



MICROSATELLITE MARKERS FOR THE STUDY OF MIXED MATING IN *HIBISCUS APONEURUS* AND *H. FLAVIFOLIUS* FROM KENYA

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ABSTRACT

In a mixed mating system, plants use both self- and cross-pollination to produce seeds. Observations of pollinator behavior from populations of two Kenyan *Hibiscus* species suggest that *H. aponeurus* uses self-pollination at higher rates than does the co-occurring *H. flavifolius*. To begin testing this hypothesis, we sought to develop a suite of variable genetic loci to use in measuring levels of selfing and outcrossing in natural populations. We tested five microsatellite primer pairs from each of four *Hibiscus* species for amplification in *H. aponeurus* and *H. flavifolius*. Eight loci were subsequently tested for genetic variation, but were found to be monomorphic in both species. Gene sequencing suggested that evolutionary changes within these loci could account for the lack of inter-individual variation.

BACKGROUND

Hibiscus aponeurus and *H. flavifolius* are morphologically and ecologically similar species that co-occur in woody savannahs of Kenya. A field study of pollinator visitation indicated that the red-flowered *H. aponeurus* was visited only about half as often as the white-flowered *H. flavifolius* (Foutch et al. 2008). Controlled pollination experiments also showed that *H. aponeurus* more often used self-fertilization to produce seeds than did *H. flavifolius*. In both species, seeds can be produced by a process called delayed autonomous self-pollination, in which styles with unpollinated stigmas curve backwards towards the anthers throughout the day. If the stigmas are pollinated during the curving process, the styles will stop curving, eventually causing the stigmas to touch the pollen on the anthers and effect self-pollination. This mechanism assures that a plant will produce at least some seeds, even when pollinator visits are few. Thus, the more a plant is visited by pollinators, the less it will self-pollinate.

QUESTION & HYPOTHESES

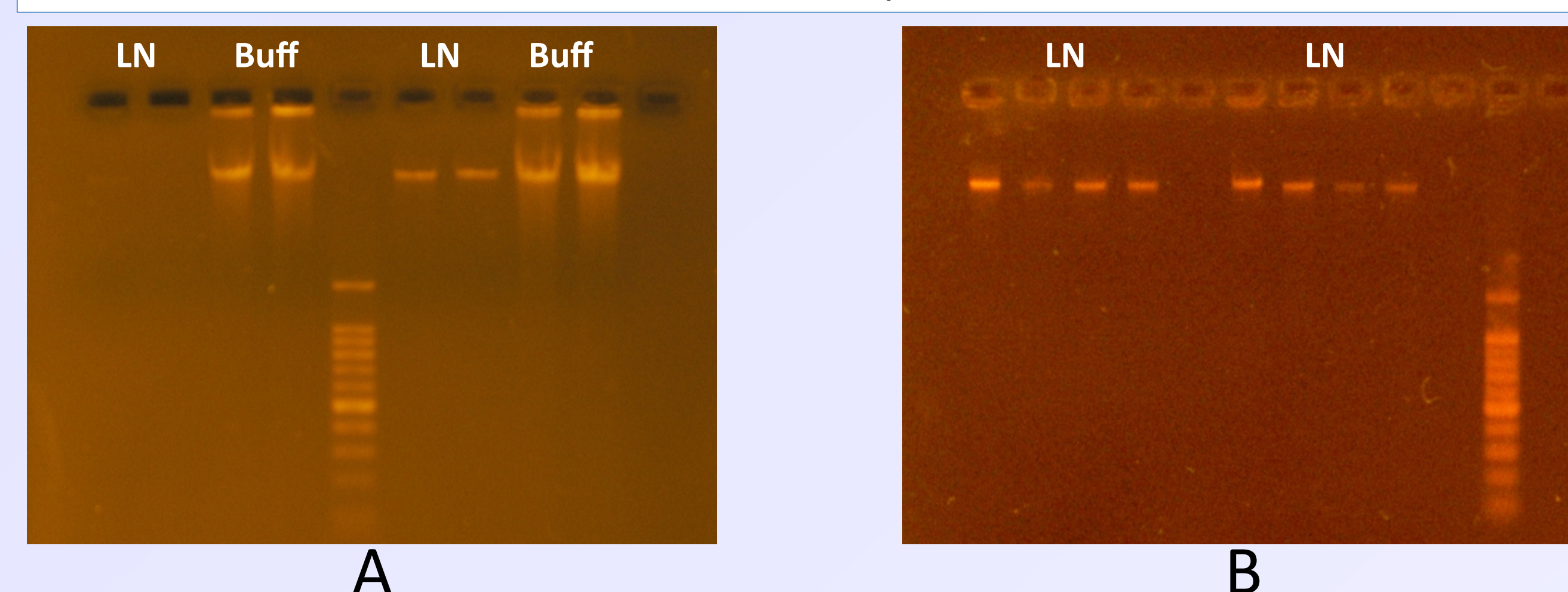
What are the levels of selfing in natural populations of *H. aponeurus* and *H. flavifolius*?

