Supplementary information for

Maja Wyczanska, Karoline Wacker, Paul S Dyer, Silke Werth

Local-scale panmixia in the lichenized fungus *Xanthoria parietina* contrasts with substantial genetic structure in its *Trebouxia* photobionts

Table S1: Groups of matching genotypes of the mycobiont *Xanthoria parietina*, showing genotype ID, region within Munich, population, and sample ID.

GenotypeID	Region	Population	Sample
A	South	Stachus	St3a
A	South	Landshuter Allee	La4a
B	South	Stachus	St5a
B	West	Botanic Gardens	B1b
C	Central	Lothstraße	Lo6c
C	Central	Lothstraße	Lo5b
C	South	Landshuter Allee	La1a
D	South	Stachus	St4a
D	South	Landshuter Allee	La6a
D	South	Flaucher	F6c
D	West	Pasing	P2a

Table S2: Groups of matching genotypes of the green algal photobiont of *Xanthoria parietina*, showing genotype ID, region within Munich, population, and sample ID.

| GenotypeID	Region	Population	Sample
A	West	Pasing	P3c
A	South	Stachus	St4c
A	South	Stachus	St3b
B	South	Landshuter Allee	La4b
B	South	Flaucher	F4c
B	North	Freimann	Fr2b
B	North	Freimann	Fr2c
C	South	Stachus	St4a
C	South	Stachus	St2a
C	South	Flaucher	F6a
C	South	Flaucher	F3a
C	North	Freimann	Fr6c
D	West	Pasing	P4b
D	West	Botanic Gardens	B6a
D	North	Freimann	Fr3b
E	West	Pasing	P1a
E	South	Flaucher	F4b
E	Allgäu	Hinterstein	A21
F	West	Pasing	P6b
F	West	Botanic Gardens	B5b
G	South	Landshuter Allee	La1a
G	North	Freimann	Fr1b
