Table S1. Genetic divergence (F_{ST}) between pairs of populations of *Alcantarea* 'inselberg' bromeliads. Population names follow the tables and figures of the main paper. All F_{ST} estimates were highly significant at p<0.005.

	BRA	GIM	GRC	IIM	IVV	MAR	NEV
BRA	0.000	0.541	0.603	0.454	0.420	0.579	0.616
GIM		0.000	0.092	0.386	0.336	0.517	0.660
GRC			0.000	0.506	0.443	0.604	0.706
IIM				0.000	0.143	0.536	0.639
IVV					0.000	0.456	0.599
MAR						0.000	0.707
NEV							0.000

Table S2. Estimates of effective population sizes (N_e) and migration rates ($N_e m$) for all studied *Alcantarea* species, including maximum likelihood estimates (MLE) and 0.025 and 0.975 percentiles. The directions of $N_e m$ are indicated by population numbers, with the first number indicating the source and the second one the receiving population. Species names are BRA, *A. brasiliana*; GEN, *A. geniculata*; IMP, *A. imperialis*; MAR, *A. martinellii*; NEV, *A. nevaresii*. Species comparisons with significantly asymmetric migration based on 95% confidence intervals are indicated in bold type.

Population	Parameter	0.025 percentile	MLE	0.975 percentile
BRA (pop1)	Ne1	2453	2610	2787
GEN (pop2)	Ne2	2248	2460	2677
IMP (pop3)	Ne3	2579	2860	3187
MAR (pop4)	Ne4	2108	2422	2810
NEV (pop5)	Ne5	1981	2190	2452
GEN -> BRA	Nem_21	0.116	0.162	0.221
IMP -> BRA	**Nem_31**	**0.123**	**0.169**	**0.230**
MAR -> BRA	Nem_41	0.074	0.110	0.157
NEV -> BRA	Nem_51	0.118	0.164	0.223
BRA -> GEN	Nem_12	0.104	0.151	0.211
IMP -> GEN	Nem_32	0.140	0.195	0.264
MAR -> GEN	Nem_42	0.098	0.141	0.199
NEV -> GEN	Nem_52	0.065	0.099	0.146
BRA -> IMP	**Nem_13**	**0.235**	**0.322**	**0.441**
GEN -> IMP	Nem_23	0.202	0.281	0.386

MAR -> IMP	Nem_43	0.191	0.268	0.374
NEV -> IMP	Nem_53	0.082	0.129	0.195
BRA -> MAR	Nem_14	0.040	0.070	0.117
GEN -> MAR	Nem_24	0.131	0.192	0.280
IMP -> MAR	Nem_34	0.148	0.216	0.312
NEV -> MAR	Nem_54	0.050	0.086	0.141
BRA -> NEV	Nem_15	0.048	0.075	0.116
GEN -> NEV	Nem_25	0.048	0.077	0.118
IMP -> NEV	Nem_35	0.044	0.071	0.111
MAR -> NEV	Nem_45	0.092	0.134	0.193

Table S3. Definition of plastid DNA haplotypes based on two Single Nucleotide Polymorphisms (SNPs) in region *petBex2-Dex2* (Ebert & Peakall, 2009), one SNP and one indel in region *ndh*A intron (Shaw et al., 2007), and fragment sizes at the two plastid microsatellite markers VgCP3 and VgCP4 (Palma-Silva et al., 2009). For references see main paper. Sequences were deposited in Genbank (submission ID: 1862480; accession numbers to be updated until online-publication).

Haplotype name	petBex2-Dex2, SNP position 123	petBex2-Dex2, SNP position 619	ndhA intron, SNP position 454	ndhA intron, Indel 456-460	VgCP3 size	VgCP4 size
H1	A	C	C	insertion	233	203
H2	T	C	C	deletion	227	204
H3	T	C	C	deletion	226	203
H4	T	C	C	deletion	226	202
H5	T	T	A	deletion	226	200