- Because the flowers of both species have been shown to use autonomous self-pollination in the field when pollinators don't visit, the populations should have a mating system that includes a mix of seeds produced by selfing and outcrossing.
- Because *H. aponeurus* is visited less often by pollinators, it will more often use delayed selfing to produce seeds and will therefore show a higher selfing rate than *H. flavifolius*.

Objective 1:

Extract clean DNA from *H. aponeurus* and *H. flavifolius*

Figure 1. Results of DNA extractions (Qiagen DNAeasy plant mini kit) from 8 seedlings each of *H. aponeurus* (A) and *H. flavifolius* (B). LN = seedlings were ground in liquid N₂ prior to adding tissue to lysis buffer; Buff = seedlings were ground directly in lysis buffer without aid of liquid N₂. In *H. aponeurus* (A), the LN method resulted in better quality DNA, while Buff method resulted in a greater quantity of DNA. During PCR, DNA extracted with both methods resulted in similar amplification of microsatellites.



Objective 2:

Choose and test the amplification of microsatellite loci from four other *Hibiscus* species.

Table 1. Number of loci (out of 5) that successfully amplified in *H. aponeurus* and *H. flavifolius*. We tested 20 microsatellite loci from four other *Hibiscus* species. A total of 11 loci successfully amplified in *H. aponeurus*, and 8 amplified in *H. flavifolius*. Only those loci that amplified with strong, single bands were considered for subsequent genotyping and sequencing.

Species for which primers were developed	<i>H. aponeurus</i>	<i>H. flavifolius</i>	Comments
<i>H. tiliaceus</i> Takayama et al. (2006)	5/5	2/5	Lots of non-specific amp.
<i>H. aridicola</i> Zhang et al. (2001)	4/5	4/5	Strong, single bands with good length
<i>H. rosa-sinensis</i> Bruna et al (2009)	2/5	2/5	Strong, single bands
<i>H. glaber</i> Ohtani et al (2008)	0/5	0/5	No amp. at any temperature

Figure 2. Variation in amplification success at different annealing temperatures in *H. aponeurus*. Microsatellites amplified better at 55°C than at 60°C. Primers from *H. aridicola* (HA primers) generally amplified well at the expected size, whereas primers from *H. tiliaceus* (Ht primers) showed a lot of non-specific amplification.

