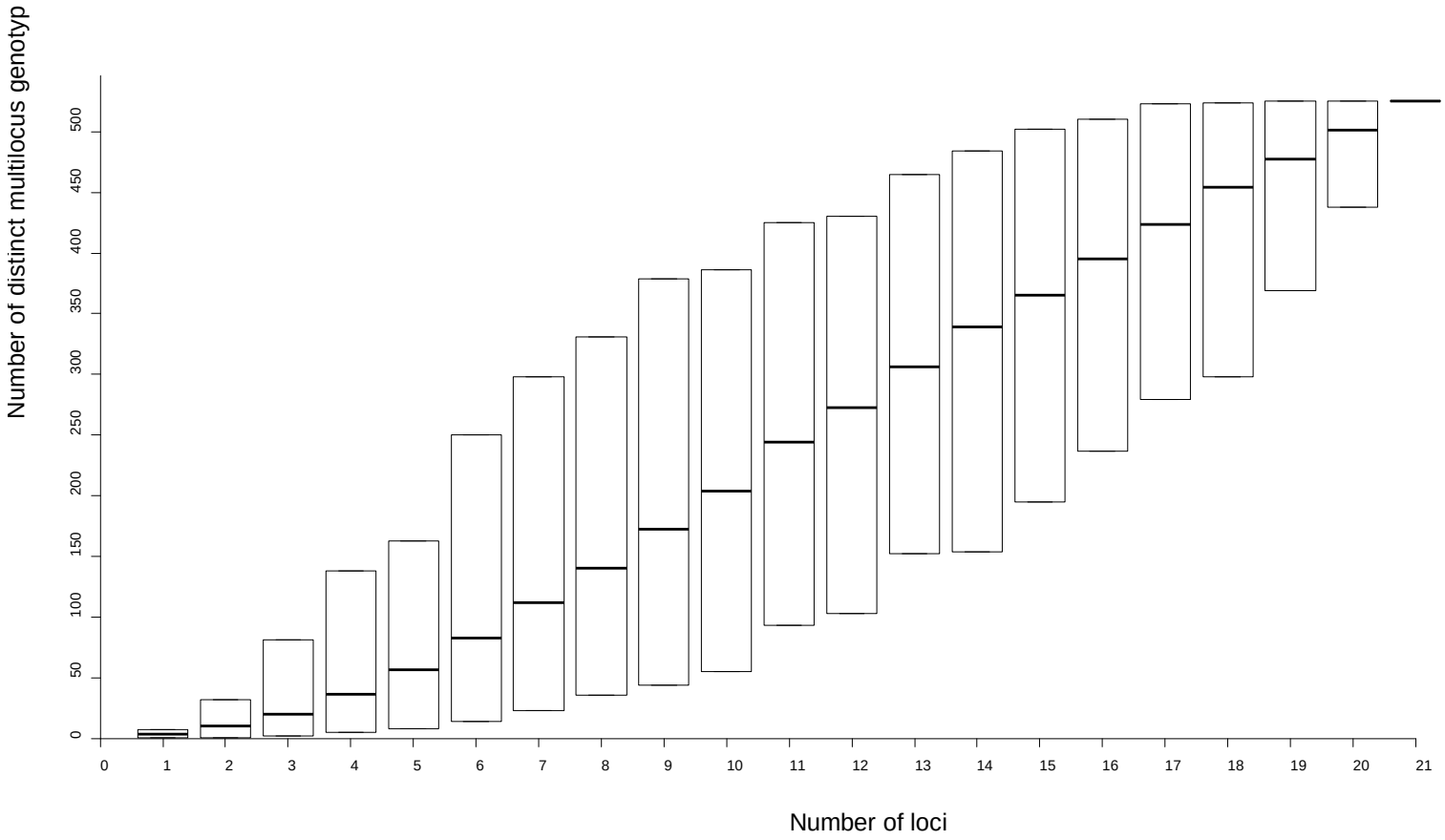
SUPPLEMENTARY DATA

TABLE S1. The history of land use in the area of sampled patches. Aereal photographs were available from seven years in the period of 1938-1993, enabling a determination of historic landuse (forest, agricultural, open roadside, agricultural roadside, or residential) over the 73 years preceeding the current study (2010 – 2011). Current patch sizes vary from 0.18 – 2.87 ha.

Year	POR	HDP	TRL	MWS	MOR	BDR
1938	Open roadside	Agricultural	Agricultural	Residential	Open roadside	Agricultural
1944	Open roadside	Agricultural	Agricultural	Residential	Open roadside	Agricultural
1955	Open roadside	Agricultural	Open roadside	Residential	Open roadside	Agricultural roadside
1967	Open roadside	Forest	Open roadside	Residential	Open roadside	Agricultural roadside
1973	Open roadside	Forest	Open roadside	Residential	Open roadside	Agricultural roadside
1980	Open roadside	Forest	Open roadside	Open roadside	Open roadside	Open roadside
1993	Open roadside	Open roadside	Open roadside	Open roadside	Open roadside	Open roadside
2010 – 2011	Open roadside	Open roadside	Open roadside	Open roadside	Open roadside	Open roadside
Patch size (ha)	0.82	0.18	0.35	0.29	0.54	2.87

FIG. S1. The power of the 21 polymorphic allozyme loci to detect distinct multilocus genotypes (a) overall and (b) in each patch. For each number of loci, the number of distinct multilocus genotypes was enumerated for 1000 random samples of all possible combinations of that number of loci. Boxes show the maximum, mean, and minimum number of multilocus genotypes.



a.

b.