H	West	Pasing	P6c
H	South	Stachus	St6c
H	Central	Lothstraße	Lo2a
I	South	Landshuter Allee	La4c
I	North	Freimann	Fr5b
I	Central	Lothstraße	Lo6a
I	Central	Lothstraße	Lo5a
I	Central	Lothstroße	Lo3a
J	South	Landshuter Allee	La5c
J	South	Flaucher	F5a
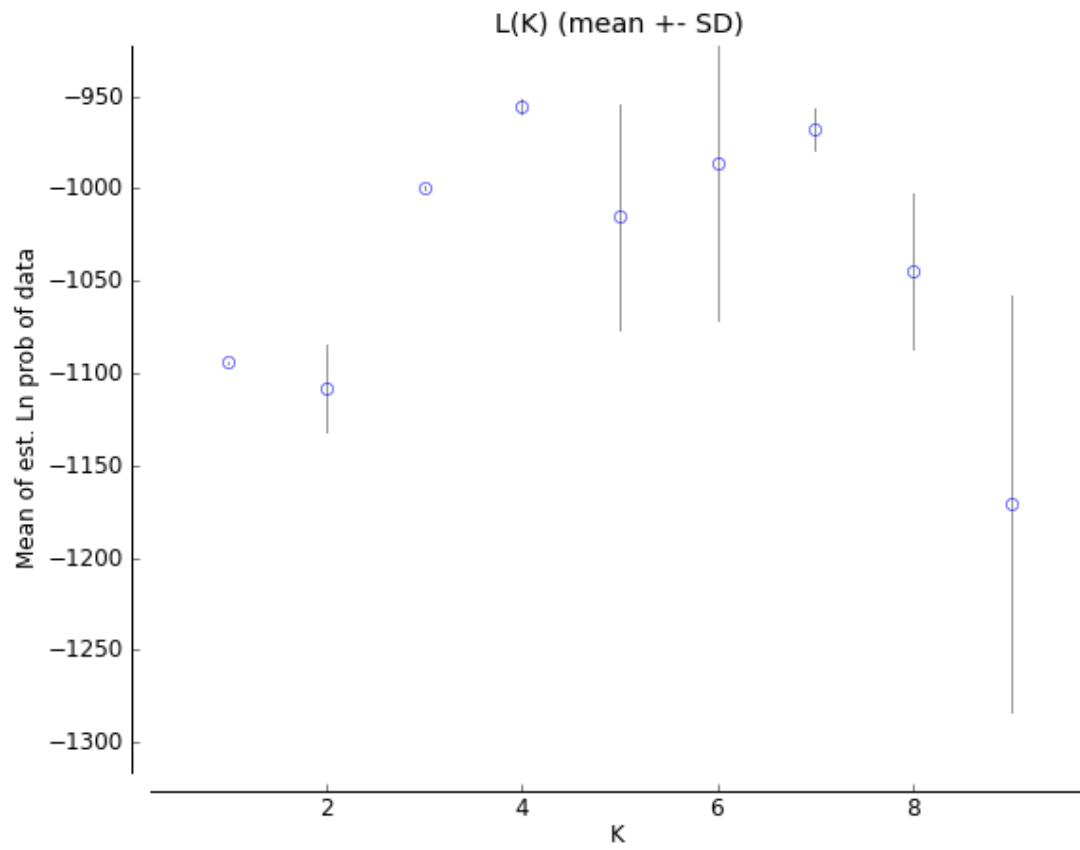
Figure S1. Bayesian analysis of population structure in the mycobiont *Xanthoria parietina*, showing the log likelihood of the data with standard deviation vs. the number of clusters K.
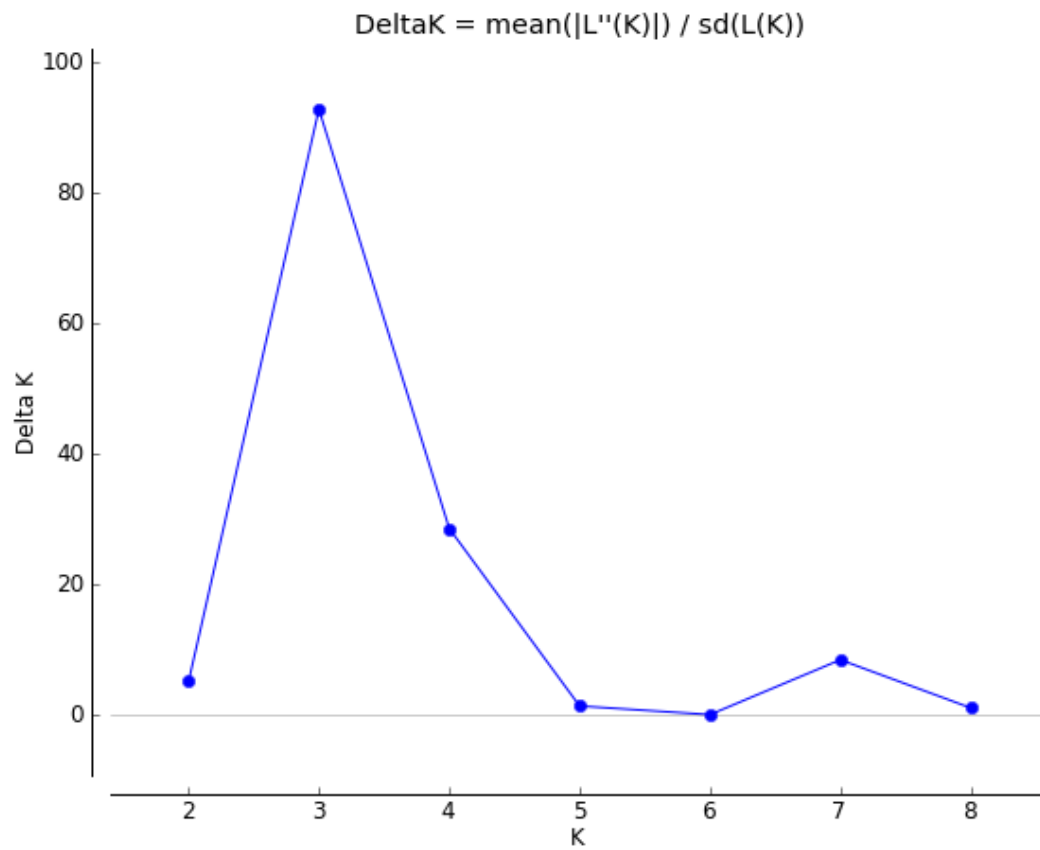
Figure S2. Bayesian analysis of population structure in the mycobiont *Xanthoria parietina*, showing delta K against the number of genetic clusters, K. The mode of this distribution is the true number of genetic clusters, here K=3.