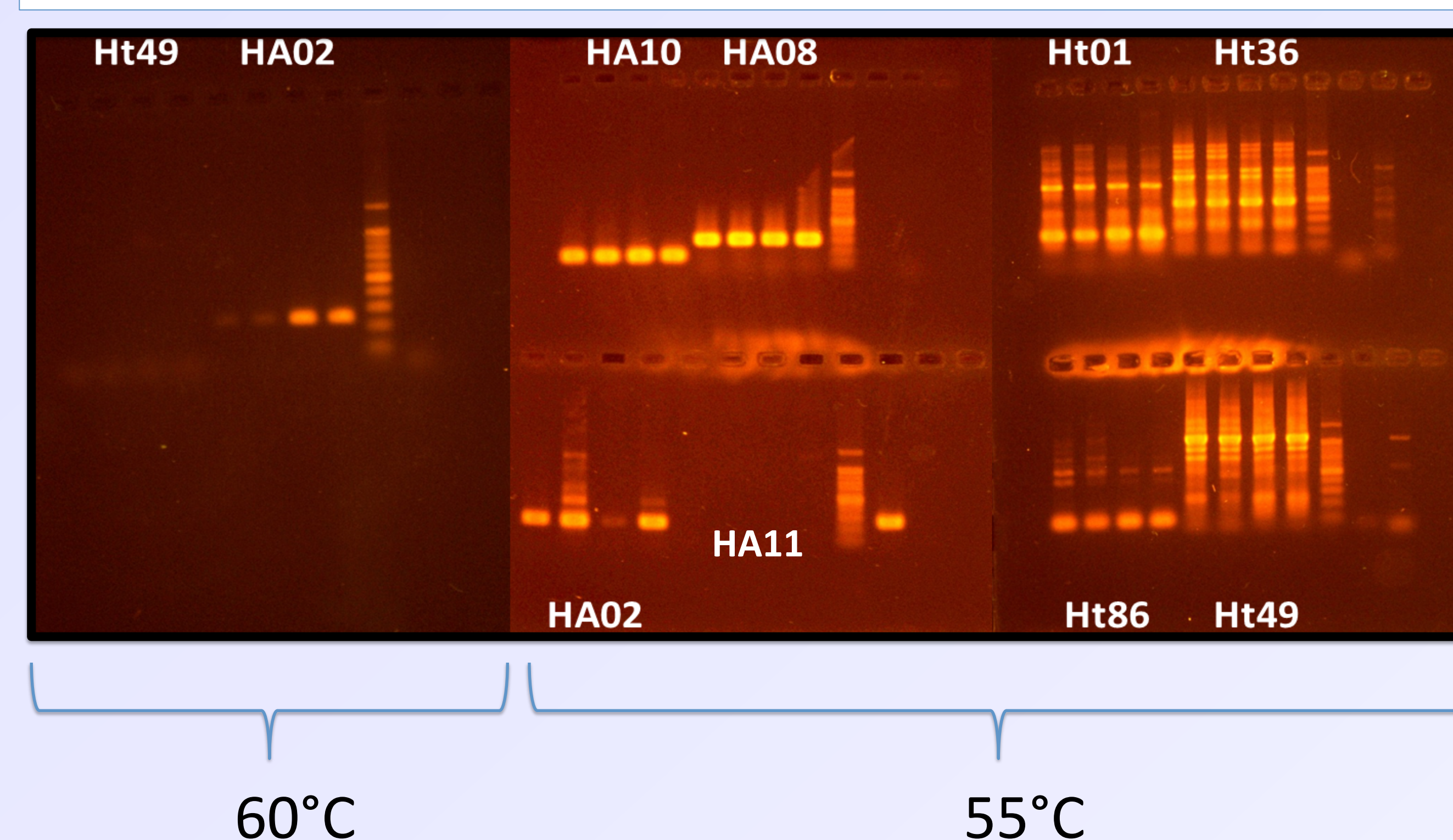
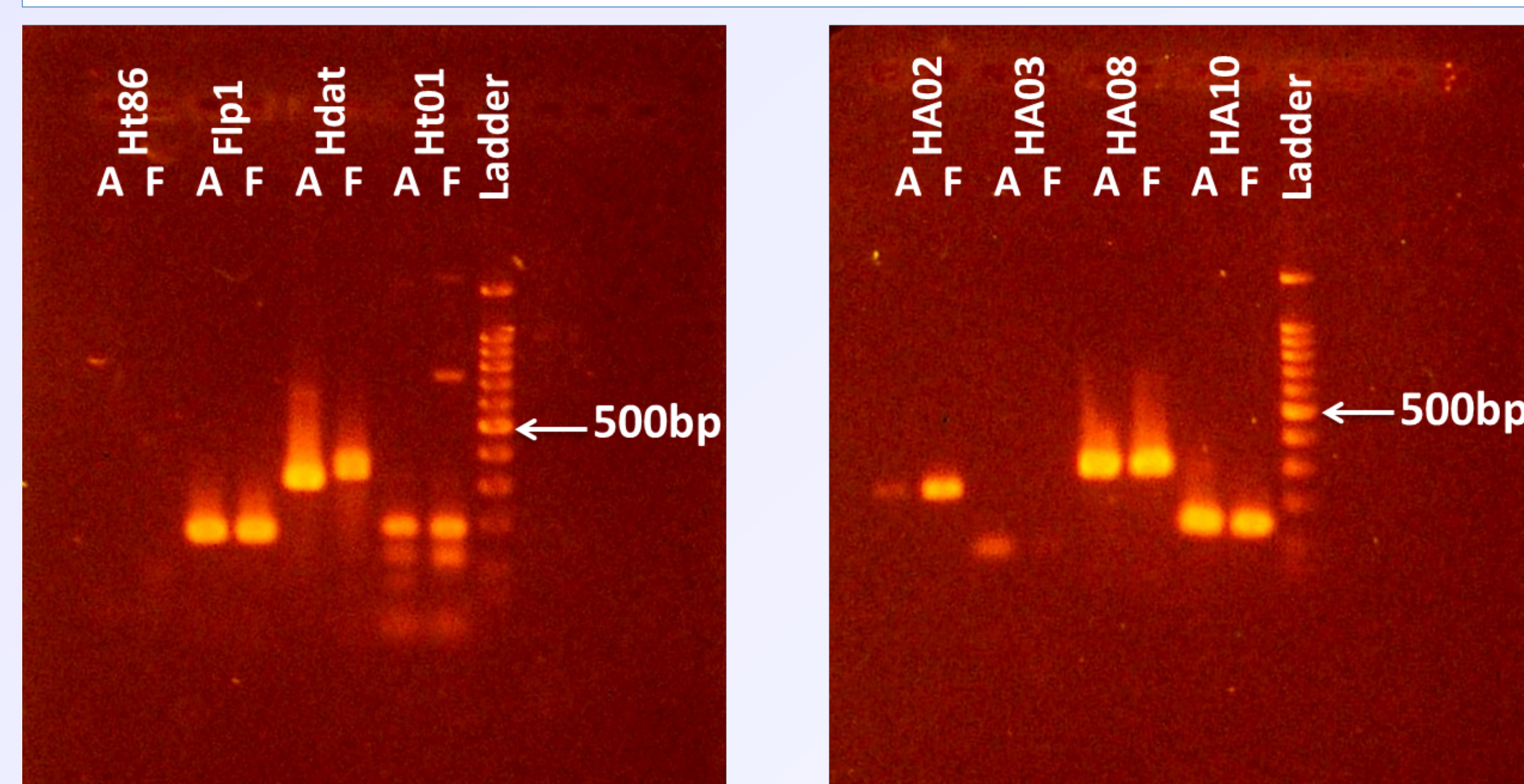