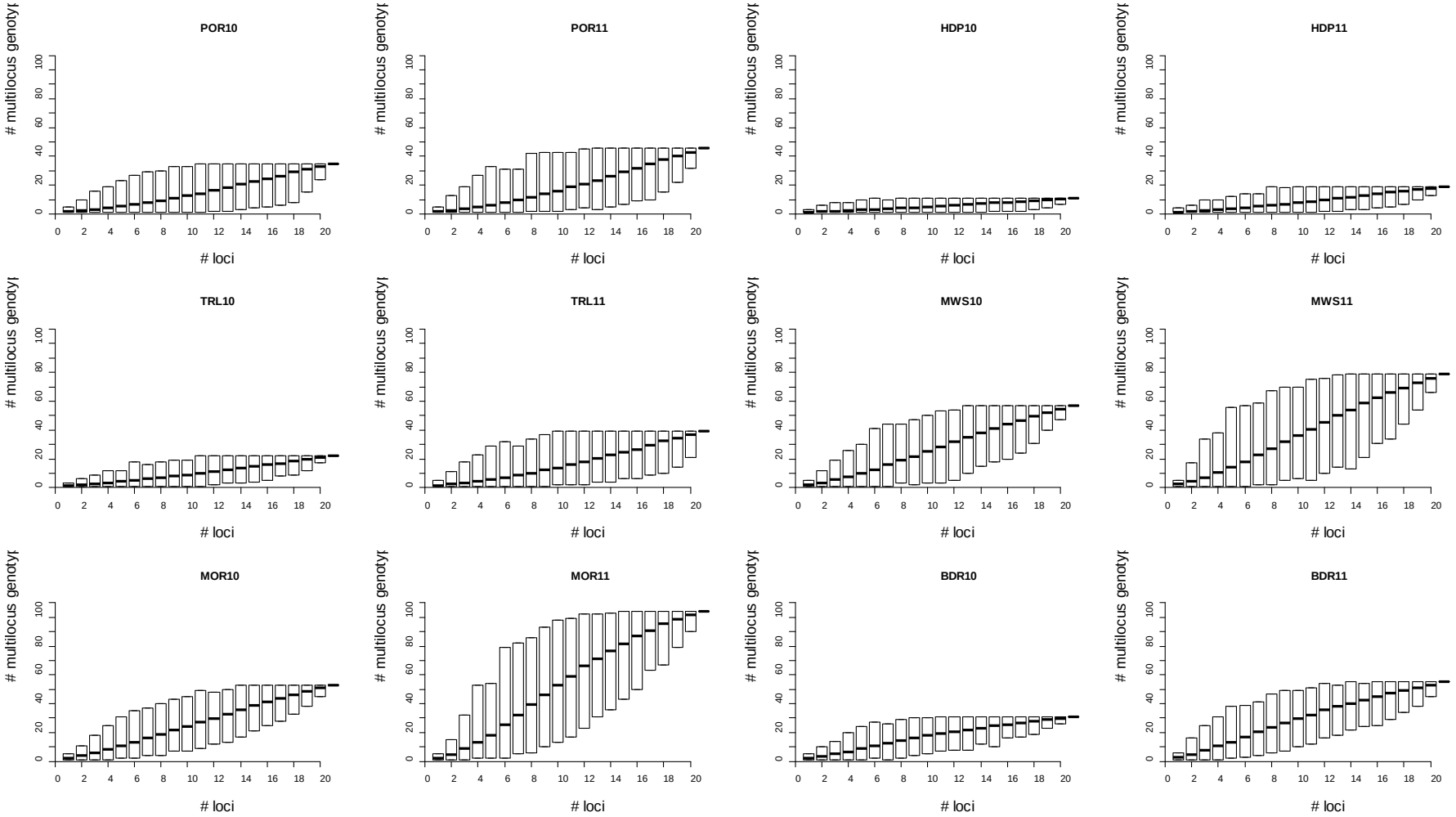