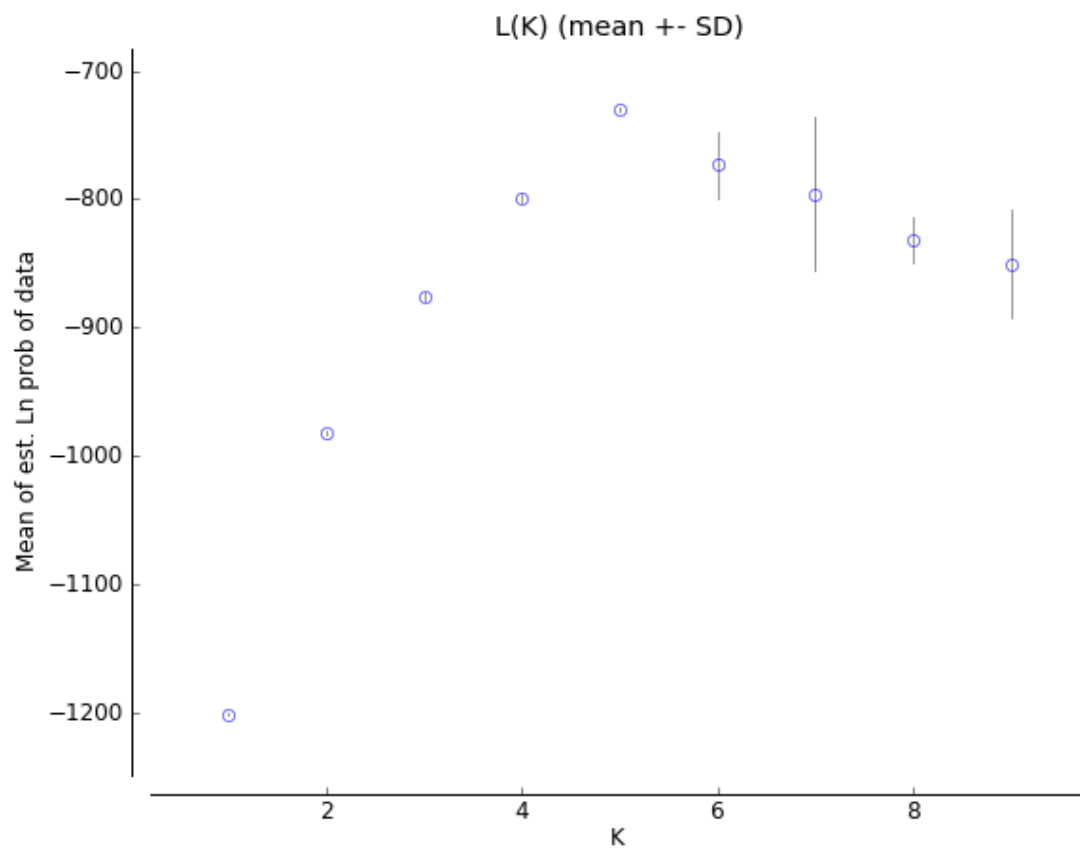
Figure S3. Bayesian analysis of population structure in the green algal photobiont *Trebouxia decolorans* associated with *Xanthoria parietina*, showing the log likelihood of the data with standard deviation vs. the number of genetic clusters K.
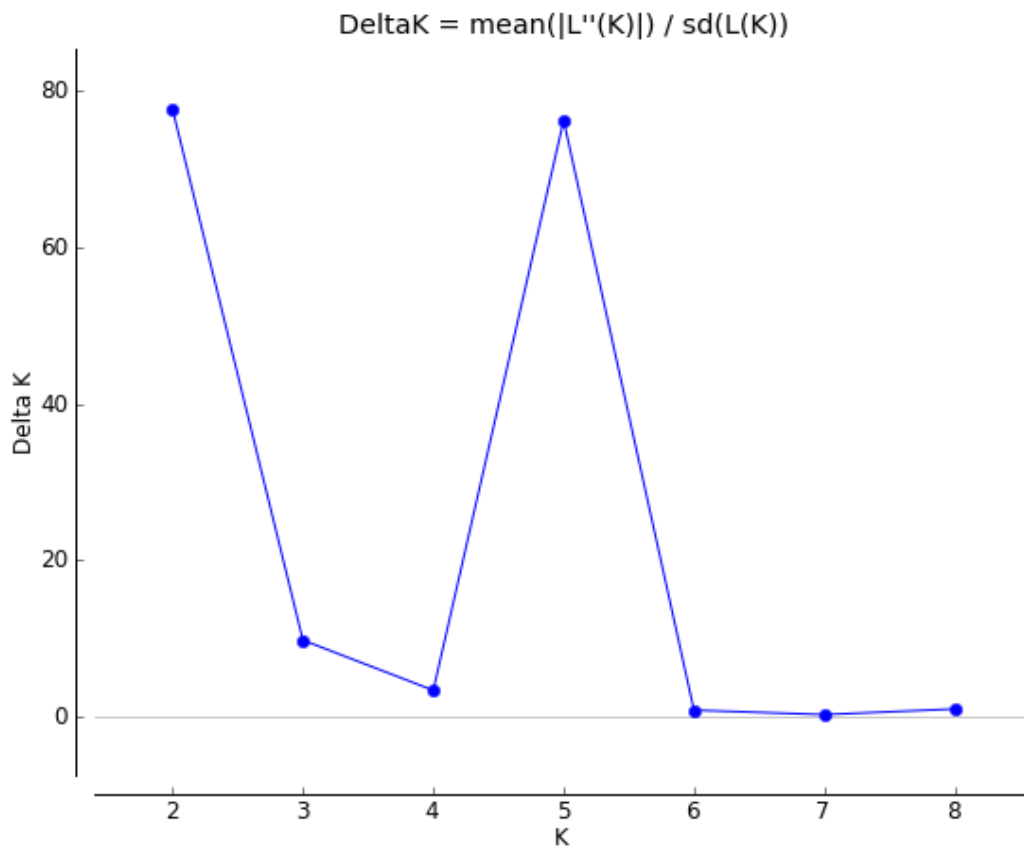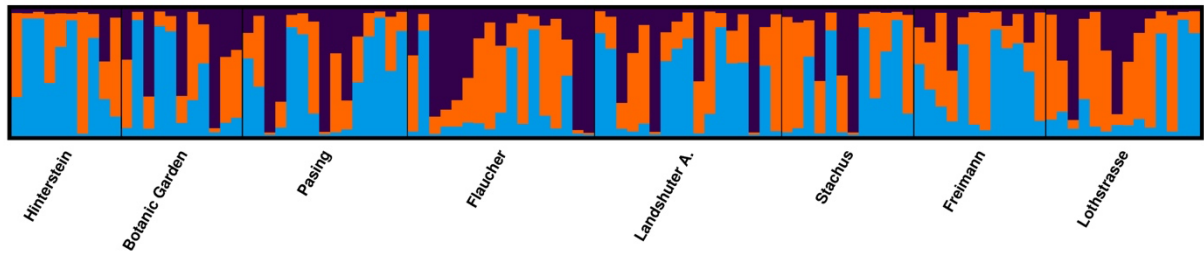
Figure S4. Bayesian analysis of population structure in the green algal photobiont *Trebouxia decolorans* associated with *Xanthoria parietina*, showing delta K against the number of genetic clusters K. The mode of this distribution is the true number of clusters.

