a Phases of speciation and genomic differentiation

Pop. 1

Pop. 2

Early phase

Intermediate phase

Complete RI

Genomic differentiation

trajectory affected by many factors
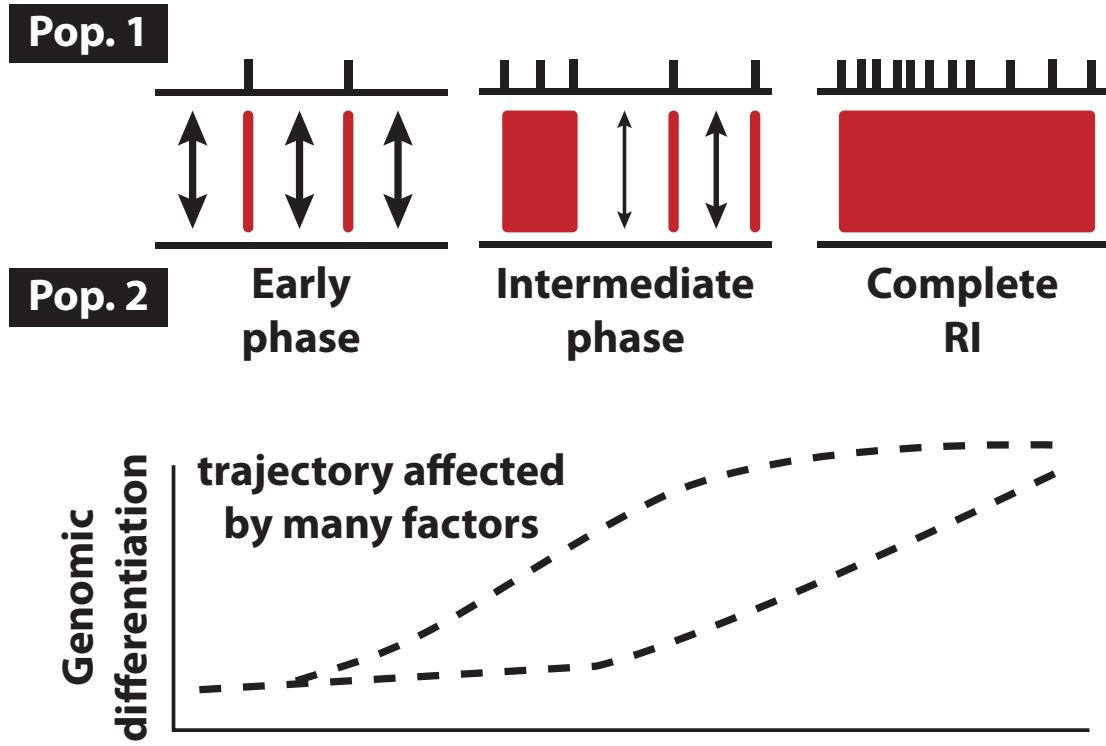
**b** Genomic differentiation in *Timema* stick-insects

Genomic differentiation

Genomic position
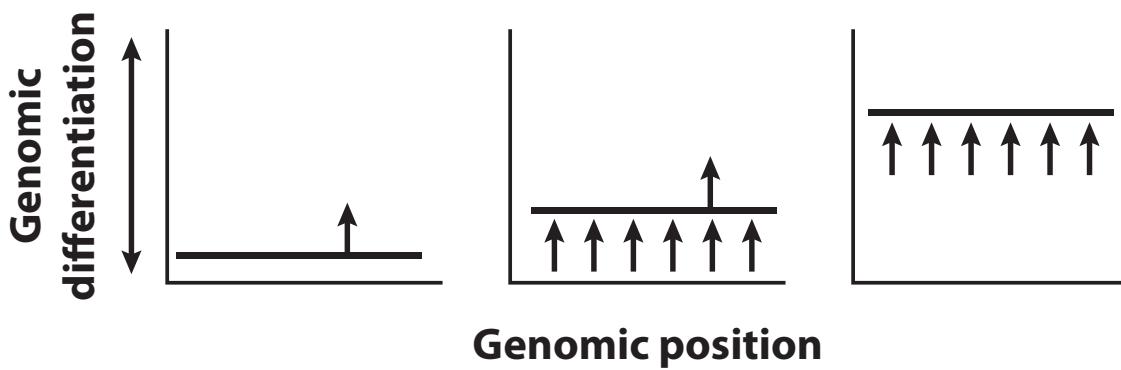
selection on colour-pattern loci

