.8 (0.3)	7.7 (1.2)	5 (0)	5.4 (0.6)	1.9 (0.3)	2.9 (0.3)	10.3 (2.6)
48	2.0 (0.8)	5 (1)	4.2 (0.4)	2.0 (0.2)	2.1 (0.2)	8.6 (1.1)	5 (0)	5.8 (0.6)	1.9 (0.2)	3.0 (0.3)	11.3 (2.3)
49	1.6 (0.7)	5 (1)	3.8 (0.3)	1.7 (0.4)	2.3 (0.5)	6.8 (1.7)	5 (0)	5.7 (0.6)	2.0 (0.2)	2.8 (0.2)	11.6 (2.2)
50	1.1 (0.2)	4 (0)	3.5 (0.3)	1.9 (0.3)	1.9 (0.3)	6.6 (1.2)	5 (0)	4.9 (0.5)	2.2 (0.2)	2.3 (0.3)	10.8 (1.5)
51	2.1 (0.7)	4 (1)	4.1 (0.4)	1.9 (0.3)	2.2 (0.3)	7.8 (1.7)	5 (0)	5.6 (0.1)	2.0 (0.3)	2.9 (0.4)	11.0 (1.6)

(Continued)

## APPENDIX 2. (Continued).

Code	PL	NOP	LOP	WOP	OPS	OPA	NIP	LIP	WIP	IPS	IPA
52	2.4 (0.2)	4 (1)	3.7 (0.5)	1.9 (0.2)	1.9 (0.3)	7.1 (1.5)	5 (0)	5.4 (0.3)	2.1 (0.3)	2.7 (0.7)	11.3 (1.4)
53	2.0 (0.2)	4 (0)	4.5 (0.7)	2.4 (0.3)	1.9 (0.2)	11.1 (2.9)	5 (0)	6.4 (0.8)	3.0 (0.3)	2.1 (0.3)	19.0 (3.4)
54	0.5 (0.0)	2 (0)	3.8 (0.3)	2.3 (0.1)	1.6 (0.2)	8.6 (0.4)	5 (0)	5.8 (0.5)	2.1 (0.1)	2.8 (0.1)	12.4 (1.8)
<i>N. glomerulosa</i> mean	1.9	4	3.8	1.8	2.1	6.9	5	5.5	2.0	2.9	11.1
<i>N. glomerulosa</i> CV	31.8	21	13.2	17.8	14.1	27.5	11	10.6	20.9	13.5	31.3
55	0.5 (0.1)	3 (1)	3.5 (0.4)	1.5 (0.2)	2.3 (0.1)	5.2 (1.1)	3 (0)	4.7 (0.4)	1.4 (0.2)	3.3 (0.3)	6.7 (1.6)
<i>N. maeviae</i> mean	0.5	3	3.5	1.5	2.3	5.2	3	4.7	1.4	3.3	6.7
<i>N. maeviae</i> CV	0.0	0	0.0	0.0	0.0	0.0	0	0.0	0.0	0.0	0.0
56	1.5 (0.1)	2 (0)	2.9 (0.3)	1.2 (0.1)	2.4 (0.2)	3.4 (0.6)	3 (0)	4.4 (0.4)	1.0 (0.1)	4.3 (0.7)	4.6 (0.5)
57	2.7 (0.3)	2 (0)	3.7 (0.7)	1.2 (0.1)	3.1 (0.6)	4.3 (0.9)	3 (0)	4.7 (0.3)	1.5 (0.3)	3.3 (0.8)	6.9 (1.4)
58	0.5 (0.0)	2 (1)	3.2 (0.1)	0.9 (0.1)	3.4 (0.4)	3.0 (0.1)	3 (1)	5.1 (0.1)	1.4 (0.3)	3.7 (0.8)	7.2 (1.6)
59	5.5 (0.3)	2 (0)	5.0 (0.4)	1.5 (0.2)	3.4 (0.5)	7.5 (1.3)	3 (0)	6.1 (0.9)	1.5 (0.2)	4.1 (0.3)	9.4 (2.7)
60	3.8 (0.5)	2 (0)	3.9 (0.1)	1.7 (0.1)	2.2 (0.1)	6.7 (0.6)	3 (0)	6.5 (0.8)	1.7 (0.1)	3.9 (0.2)	11.0 (2.3)
