

APPENDICES

Appendix 1: Unique aphid clonal lineages were identified using six published microsatellite markers (Sloane *et al.*, 2001; Wilson *et al.*, 2004) and PCR methods were modified from these studies. Three individuals from each isofemale colony were genotyped separately. One microsatellite primer from each pair was 5' labeled with fluorescent dyes. Loci with overlapping lengths were labeled with dyes of different wavelengths (loci-dye: myz2-6FAM, myz3-6FAM, M40-6FAM, M86-HEX [Sigma-Aldrich], M49-PET [Applied Biosystems], and myz9-HEX [Invitrogen]). All six microsatellite were composed of dinucleotide repeats. DNA from a single aphid was extracted using 5% Chelex 100 resin (Bio-Rad) and incubated for 35min at 56°C and for 15min at 95°C. Samples were then centrifuged at 12000rpm for 2min and the supernatant retained. PCR reactions were 10µL in volume that included 0.6 units of *Taq* polymerase (New England Biolabs), 1µL of 10x Mg-free standard reaction buffer, 0.2mM dNTP, 1µM of forward and reverse primer, 1.5mM MgCl₂, and 0.8µL of DNA extract. Touchdown PCR was used to amplify these loci. Two different PCR cycling programs were used that follow those of Sloane *et al.* (2001) except that one additional amplification cycle was added to the last annealing temperature. Loci myz2, myz9, M40, and M86 used PCR program PMS1 and myz3 and M49 used PMS2. The lengths of PCR products were determined using an ABI 3100 Genetic Analyzer, using the GeneScan 500 LIZ size standard, and *GeneMapper* software (Applied Biosystems).

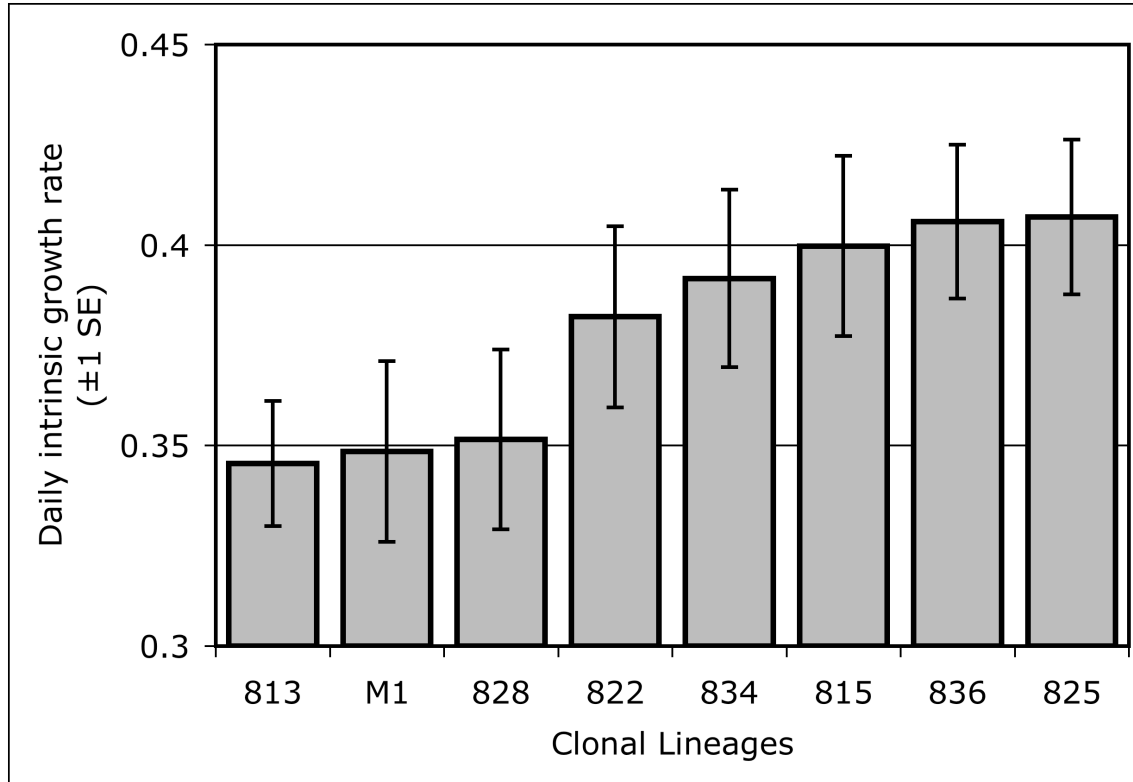
Appendix 2: The multilocus microsatellite genotypes of the 10 clonal *M. persicae* lineages collected at the Motte-Rimrock Reserve. Numbers represent the length of each allele at each locus. Unique clones have alleles of unique length or unique combinations of alleles. The total number of unique alleles and unique genotypes are listed for each locus.