differentiation in mate choice / CHCs
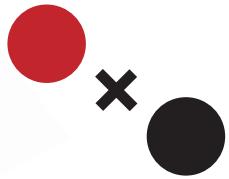
complete RI /spatial separation

a Ecotypes and host plants

Adenostoma

♂

Ceanothus

♂

b Hidden Markov Model analysis of heterogeneous genetic differentiation

HV *T. cristinae*

R12 *T. cristinae*

MR1 *T. cristinae*

LAPRC *T. cristinae*

F_{ST}
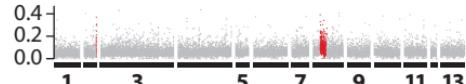
Genomic position (LG)

c Allele frequency cline

centre = 2.64 (2.57-2.70)
width = 1.79 (1.58-2.05)

Stripe allele frequency

Adenostoma
Ceanothus

Transect location (km)
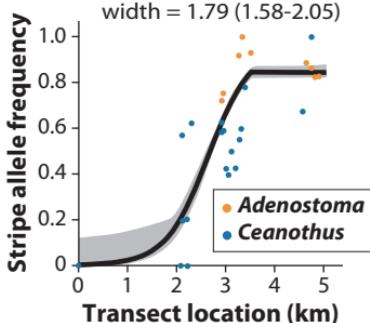
d Differentiation between experimental populations on different hosts

F_{ST}

Genomic position (LG)
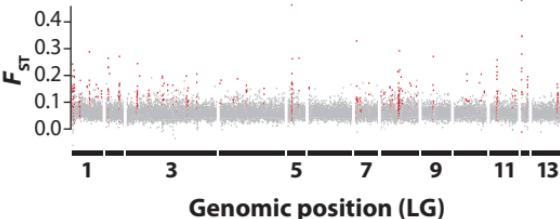
e Number of high F_{ST} windows and linkage group size

LG8

Number of high F_{ST} windows

Linkage group size
(number of 20 kb windows)
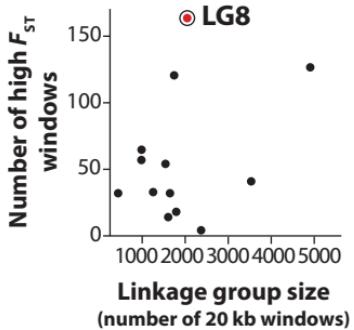
a **Perfuming experiments**

Cumulative successful copulation vs. Time to copulation (minutes)
- no perfume
- conspecific perfume
- heterospecific perfume
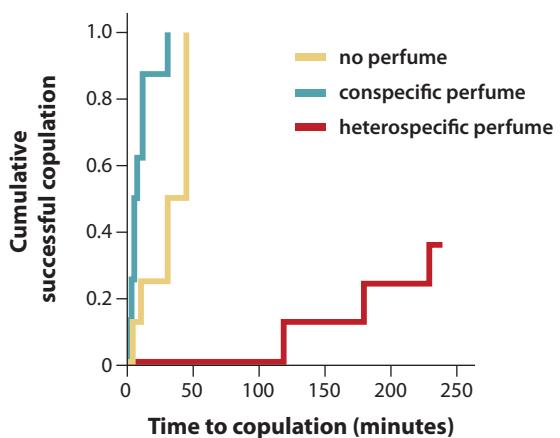
b **Profiles of methylated CHCs**