Figure 3. Amplification differences between *H. aponeurus* and *H. flavifolius* were evident. Amplification within the same locus in the two species differed in quantity and quality. There was also a difference in the amount of nonspecific amplification between the two species in the Ht01 microsatellite locus.



Objective 3:

Test microsatellite loci for levels of variation

Table 2. We chose 7 loci to test for levels of variability: 4 from *H. aridicola*, 1 from *H. tiliaceus*, and 2 from *H. rosa-sinensis*. Forward primers were fluorescently tagged, and amplification products were genotyped using an ABI 3130 genetic analyzer. We tested 12 individuals per locus per species and found no variation at any locus. At each locus, all individuals were homozygous for a single allele.

Locus	Repeat motif	Expected size (bp)	Primer sequences (5'-3')
HA-02	AG	410-445	F: CTGAATGCCAGAATGACT R: CAGGCCAAAGAGGAAGAT
HA-03	CT	141-154	F: ATCATTATCATCTTCGTTTC R: AAGGGACCAAAGTCTCAA
HA-08	CTTCT	230-242	F: CACTTCCACGAAGCTCTTAC R: GGAGATAAACAGAAAAGGGTA
HA-10	GT	197-204	F: CCCAAACCTCTATCATCT R: ATATCCCTTAGTTCTGCT
Ht-86	GA	94-99	F: GGACTTTTCTGTTTCTTTCTCGTAG R: ATGCTTTTCAGTTCTTGACAAATG
H-DAT2	TTA	400-480	F: TGTCAGCTGTCAAGGGTGA R: CCGATCCGTGTTTTTCAAGT
H-MAFLP1	CT	159-169	F: AGCCTGTCACCAACAAA R: GAGAGCTTACGAAGCGGAGA

Figure 4. Nucleotide sequence of H-dat2 microsatellite locus from *H. aponeurus* and *H. flavifolius* (primer sequences in green; variable sites in red). The locus length is ~100-150 bp shorter than expected, and there is no evidence of the TTA repeat motif (cf. Table 2). These results indicate that the locus has undergone extensive evolutionary change since the *H. flavifolius*/*H. aponeurus* lineage split from the *H. rosa-sinensis* lineage within the *Hibiscus* genus. They also help explain our finding of only a single allele within our populations. Similar results would be expected if we sequenced the 7 other loci that were also monomorphic.

<i>H. fl.</i>	TGTCAGCCT	GGCGAAGGGT	GAATTTCTTA	TTTCTTATTA	TTAATTTATT	GATTTCTTAT	60
<i>H. ap.</i>	TGTCAGCCT	GGCGAAGGGT	GAATTTCTTA	TTTCTTATTA	TTGATTTATT	GATTTCTTAT	60
<i>H. fl.</i>	TATTGAGTTT	ATATTATATA	TAATTTATAT	TAGATGTTAG	AATATTAATT	CTATTATATA	120
<i>H. ap.</i>	TATTGAGTTT	ATATTATATA	TAATTTATAT	TAGATGTTAG	AATATTAATT	CTATTATATA	120
<i>H. fl.</i>	TTTATATATT	CTAATATATA	TTCTAACTTA	TTTATATATT	TTATTTAGAA	TAATATAATT	180
<i>H. ap.</i>	TTTATATATT	CTAATATATA	TTCTAACTTA	TTT-----	-----	--ATATAATT	161
<i>H. fl.</i>	TTATTTAGAA	TATATCTAT	TTAAATTAAT	ATTTAATATT	ATTATTTTTT	ATATTCTTTT	240
<i>H. ap.</i>	TTATTTAGAA	TATATCTAT	TTAAATTAAT	ATTTAATATT	ATTATTTTTT	ATATTCTTTT	221
<i>H. fl.</i>	TATATCATT	ATTTTCATT	ATTTTCATTG	CAT			253
<i>H. ap.</i>	TATATCATT	ATTTTCATT	ATTTTCATTG	CATTTTCGATT	CAAAAAAAAA	GGAAGGAATT	281
<i>H. fl.</i>							
<i>H. ap.</i>	ATAAACTTGA	AAAACACGGA	TCGGA				306

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