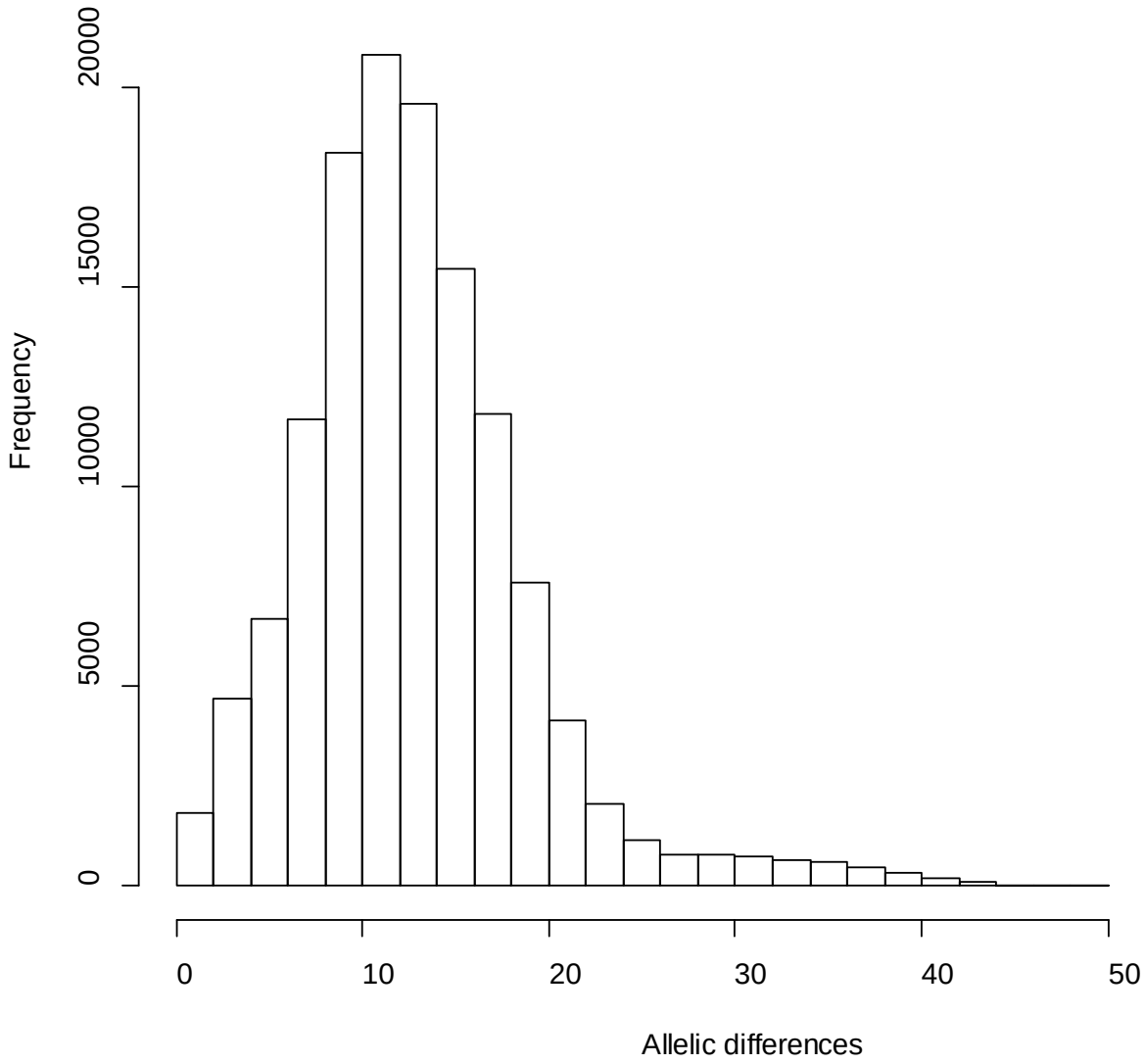