Pentacosanes | Heptacosanes | Nonacosanes

♀ *Adenostoma*

♀ *Ceanothus*

Response (pA) vs. Retention time (minutes)
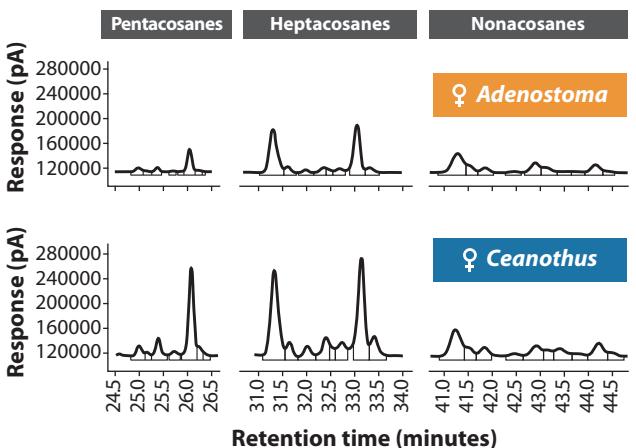
c **CHC differences between ecotypes and sexes**

Principal component 2 vs. Principal component 1
- Male *A*
- Male *C*
- Female *A*
- Female *C*
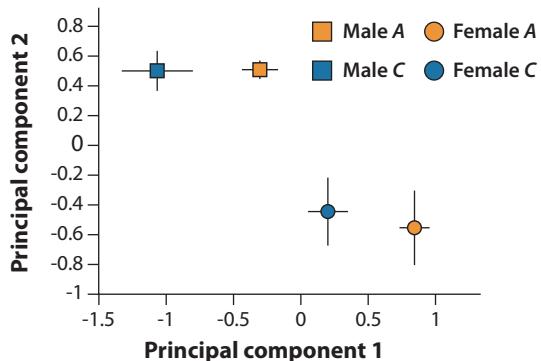
d **CHCs, sexual isolation (SI), and genomic differentiation (GD)**

Density vs. Effect of CHCs
- SI, F, pp > 0 = 0.97
- SI, M, pp > 0 = 0.38
- GD, F, pp > 0 = 0.99
- GD, M, pp > 0 = 0.24
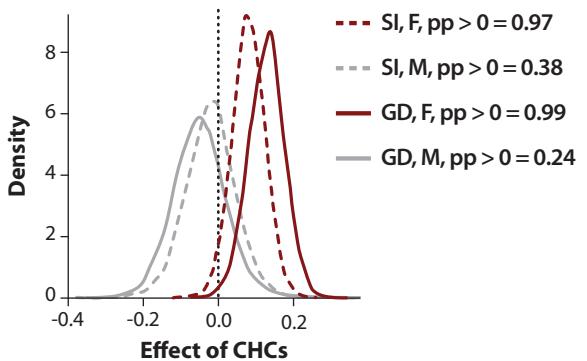
e **Hyper-parameter estimates of genetic architecture**

Median proportion variance explained (PVE) vs. Trait

0.58*** | 0.01 | 0.04** | 0.03* | 0.02** | 0.01* | 0.04***

% striped, fpenta, fhepta, fnona, mpenta, mhepta, mnona
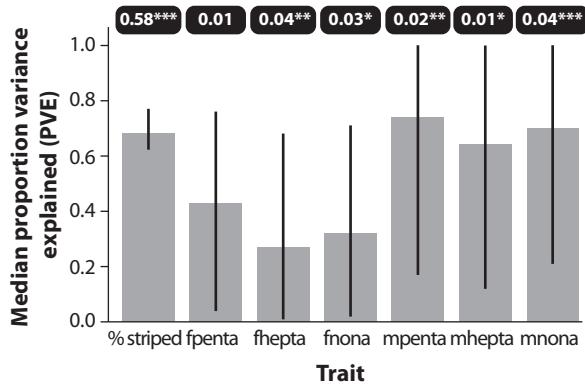
f **Number of trait-associated SNPs and linkage group size**
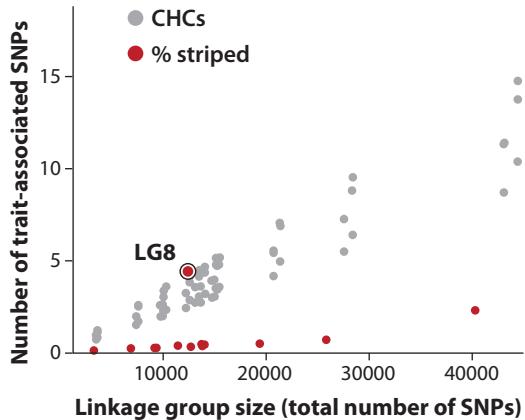
Number of trait-associated SNPs vs. Linkage group size (total number of SNPs)
- CHCs
- % striped