Clonal Lineage	Microsatellite Loci					
	myz2	myz3	myz9	M40	M49	M86
813	188/202	119	203/209	125	156/171	98/135
815	186/196	115/121	195/207	121/125	201/203	110/112
820	162/186	105/115	207/209	125/131	166	117/133
822	186/198	117/119	195/223	121/131	138/156	123
825	186/198	117/ 119*	221/223	119/125	152/166	117/140*
828	186/188	117	195/209	121	154	135
831	186/188	117	195/209	119/121	154	117/135
834	174	117	195/223	121/133	138/ *	98/100
836	174/188	117	203	121/133	136/156	110/123
M1	172/186	113/119	207 / 238*	121/125	143/179	108/112
# Alleles	8	6	7	5	11	9 or 10
# Genotypes	8	5	8	8	8 or 9	10

* alleles where microsatellite lengths were inconsistent due to bad amplification.

Appendix 3: A preliminary experiment measured intrinsic growth rate in the aphid clonal lineages. Two of the ten lineages could not be tested due to contamination. On day 0 of the experiment each *H. incana* plant (the unit of replication) received 12 apterous third instar *M. persicae* from a single clonal lineage. Each clonal treatment was replicated three times. Population size was measured, by counting all aphids, on days 3, 6, 9, 12, and 23. Because it took longer than a full day to count all the aphids certain treatments were counted on day 13 and others on days 24 and 25. We tested for differences in growth rate by fitting an exponential growth model to the population dynamics observed on days 0 to 13 because after this day population growth declined. We fit a linear mixed-effect model (LME) with a linear exponential growth equation with a common intercept (mean density of aphids on day 0) across treatments. Thus the dependent variable was LN(x) transformed number of aphids, the fixed effect was aphid treatments and day (as the main covariate). Given that plants were repeatedly counted violating the assumption of independent observations we set unique plant identity as a random effect on population growth rate and used an autoregressive correlation error structure (Pinheiro & Bates, 2000). Increasing variance through time was modeled by using a variance function within the LME that increases with the power of the variance covariate (varPower). All analyses were implemented in R (v. 2.11.1; R Development Core Team, 2009) using the ‘nlme’ package (Pinheiro *et al.*, 2011).

Appendix 4: Daily intrinsic growth rates, from the preliminary experiment (Appendix 3) for the eight clonal lineages during population exponential growth in pure (single clone) populations. Significant variation was detected using a linear mixed-effect model.



Appendix 5: Planned contrast weight matrix used to test the *a priori* hypotheses comparing each evolution treatment to its corresponding no-evolution expectation that matched the initial clonal frequency.

Aphid Treatments	Hypothesis 1: A-B vs. Pure A and Pure B	Hypothesis 2: B-C vs. Pure B and Pure C	Hypothesis 3: A-C vs. Pure A and Pure C
Pure clone A	-0.25	0	-0.25
Pure clone B	-0.75	-0.25	0
Pure clone C	0	-0.75	-0.75
Evolution A-B	+1	0	0
Evolution B-C	0	+1	0
Evolution A-C	0	0	+1