POR10
POR11
HDP10
HDP11
TRL10
TRL11
MWS10
MWS11
MOR10
MOR11
BDR10
BDR11
multilocus genotype
loci

FIG. S2. Distribution of allelic distances separating all unique multilocus genotypes (a) overall and (b) in each patch. The lack of a minor bimodal peak at small allelic distances suggests that somatic mutations and scoring error do not have a major influence on this dataset. Thus, it would not be appropriate to define a threshold for combining distinct multilocus genotypes into closely related multilocus clonal lineages.

a.



b.

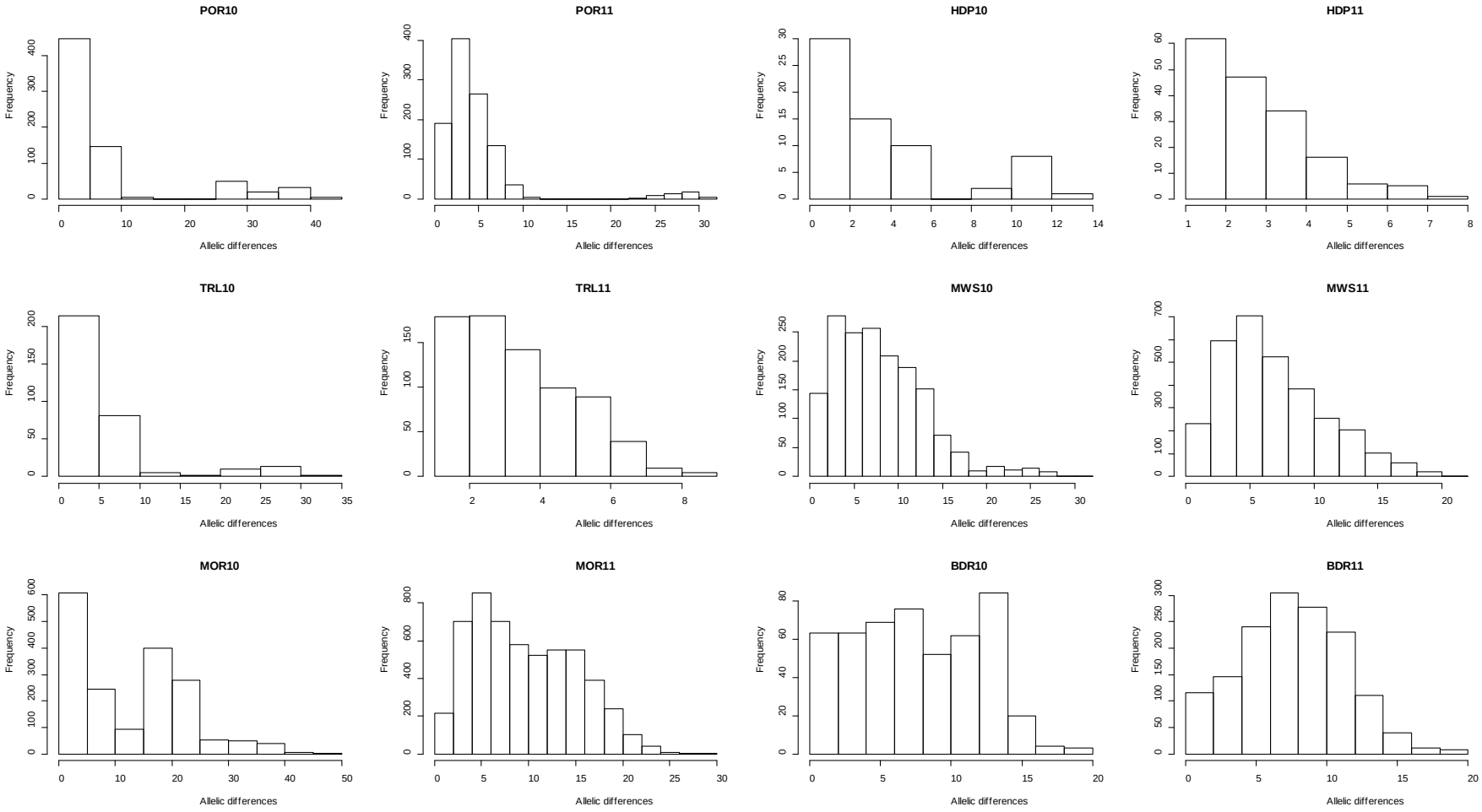
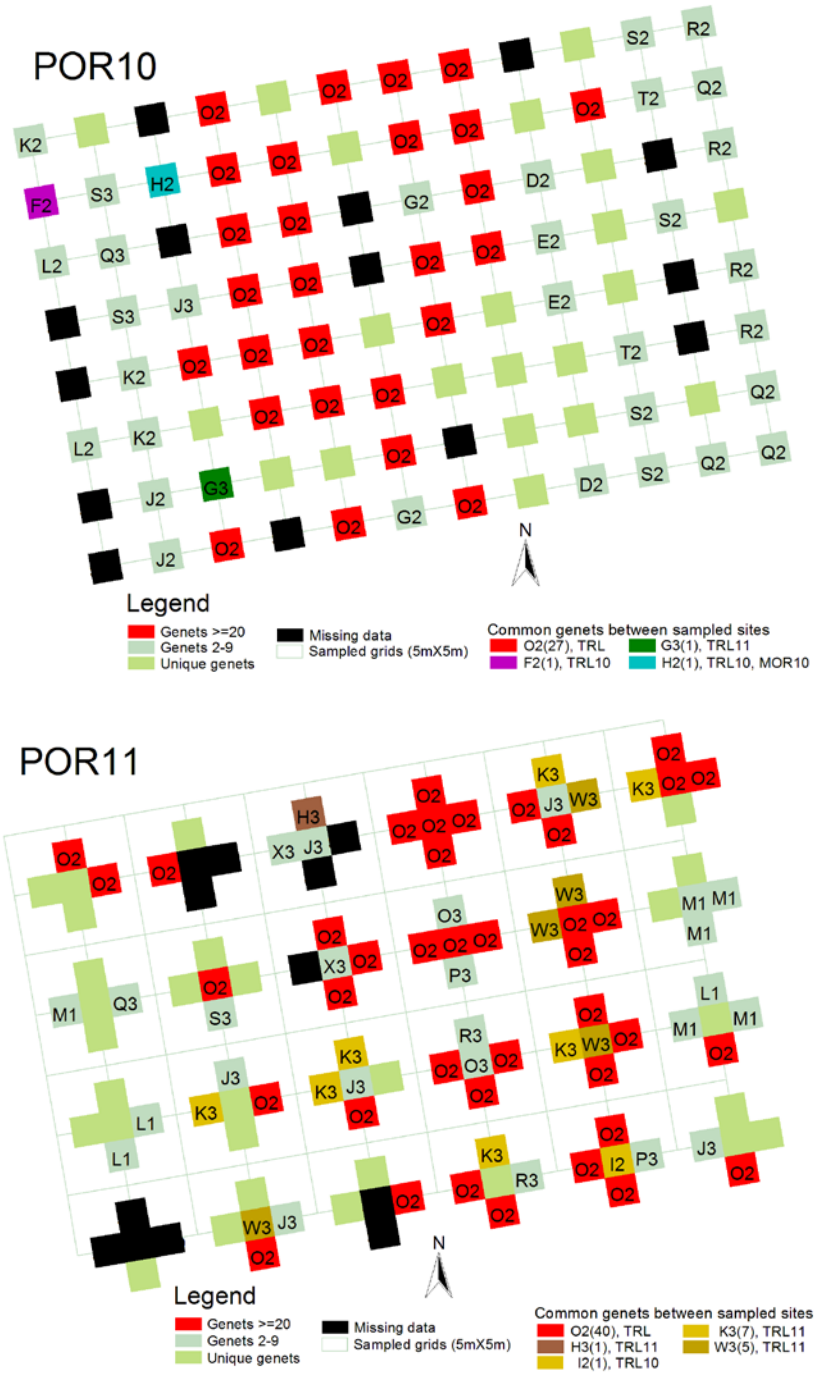
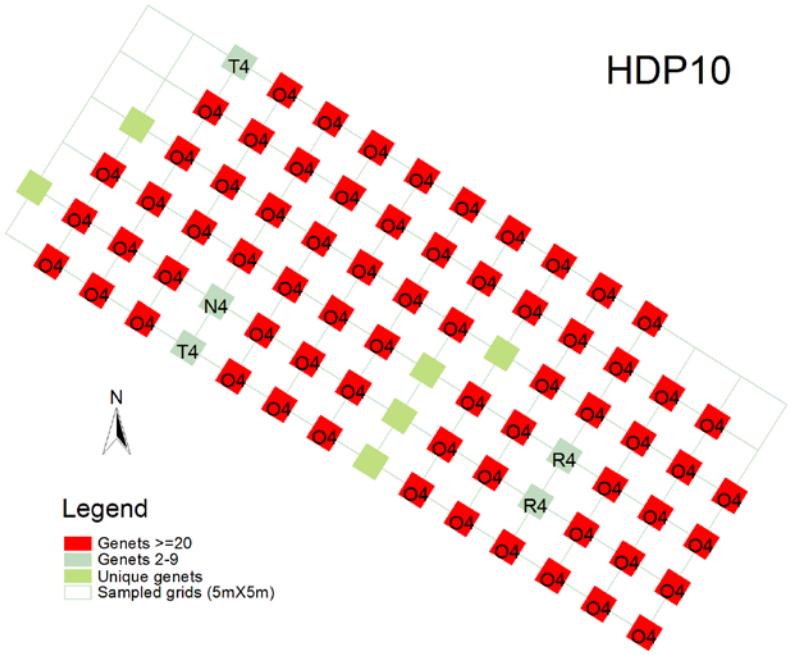
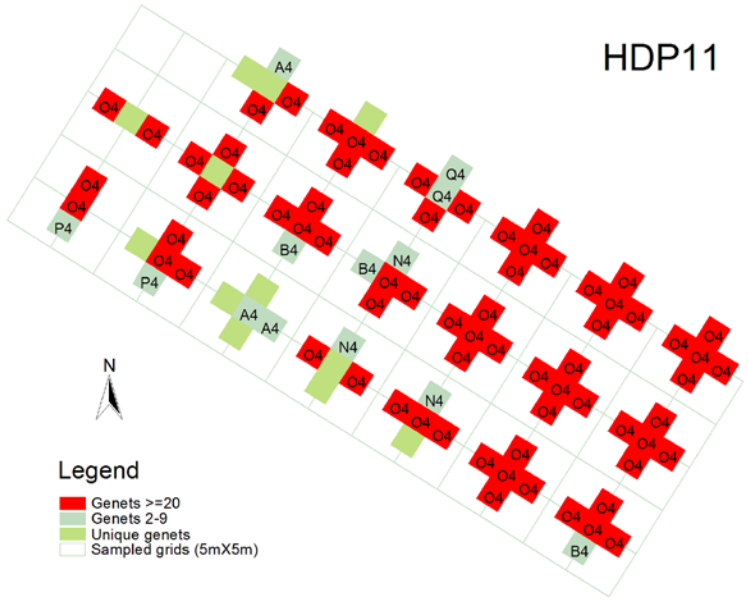