LG8

Hidden Markov Model analysis of heterogeneous genetic differentiation
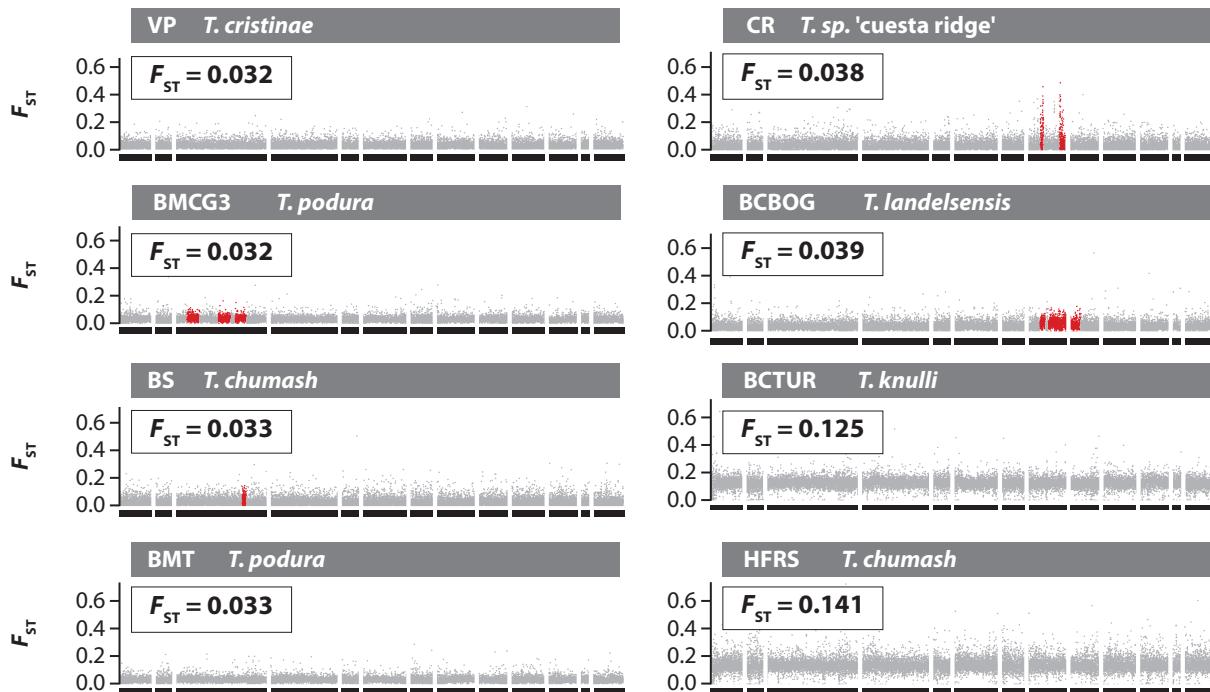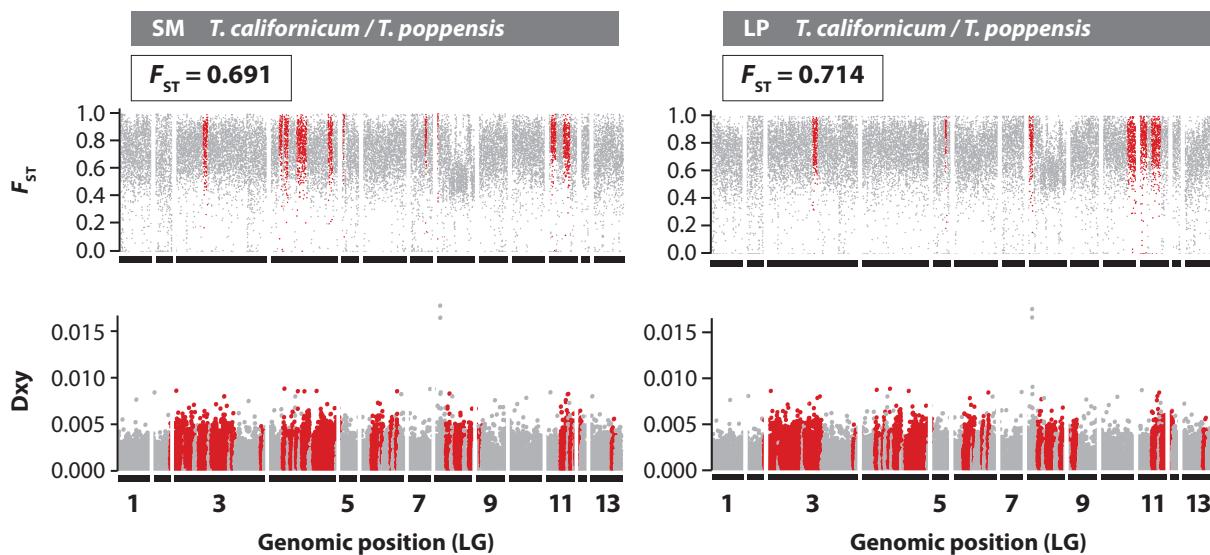
a A gap in genomic differentiation in sympatry in *Timema*

