

Supplementary Table 1. Data for individual females tested in insectary host preference tests. Data are the number of eggs laid on *Passiflora menispermifolia* and *P. vitifolia* during the course of the trial.

a) *Heliconius cydno*

Individual	<i>P. menispermifolia</i>	<i>P. vitifolia</i>
109	5	13
110	1	32
163	13	10
167	14	16
168a	11	3
c84	13	13
c94	7	11
1183	9	3
1084	1	17
c70	20	17
c72	25	24
c71	8	7
c99	8	3

b) *Heliconius melpomene*

Individual	<i>P. menispermifolia</i>	<i>P. vitifolia</i>
15	26	0
16	37	0
17	18	0
31	16	0
32	5	0
33	33	0
34	25	0
35	9	0
40	19	0
49	20	0
50	19	0
51	2	0
52	36	0
53	25	0
56	23	0
57	11	0
58	12	0
59	8	0
90	17	0
92	25	0
93	13	0
111	5	0

c) First generation hybrids

Individual	<i>P. menispermifolia</i>	<i>P. vitifolia</i>
4	16	3
5	28	2
7	0	0
10	19	0
11	23	11
20	19	15
21	0	0
116	50	0
126	9	0
132	13	0
134	3	0
155	2	0
205	0	0
206	3	0
210	3	0
215	0	0
220	0	0
229	0	0
232	0	0
a	26	0

d) Backcross to *H. melpomene*

Individual	<i>P. menispermifolia</i>	<i>P. vitifolia</i>
88	29	0
119a	52	0
124	19	0
125	21	0
136	18	0
168	16	0
175	24	0
183	10	0
228	49	0
236	18	0
240	31	0
248	20	0
251	20	0
283	19	0
290	0	0
291	0	0
300	31	0
349	22	0

e) Backcross to *H. cydno* (including brood and colour pattern genotypes)

Individual	Brood	<i>B</i> locus	<i>Yb</i> locus	<i>Ac</i> locus	<i>P. menispermifolia</i>	<i>P. vitifolia</i>
253	C10	<i>bb</i>	<i>YbYb</i>	<i>Acac</i>	0	0
254	C10	<i>bb</i>	NA	<i>acac</i>	0	0
255	C10	<i>Bb</i>	<i>YbYb</i>	<i>Acac</i>	0	0
263	C10	<i>bb</i>	<i>YbYb</i>	<i>Acac</i>	0	0
267	C8	<i>Bb</i>	<i>Ybyb</i>	<i>acac</i>	22	7
275	C8	<i>Bb</i>	<i>YbYb</i>	<i>acac</i>	18	11
286	C10	<i>bb</i>	<i>YbYb</i>	<i>Acac</i>	18	6
287	C8	<i>bb</i>	<i>Ybyb</i>	<i>acac</i>	24	5
293	C8	<i>bb</i>	NA	<i>Acac</i>	0	0
296	C11	<i>bb</i>	<i>Ybyb</i>	<i>Acac</i>	0	0
305	C8	<i>Bb</i>	<i>YbYb</i>	<i>Acac</i>	0	0
307	C14	<i>Bb</i>	<i>Ybyb</i>	<i>acac</i>	5	5
312	C8	<i>bb</i>	<i>YbYb</i>	<i>Acac</i>	0	0
314	C11	<i>bb</i>	<i>YbYb</i>	<i>Acac</i>	17	0
320	C8	<i>bb</i>	<i>YbYb</i>	<i>Acac</i>	14	0
321	C8	<i>Bb</i>	<i>Ybyb</i>	<i>acac</i>	8	2
323	C14	<i>Bb</i>	<i>YbYb</i>	<i>acac</i>	22	13
326	C8	<i>bb</i>	<i>Ybyb</i>	<i>Acac</i>	0	0
326a	C8	<i>Bb</i>	<i>Ybyb</i>	<i>acac</i>	25	14
330	C8	<i>Bb</i>	<i>YbYb</i>	<i>Acac</i>	0	0
374	C18	<i>bb</i>	<i>Ybyb</i>	<i>Acac</i>	5	4
375	C18	<i>Bb</i>	<i>Ybyb</i>	<i>acac</i>	23	15
376	C18	<i>bb</i>	<i>Ybyb</i>	<i>acac</i>	0	0
378	C8	<i>bb</i>	<i>Ybyb</i>	<i>Acac</i>	0	0
382	C8	<i>bb</i>	<i>YbYb</i>	<i>acac</i>	24	9
383	C8	<i>bb</i>	<i>YbYb</i>	<i>acac</i>	0	0
393	C18	<i>Bb</i>	<i>YbYb</i>	<i>acac</i>	0	0
397	C10	<i>bb</i>	<i>Ybyb</i>	<i>acac</i>	30	4
411	C10	<i>Bb</i>	<i>YbYb</i>	<i>acac</i>	0	0
423	C10	<i>Bb</i>	<i>YbYb</i>	<i>Acac</i>	23	0
427	C18	<i>bb</i>	<i>Ybyb</i>	<i>Acac</i>	0	0
430	C18	<i>bb</i>	<i>YbYb</i>	<i>Acac</i>	0	0
444	C18	<i>bb</i>	NA	<i>Acac</i>	0	0
454	C18	<i>bb</i>	<i>Ybyb</i>	<i>acac</i>	0	0
465	C18	<i>bb</i>	<i>Ybyb</i>	<i>acac</i>	21	0
456	C18	<i>bb</i>	<i>YbYb</i>	<i>Acac</i>	0	0
471	C10	<i>bb</i>	<i>YbYb</i>	<i>acac</i>	0	0
481	C18	<i>Bb</i>	<i>YbYb</i>	<i>Acac</i>	0	0
484	C18	<i>Bb</i>	<i>Ybyb</i>	<i>Acac</i>	27	0
487	C21	<i>Bb</i>	<i>YbYb</i>	<i>acac</i>	9	1
542	C24	<i>Bb</i>	<i>Ybyb</i>	<i>acac</i>	21	0
2012_166	E2	<i>Bb</i>	<i>YbYb</i>	<i>acac</i>	0	0
2012_182	E4	<i>bb</i>	<i>Ybyb</i>	<i>Acac</i>	0	0
2012_201	E5	<i>Bb</i>	<i>YbYb</i>	<i>Acac</i>	0	0
2013_596	H5	<i>bb</i>	<i>YbYb</i>	<i>Acac</i>	30	9
2013_607	H5	<i>Bb</i>	<i>YbYb</i>	<i>Acac</i>	5	2

Supplementary figure 1. The phenotypes of *Heliconius melpomene* (left), *H. cydno* (right), and a heterozygote (middle) at the loci studied here: i) red forewing band *B* locus, ii) the anterior part of the white forewing hourglass *Ac* locus, iii) the yellow hindwing bar *Yb* locus. The *B* and *Ac* loci have dominant alleles in *H. melpomene*; heterozygotes can only be distinguished in the backcross to *H. cydno*. The *Yb* locus is partially dominant so that heterozygotes can be distinguished in both backcrosses. In each pair of wings the lower surface is shown to the left and the upper surface on the right. Colour pattern loci genotypes are shown below each butterfly.



Supplementary Figure 2. Inheritance of sex-linked (W and Z) and autosomal (A) alleles in the crosses used to explore host acceptance in *Heliconius cydno* and *H. melpomene*. White boxes represent alleles inherited from *H. cydno* and red boxes alleles from *H. melpomene*. Note that females are the heterogametic sex in the Lepidoptera.