A. Mycobiont

Hinterstein
Botanic Garden
Pasing
Flaucher
Landshuter A.
Stachus
Freimann
Lothstrasse

B. Photobiont

Hinterstein
Botanic Garden
Pasing
Flaucher
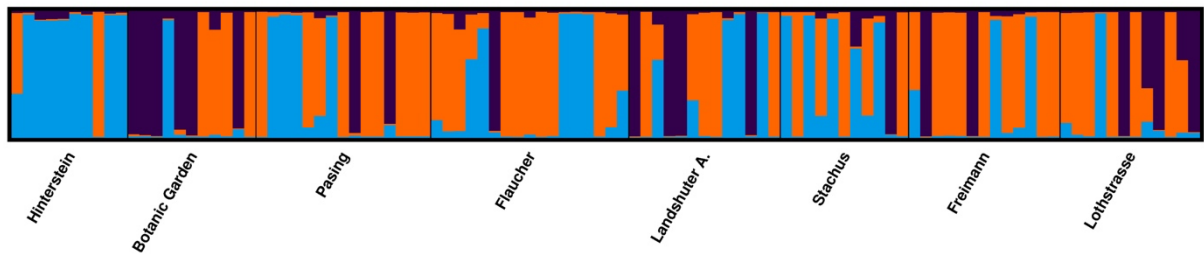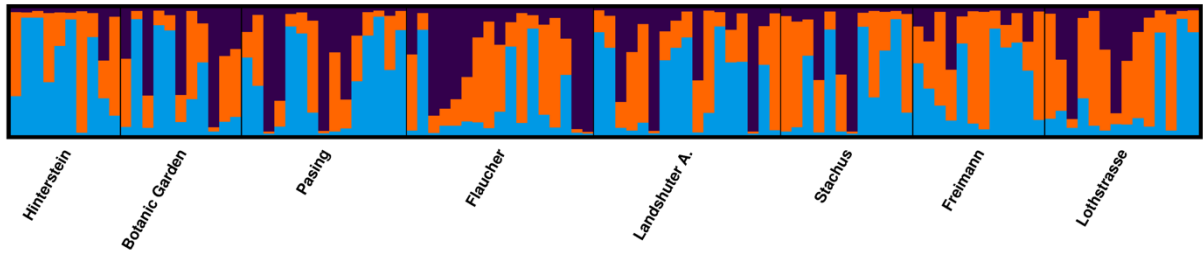Landshuter A.
Stachus
Freimann
Lothstrasse