Mean F_{ST} vs. Rank of mean F_{ST}
- red: between species
- grey: within species
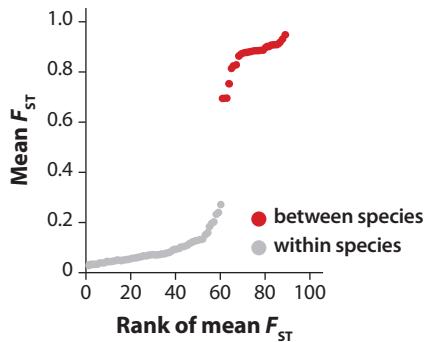
b Mean differentiation per species and species pair

Mean F_{ST} vs. Rank of mean F_{ST}

T. chumash - T. podura
T. californicum - T. poppensis
T. bartmani - T. podura

T. poppensis
T. californicum
T. cristinae
T. landelsensis
T. bartmani
T. chumash
T. sp. 'Cuesta ridge'
T. podura
T. knulli

c Genealogical sorting index

Density vs. Genealogical sorting index (GSI)
- red: species
- grey: conspecific host ecotypes within localities
- purple: geographic localities within species
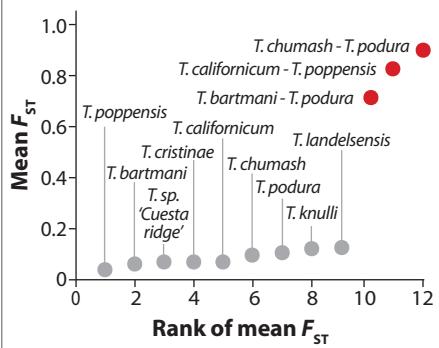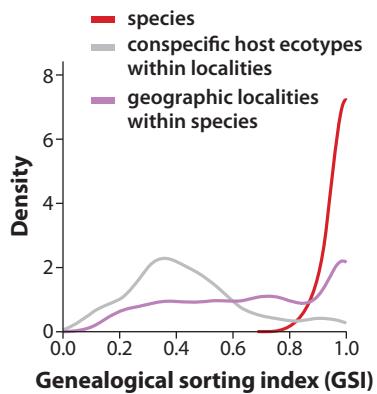
d Dated *Timema* phylogeny

Northern Clade
- SM
- FROCK
- TBARN
- LP
- MM — *T. poppensis*
- BCE
- BCTUR
- BCWP
- H1M37
- HB — *T. knulli*
- 101SS — *T. petita*
- SM
- LP
- LICK — *T. californicum*
- BCBOG
- BCOG
- BCHC
- BCSUM — *T. landelsensis*
- CR — *T. sp. 'Cuesta ridge'*