61	1.5 (0.0)	2 (0)	4.4 (0.4)	1.3 (0.2)	3.3 (0.8)	5.9 (0.4)	3 (0)	5.0 (0.4)	1.2 (0.1)	4.2 (0.0)	6.0 (0.9)
62	2.2 (0.5)	2 (0)	4.0 (0.7)	1.4 (0.3)	2.9 (0.6)	5.7 (1.7)	3 (0)	5.3 (0.6)	1.6 (0.2)	3.3 (0.4)	8.5 (1.9)
63	3.9 (0.5)	2 (0)	3.2 (0.2)	1.0 (0.1)	3.1 (0.1)	3.3 (0.4)	3 (0)	4.7 (0.2)	1.5 (0.1)	3.1 (0.3)	7.2 (0.2)
64	4.4 (0.3)	2 (1)	5.0 (1.0)	1.2 (0.5)	4.4 (0.9)	6.2 (3.6)	3 (0)	6.1 (1.6)	1.7 (0.2)	3.5 (0.7)	10.9 (3.6)
65	?	3 (0)	4.3 (0.0)	1.8 (0.0)	2.3 (0.0)	7.9 (0.0)	3 (0)	5.6 (0.0)	1.1 (0.0)	5.3 (0.0)	6.0 (0.0)
<i>N. ulicina</i> mean	2.9	2	4.0	1.3	3.1	5.4	3	5.4	1.4	3.9	7.8
<i>N. ulicina</i> CV	55.8	15	18.6	21.8	21.2	33.1	0	13.3	17.2	16.7	27.4
Total mean	2.7	3	4.0	1.6	2.7	6.5	5	5.8	1.7	3.5	10.1
Total CV	70.5	34	16.2	21.8	25.9	29.5	18	17.6	23.2	23.3	34.6

Code	NFC	ALL	ALW	ALS	ALA	CL	CW	CS	CA
1	5 (0)	4.7 (0.3)	1.4 (0.0)	3.4 (0.3)	6.5 (0.3)	1.5 (0.5)	0.5 (0.1)	3.1 (1.4)	0.8 (0.1)
2	5 (0)	4.6 (0.1)	1.6 (0.0)	2.8 (0.1)	7.6 (0.1)	1.5 (0.1)	0.4 (0.1)	3.7 (0.9)	0.6 (0.2)
3	5 (0)	4.8 (0.3)	1.6 (0.1)	3.0 (0.3)	7.7 (0.6)	1.3 (0.1)	0.4 (0.1)	3.2 (0.9)	0.5 (0.1)
4	5 (0)	4.4 (0.2)	1.7 (0.2)	2.5 (0.2)	7.7 (1.3)	1.3 (0.2)	0.6 (0.0)	2.3 (0.2)	0.7 (0.1)
5	5 (0)	4.2 (0.3)	1.3 (0.1)	3.3 (0.4)	5.5 (0.8)	1.1 (0.1)	0.4 (0.1)	3.0 (0.4)	0.4 (0.1)
6	5 (0)	4.7 (0.3)	2.0 (0.4)	2.3 (0.3)	9.5 (2.3)	1.4 (0.2)	0.8 (0.1)	1.8 (0.3)	1.1 (0.3)
7	5 (0)	4.5 (0.3)	1.6 (0.1)	2.8 (0.0)	7.3 (1.0)	1.6 (0.1)	0.5 (0.1)	3.0 (0.5)	0.8 (0.3)
8	5 (0)	4.7 (0.2)	1.6 (0.1)	3.0 (0.1)	7.4 (0.8)	1.7 (0.3)	0.7 (0.1)	2.7 (0.7)	1.1 (0.1)
9	5 (0)	5.0 (0.1)4	1.8 (0.1)	2.7 (0.3)	9.3 (0.5)	1.7 (0.2)	0.6 (0.0)	2.7 (0.2)	1.1 (0.2)
10	5 (0)	5.4 (0.5)	1.8 (0.1)	3.0 (0.3)	9.6 (1.2)	1.7 (0.1)	0.6 (0.1)	2.8 (0.4)	1.0 (0.2)
11	5 (0)	?	?	?	?	?	?	?	?