POR10
POR11
HDP10
HDP11
TRL10
TRL11
MWS10
MWS11
MOR10
MOR11
BDR10
BDR11
Frequency
Allelic differences

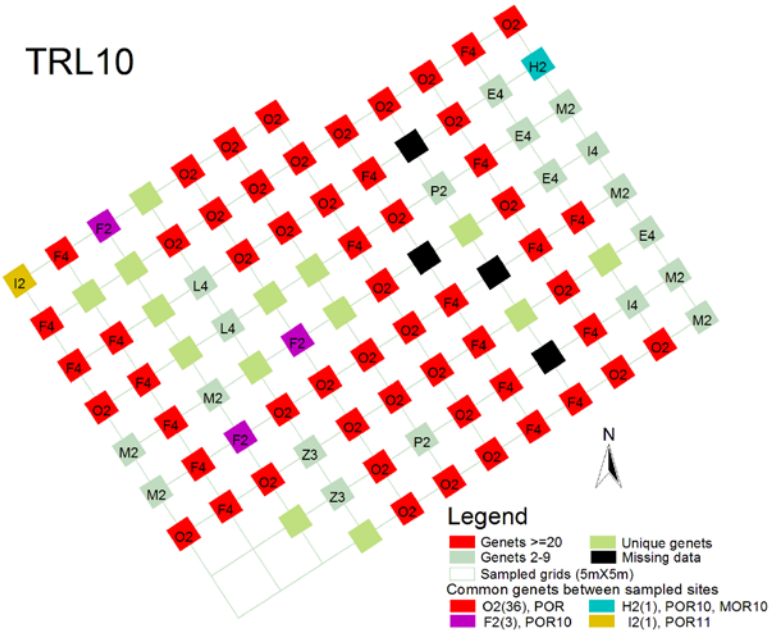
FIG. S3. Maps of clones in all patches. A common alphanumeric naming system is used throughout to allow identification of clones occurring in multiple patches. Genets are shown in boxes collared according to their frequency (red ≥20 occurrences; purple = 10-19; blue = 2-9; green = 1). Genets that were detected infrequently overall, but which occurred in multiple populations are uniquely colored (frequency listed in parentheses; see Table 2 in main text).



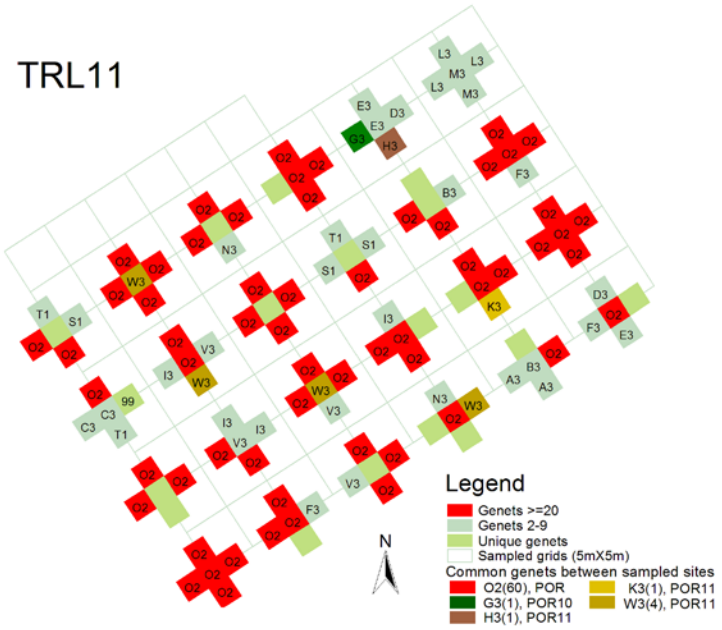

HDP10
T4
N4
T4
R4
R4
N
Legend
Genets >=20
Genets 2-9
Unique genets
Sampled grids (5mX5m)

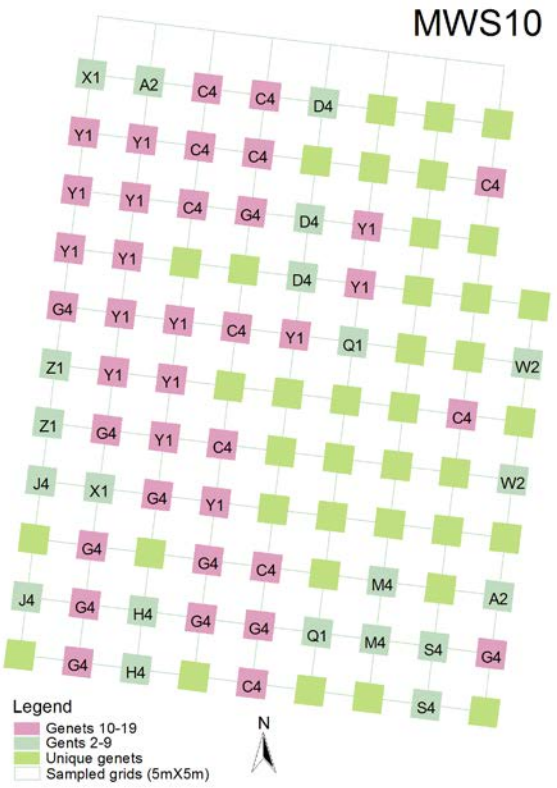

HDP11
A4
P4
P4
B4
B4
N4
A4
A4
N4
N4
B4
N
Legend
Genets >=20
Genets 2-9
Unique genets
Sampled grids (5mX5m)