Santa Barbara Clade
- R23
- R9
- OUT
- VP
- ECCAMP
- BY — *T. cristinae*

Southern Clade
- BS
- BME
- BMT
- DZ243
- PF243
- BMLC
- BMCG3
- PCT8000ft
- PCTCR
- BMPCT
- BMOKC
- SRHWY — *T. podura*
- BMCG3
- PCT8000ft
- PCTCR
- BMPCT
- BMP90
- JL — *T. bartmani*
- SRTH — *T. boharti*
- HFRBP
- HF6
- HF4
- HFRS
- HFTP
- GR806
- GR603
- GR104
- BALD
- BMT
- BS
- PF243
- DZ243 — *T. chumash*

Millions of years (Ma): 50 40 30 20 10 0

a Sexual isolation within and between species

■ among populations ■ among species

Frequency

I_{PSI} (sexual isolation)
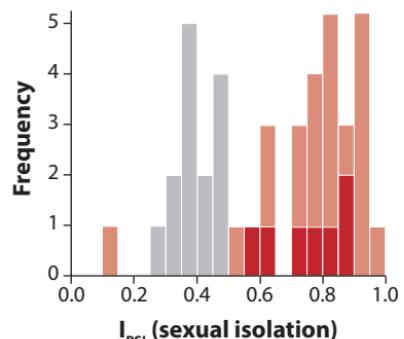
b Morphological differentiation within and between species (males)

Frequency

Morphological distance (males)
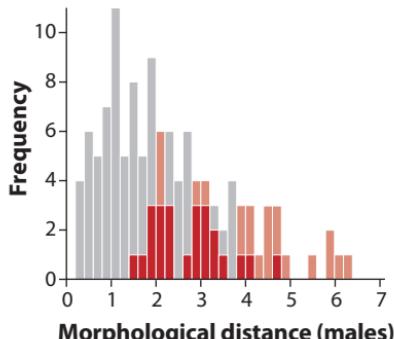
c Morphological differentiation within and between species (females)

Frequency

Morphological distance (females)
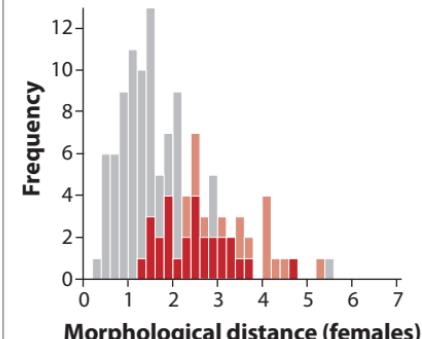
d Sexual isolation against time

$r^2 = 0.23$

I_{PSI} (sexual isolation)

Divergence time (Ma)
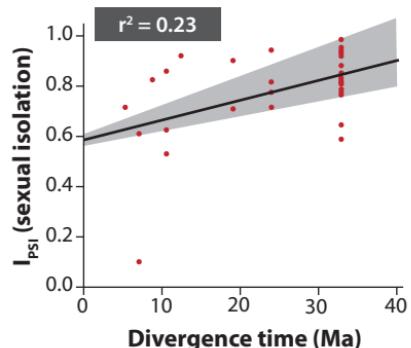
e Morphological differentiation against time (males)

$r^2 = 0.18$

Morphological distance (males)

Divergence time (Ma)
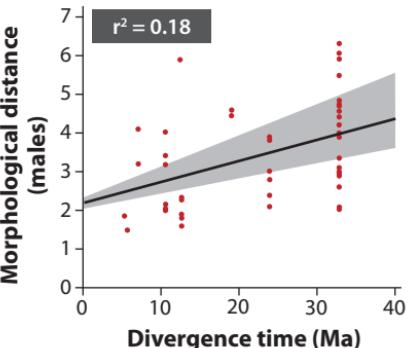
f Morphological differentiation against time (females)

$r^2 = 0.06$

Morphological distance (females)

Divergence time (Ma)