12	5 (0)	6.1 (0.6)	2.4 (0.2)	2.6 (0.3)	14.7 (1.9)	2.3 (0.3)	0.9 (0.2)	2.7 (0.4)	2.1 (0.7)
13	5 (0)	6.0 (0.1)	2.4 (0.1)	2.5 (0.1)	14.7 (0.7)	2.1 (0.2)	1.0 (0.0)	2.2 (0.3)	2.1 (0.2)
14	5 (0)	5.1 (0.3)	1.7 (0.2)	3.0 (0.3)	8.6 (1.4)	2.5 (0.3)	0.6 (0.1)	4.3 (0.2)	1.5 (0.4)
15	5 (0)	6.7 (0.3)	2.1 (0.2)	3.3 (0.2)	14.0 (1.9)	2.6 (0.3)	1.0 (0.1)	2.5 (0.2)	2.6 (0.5)
16	5 (0)	6.0 (0.3)	2.0 (0.2)	3.1 (0.2)	11.8 (1.8)	2.7 (0.2)	0.5 (0.1)	5.0 (0.7)	1.4 (0.1)
17	5 (0)	5.8 (0.4)	2.1 (0.3)	2.8 (0.3)	12.1 (2.3)	2.1 (0.2)	0.9 (0.1)	2.4 (0.4)	1.9 (0.3)
18	5 (0)	6.1 (0.1)	2.0 (0.1)	3.0 (0.2)	12.4 (1.0)	2.0 (0.5)	1.0 (0.4)	3.0 (0.7)	3.2 (1.4)
19	5 (0)	5.2 (0.0)	2.1 (0.0)	2.4 (0.0)	11.0 (0.0)	3.0 (0.2)	1.3 (0.5)	2.7 (1.2)	3.9 (1.6)
20	5 (0)	5.2 (0.0)	2.1 (0.0)	2.4 (0.0)	11.0 (0.0)	3.0 (0.2)	1.3 (0.5)	2.7 (1.2)	3.9 (1.6)
<i>N. axillaris</i> mean	5	5.2	1.9	2.9	9.9	2.0	0.7	3.0	1.5
<i>N. axillaris</i> CV	0	13.6	16.6	10.4	28.2	30.2	35.5	25.0	63.4
21	5 (0)	6.2 (0.2)	1.9 (0.1)	3.2 (0.2)	12.0 (0.8)	2.8 (0.4)	0.8 (0.0)	3.7 (0.7)	2.1 (0.3)
22	5 (0)	5.6 (1.0)	2.3 (0.4)	2.4 (0.1)	13.3 (4.3)	2.1 (0.4)	0.7 (0.1)	3.0 (0.4)	1.4 (0.4)
23	5 (0)	?	?	?	?	2.1 (0.1)	0.7 (0.1)	3.1 (0.5)	1.5 (0.2)
24	5 (0)	5.0 (0.1)	1.8 (0.2)	2.8 (0.2)	8.8 (0.8)	2.1 (0.2)	0.5 (0.1)	3.8 (0.6)	1.1 (0.1)
25	5 (0)	5.2 (0.3)	1.5 (0.1)	3.6 (0.5)	7.6 (0.4)	2.7 (0.3)	0.6 (0.1)	4.3 (0.8)	1.8 (0.6)
26	3 (1)	5.6 (0.3)	2.0 (0.2)	2.8 (0.2)	11.3 (1.5)	2.1 (0.4)	0.6 (0.0)	3.6 (0.6)	1.3 (0.3)
27	5 (0)	6.6 (0.2)	1.7 (0.1)	3.9 (0.3)	11.2 (0.8)	3.1 (0.4)	0.6 (0.1)	5.2 (0.5)	1.9 (0.4)
28	3 (1)	4.7 (0.2)	1.4 (0.1)	3.4 (0.1)	6.6 (0.8)	1.6 (0.1)	0.5 (0.1)	3.5 (1.0)	0.8 (0.2)
29	5 (0)	4.4 (0.0)	2.0 (0.0)	2.2 (0.0)	8.7 (0.0)	2.0 (0.0)	0.5 (0.0)	4.0 (0.0)	1.0 (0.0)
<i>N. fuegiana</i> mean	5	5.4	1.8	3.0	10.0	2.3	0.6	3.8	1.4
<i>N. fuegiana</i> CV	19	14.0	16.8	19.7	23.4	20.9	15.7	17.6	30.9