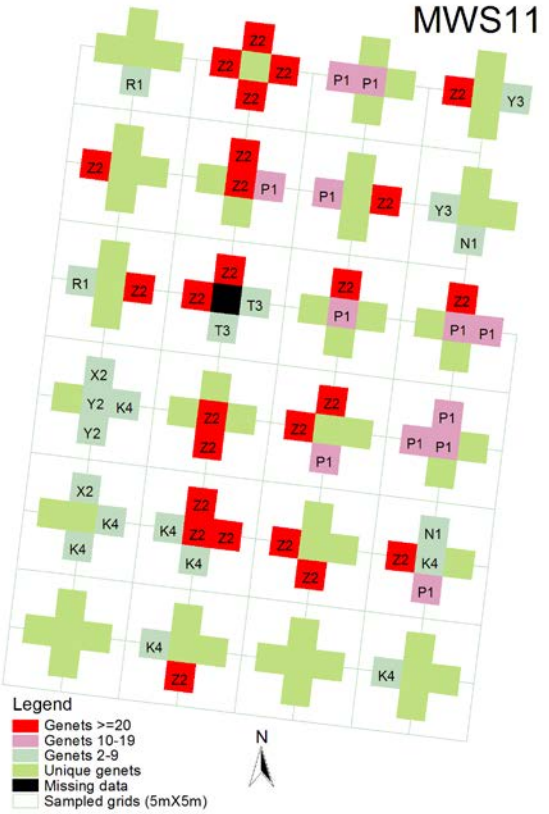
TRL10

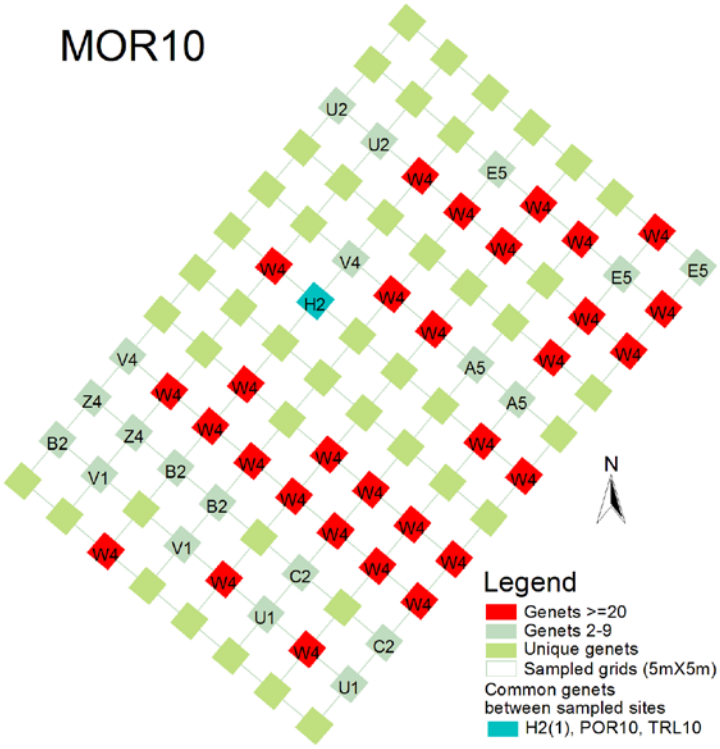

N
Legend
Genets >=20
Genets 2-9
Sampled grids (5mX5m)
Unique genets
Missing data
Common genets between sampled sites
O2(36), POR
F2(3), POR10
H2(1), POR10, MOR10
I2(1), POR11