Figure S5. Bayesian analysis of population structure in *Xanthoria parietina*, based on STRUCTURE. The plot shows each individual as a vertical bar, with affiliation to genetic clusters shown by colors. A*. Xanthoria parietina* mycobiont. B. *Trebouxia decolorans* photobiont of *X. parietina*. The plot was created with CLUMPAK (http://clumpak.tau.ac.il, date accessed: 29.3.2021) (Kopelman *et al.* 2015) and compiled in GIMP v. 2.8.22.
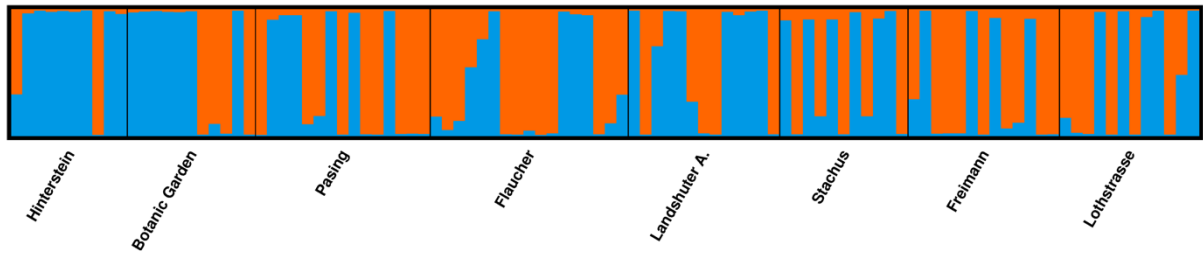
Figure S6. Bayesian analysis of population structure in *Xanthoria parietina*, based on STRUCTURE. The plot shows each individual as a vertical bar, with affiliation to genetic clusters shown by colors. A. *Xanthoria parietina* mycobiont (K=3). B. *Trebouxia decolorans* photobiont of *X. parietina* (K=2). The plot was created with CLUMPAK (http://clumpak.tau.ac.il, date accessed: 29.3.2021) (Kopelman *et al.* 2015) and compiled in GIMP v. 2.8.22.

Methods population trees

Population trees were computed in PHYLIP v. 3.697 (Felsenstein 1989). Using the "gendist" module, genetic distance matrices were created and with seqboot, bootstrapping was performed. A neighbor-joining tree was made, using the "Neighbor" Program of PHYLIP and then a consensus tree was created with the "Consense" Program. The final population tree was visualized with the software FigTree v. 1.4.4 (http://tree.bio.ed.ac.uk/software/figtree/).
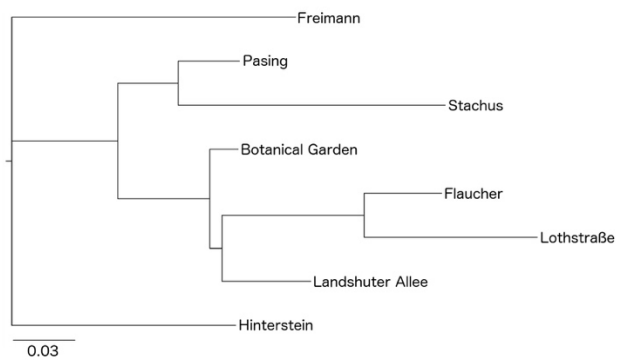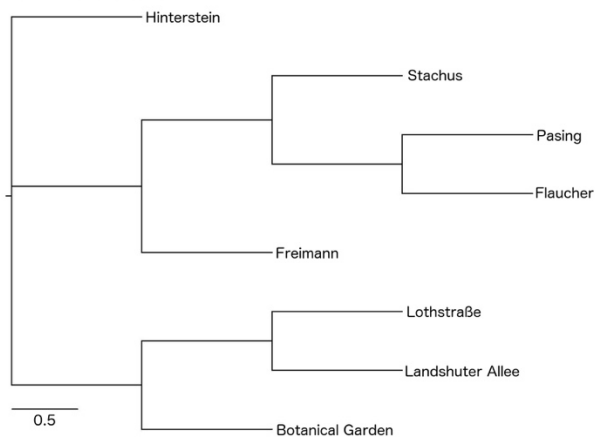
A. Mycobiont

B. Photobiont

Figure S7: Population tree of eight populations of *Xanthoria parietina*, with Hinterstein (Oberallgäu) as an outgroup for seven populations sampled in the city of Munich, Bavaria, Germany. A. Mycobiont. B. Photobiont.

References

Felsenstein, J. (1989) PHYLIP - Phylogeny inference package (Version 3.2). *Cladistics* **5:** 164-166.

Kopelman, N. M., Mayzel, J., Jakobsson, M., Rosenberg, N. A. & Mayrose, I. (2015) CLUMPAK: a program for identifying clustering modes and packaging population structure inferences across K. *Molecular Ecology Resources* **15:** 1179-1191.