30	5 (0)	4.1 (0.0)	1.9 (0.0)	2.2 (0.0)	7.7 (0.0)	2.1 (0.0)	1.1 (0.0)	1.8 (0.0)	2.3 (0.0)
31	5 (0)	4.3 (0.1)	1.7 (0.4)	2.5 (0.6)	7.5 (1.5)	1.5 (0.1)	0.7 (0.1)	2.0 (0.3)	1.1 (0.0)
32	5 (0)	5.0 (0.2)	2.1 (0.3)	2.4 (0.2)	10.9 (1.7)	2.3 (0.4)	0.9 (0.1)	2.5 (0.4)	2.1 (0.6)
33	5 (0)	4.8 (0.3)	1.8 (0.1)	2.6 (0.2)	8.8 (1.0)	1.6 (0.2)	0.8 (0.1)	2.1 (0.3)	1.2 (0.2)
34	3 (0)	4.1 (0.3)	1.7 (0.2)	2.4 (0.4)	7.0 (1.3)	1.3 (0.1)	0.7 (0.1)	2.0 (0.4)	0.9 (0.2)
35	5 (0)	4.6 (0.5)	1.9 (0.2)	2.5 (0.3)	8.6 (1.7)	1.6 (0.2)	0.8 (0.1)	1.9 (0.3)	1.4 (0.3)
36	5 (1)	4.7 (0.3)	2.0 (0.2)	2.3 (0.2)	9.7 (1.3)	1.5 (0.2)	0.8 (0.1)	1.8 (0.3)	1.2 (0.2)
37	5 (0)	4.9 (0.6)	2.0 (0.3)	2.5 (0.3)	10.0 (2.4)	1.4 (0.2)	0.7 (0.2)	2.2 (0.6)	1.0 (0.3)
38	3 (0)	4.4 (0.4)	1.8 (0.2)	2.4 (0.2)	7.9 (1.3)	1.5 (0.2)	0.6 (0.1)	2.7 (0.7)	0.9 (0.2)
39	5 (0)	5.1 (0.2)	2.0 (0.1)	2.5 (0.2)	10.3 (0.9)	1.5 (0.1)	0.8 (0.1)	1.9 (0.2)	1.3 (0.2)
40	5 (1)	5.2 (0.2)	2.0 (0.2)	2.7 (0.3)	10.2 (1.2)	2.3 (0.3)	1.0 (0.1)	2.3 (0.4)	2.3 (0.4)
41	5 (0)	4.9 (0.5)	1.9 (0.2)	2.6 (0.3)	9.4 (1.7)	2.2 (0.3)	1.0 (0.1)	2.1 (0.2)	2.2 (0.5)

(Continued)



## APPENDIX 2. (Continued).

Code	NFC	ALL	ALW	ALS	ALA	CL	CW	CS	CA
42	5 (0)	5.5 (0.1)	2.0 (0.1)	2.8 (0.1)	10.7 (0.9)	2.2 (0.1)	1.2 (0.1)	1.8 (0.2)	2.6 (0.3)
43	5 (0)	4.8 (0.3)	1.9 (0.2)	2.5 (0.2)	9.3 (1.4)	1.7 (0.2)	0.9 (0.1)	1.8 (0.3)	1.6 (0.2)
44	5 (0)	5.0 (0.3)	1.9 (0.2)	2.6 (0.2)	9.6 (1.1)	1.9 (0.2)	0.9 (0.2)	2.2 (0.5)	1.6 (0.4)
45	5 (1)	4.1 (0.2)	1.6 (0.1)	2.6 (0.2)	6.5 (0.7)	1.6 (0.2)	0.9 (0.1)	1.9 (0.2)	1.4 (0.2)
46	5 (0)	4.8 (0.4)	1.7 (0.1)	2.8 (0.2)	8.2 (0.8)	2.2 (0.2)	0.9 (0.2)	2.6 (0.6)	2.0 (0.4)
47	5 (0)	4.7 (0.4)	1.9 (0.1)	2.4 (0.2)	9.1 (1.2)	2.2 (0.2)	0.8 (0.2)	2.3 (0.4)	2.1 (0.5)
48	5 (0)	4.5 (0.3)	1.6 (0.2)	2.8 (0.2)	7.2 (1.1)	1.9 (0.3)	0.9 (0.1)	2.1 (0.4)	1.8 (0.3)
49	5 (0)	4.1 (0.2)	1.6 (0.2)	2.6 (0.2)	6.6 (0.9)	2.0 (0.3)	0.8 (0.1)	2.5 (0.4)	1.5 (0.4)