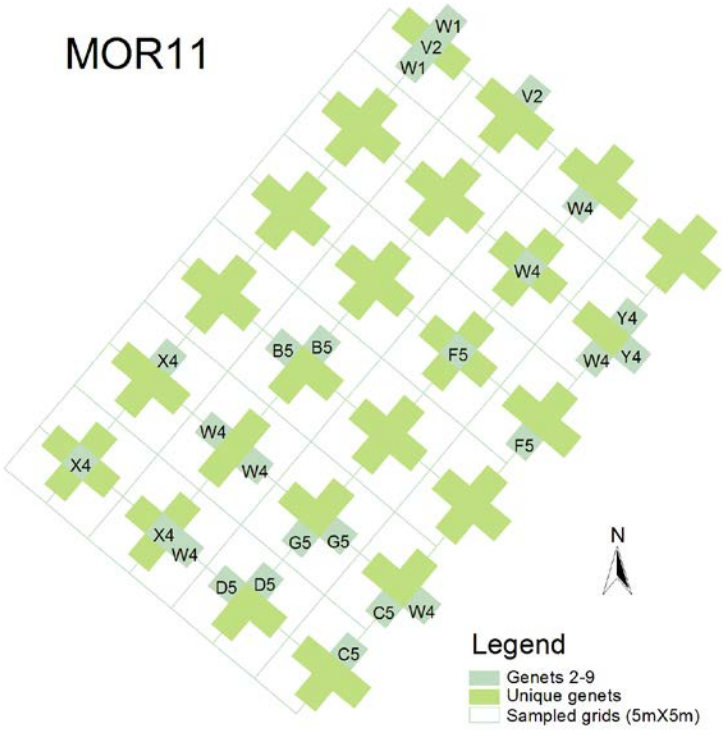
TRL11

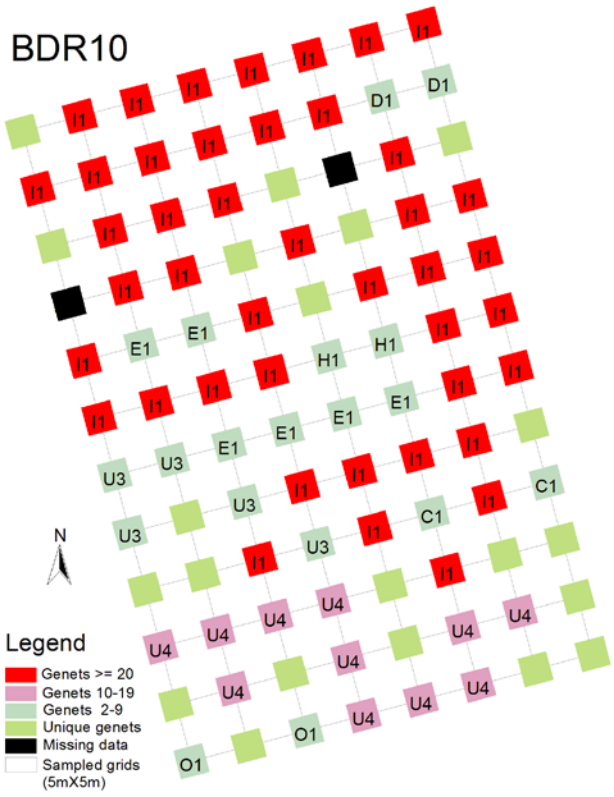

N
Legend
Genets >=20
Genets 2-9
Unique genets
Sampled grids (5mX5m)
Common genets between sampled sites
O2(60), POR
G3(1), POR10
H3(1), POR11
K3(1), POR11
W3(4), POR11

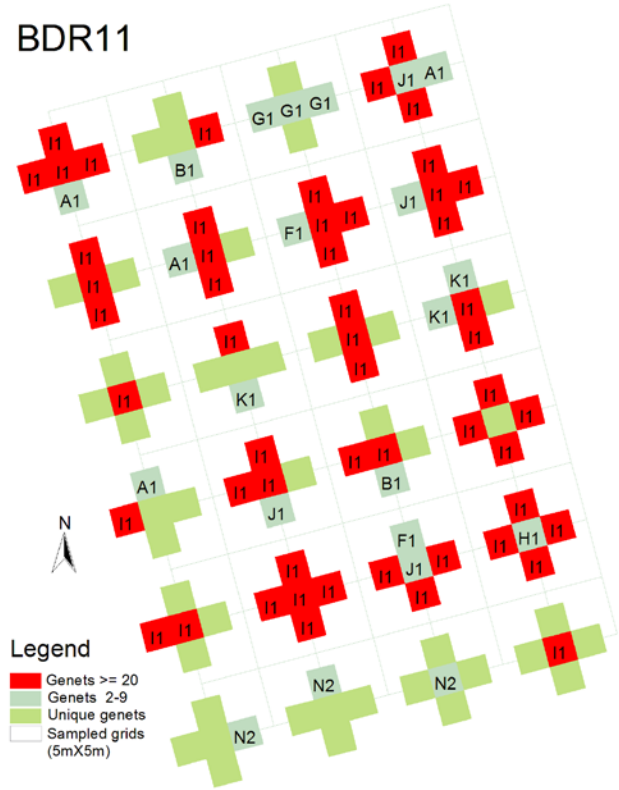

MWS10
X1 A2 C4 C4 D4
Y1 Y1 C4 C4
Y1 Y1 C4 G4 D4 Y1 C4
Y1 Y1 D4 Y1
G4 Y1 Y1 C4 Y1 Q1 W2
Z1 Y1 Y1 C4
Z1 G4 Y1 C4 W2
J4 X1 G4 Y1
G4 G4 C4 M4 A2
J4 G4 H4 G4 G4 Q1 M4 S4 G4
G4 H4 C4 S4
Legend
Genets 10-19
Gents 2-9
Unique genets
Sampled grids (5mX5m)
N


MWS11
R1 Z2 Z2 Z2 P1 P1 Z2 Y3
Z2 Z2 Z2 P1 P1 Z2 Y3 N1
R1 Z2 Z2 Z2 T3 T3 Z2 P1 Z2 P1 P1
X2 Y2 K4 Y2 Z2 Z2 Z2 Z2 P1 P1 P1 P1
X2 K4 K4 K4 Z2 Z2 Z2 Z2 Z2 N1 Z2 K4 P1
K4 Z2 K4
Legend
Genets >=20
Genets 10-19
Genets 2-9
Unique genets
Missing data
Sampled grids (5mX5m)
N


MOR10
U2
U2
E5
V4
E5
E5
H2
V4
A5
Z4
A5
Z4
B2
B2
V1
B2
V1
C2
U1
C2
U1
N
Legend
Genets >=20
Genets 2-9
Unique genets
Sampled grids (5mX5m)
Common genets
between sampled sites
H2(1), POR10, TRL10


MOR11
W1
V2
W1
V2
W4
W4
Y4
B5
B5
F5
W4
Y4
X4
W4
F5
X4
W4
X4
G5
G5
W4
D5
D5
C5
W4
C5
N
Legend
Genets 2-9
Unique genets
Sampled grids (5mX5m)


BDR10
N
Legend
Genets >= 20
Genets 10-19
Genets 2-9
Unique genets
Missing data
Sampled grids
(5mX5m)


BDR11
N
Legend
Genets >= 20
Genets 2-9
Unique genets
Sampled grids
(5mX5m)