50	5 (0)	4.3 (0.2)	1.5 (0.1)	2.8 (0.2)	6.6 (0.6)	2.0 (0.1)	0.9 (0.1)	2.2 (0.2)	1.8 (0.2)
51	5 (0)	4.4 (0.4)	1.6 (0.2)	2.7 (0.3)	7.2 (1.2)	1.9 (0.3)	0.9 (0.1)	2.0 (0.3)	1.8 (0.4)
52	5 (0)	4.1 (0.1)	1.4 (0.2)	3.0 (0.4)	5.6 (0.9)	2.2 (0.1)	0.9 (0.1)	2.4 (0.4)	2.1 (0.3)
53	5 (0)	5.9 (0.2)	2.2 (0.2)	2.7 (0.1)	12.9 (1.5)	2.2 (0.3)	0.7 (0.1)	3.0 (0.2)	1.7 (0.4)
54	5 (0)	5.2 (0.1)	2.0 (0.4)	2.7 (0.6)	10.3 (2.1)	2.3 (0.3)	0.9 (0.3)	2.6 (0.7)	2.2 (1.0)
<i>N. glomerulosa</i> mean	5	4.7	1.8	2.6	8.7	1.9	0.9	2.2	1.7
<i>N. glomerulosa</i> CV	11	10.2	10.9	7.1	20.0	17.0	15.9	14.8	28.8
55	3 (0)	4.2 (0.2)	2.0 (0.1)	2.1 (0.1)	8.5 (0.9)	1.6 (0.1)	0.5 (0.1)	3.0 (0.3)	0.9 (0.2)
<i>N. maeviae</i> mean	3	4.2	2.0	2.1	8.5	1.6	0.5	3.0	0.9
<i>N. maeviae</i> CV	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
56	2 (1)	3.8 (0.3)	1.5 (0.0)	2.5 (0.2)	5.8 (0.4)	1.5 (0.1)	0.4 (0.1)	3.4 (0.6)	0.6 (0.1)
57	2 (0)	2.8 (0.2)	1.4 (0.2)	2.0 (0.3)	4.1 (0.8)	1.0 (0.0)	0.3 (0.1)	3.2 (0.5)	0.3 (0.1)
58	3 (1)	4.5 (0.1)	2.0 (0.1)	2.2 (0.0)	9.3 (0.4)	1.9 (0.1)	0.5 (0.1)	3.8 (1.3)	1.0 (0.2)
59	2 (1)	5.1 (0.5)	1.7 (0.2)	2.9 (0.1)	8.9 (1.8)	2.2 (0.2)	0.6 (0.1)	3.6 (0.2)	1.3 (0.3)
60	3 (1)	4.5 (0.1)	1.8 (0.2)	2.5 (0.2)	8.2 (0.8)	2.2 (0.1)	0.8 (0.0)	2.8 (0.2)	1.7 (0.1)
61	2 (0)	4.2 (0.2)	1.2 (0.2)	3.3 (0.2)	5.2 (0.9)	1.5 (0.2)	0.4 (0.0)	3.7 (0.0)	0.6 (0.1)
62	2 (1)	4.4 (0.3)	1.8 (0.2)	2.4 (0.2)	8.2 (1.5)	1.7 (0.2)	0.8 (0.1)	2.2 (0.4)	1.3 (0.2)
63	2 (0)	4.0 (0.2)	1.6 (0.1)	2.5 (0.2)	6.4 (0.3)	1.8 (0.2)	0.4 (0.1)	4.1 (0.4)	0.8 (0.2)
64	2 (1)	4.8 (0.8)	1.6 (0.3)	2.9 (0.3)	7.9 (2.5)	2.1 (0.4)	0.5 (0.1)	4.2 (0.2)	1.1 (0.3)
65	3 (0)	4.6 (0.0)	1.4 (0.0)	3.4 (0.0)	6.2 (0.0)	1.7 (0.0)	0.6 (0.0)	3.0 (0.0)	1.0 (0.0)
<i>N. ulicina</i> mean	2	4.3	1.6	2.7	7.0	1.8	0.5	3.4	1.0
<i>N. ulicina</i> CV	21	14.4	14.8	17.0	24.2	20.5	27.5	17.8	40.6
Total mean	4	4.9	1.8	2.7	9.0	1.9	0.7	2.9	1.5
Total CV	24	14.7	14.5	13.8	26.2	23.8	29.5	28.6	45.8

