

Detection of the genomic signature of selection

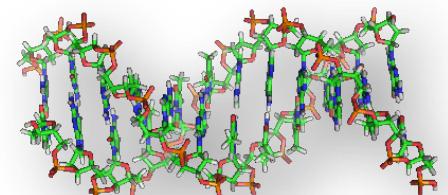
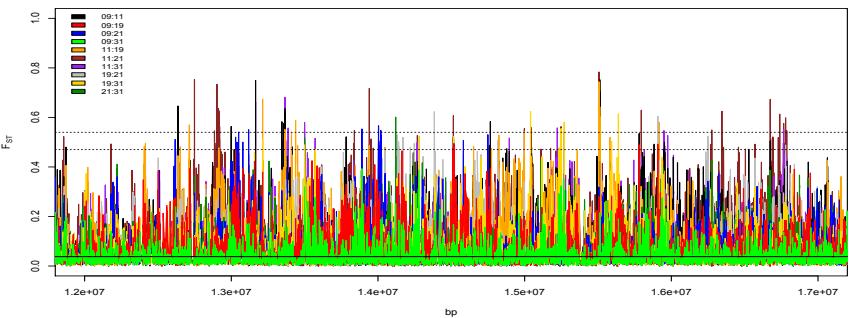
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May 17th, 2017



Diversity and adaptation



Why is there so much variation among and within species?



How do organisms adapt to their environment?

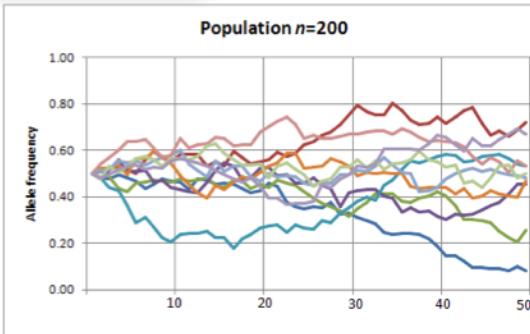


Genetic diversity

- Evolutionary changes at the molecular level are caused by...

Neutral processes

- Mutations



- Genetic drift



- Population history

Mutations

- ❖ Small scale:

- Point mutations (SNPs)
- Deletions
- Insertions

- ❖ Large scale:

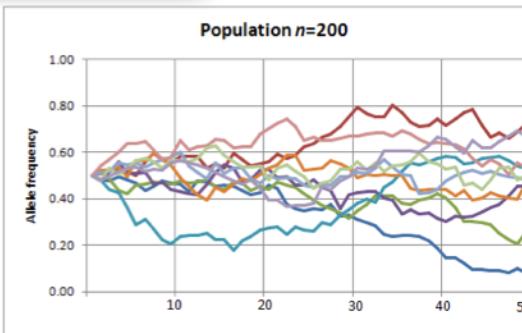
- Copy number variation
- Translocations
- Inversions

Genetic diversity

- Evolutionary changes at the molecular level are caused by...

Neutral processes

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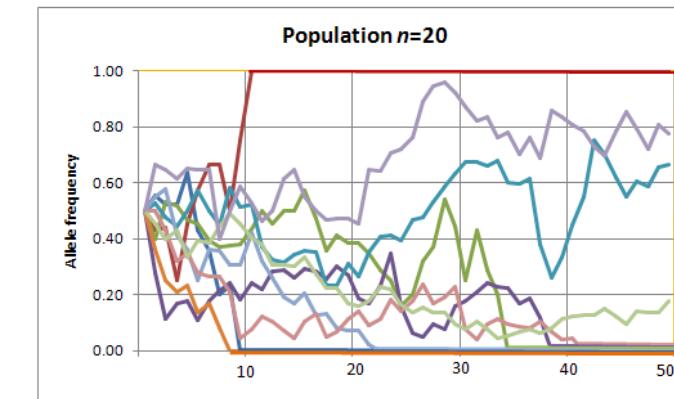
- Genetic drift



- Population history

Genetic drift

- ❖ Change of allele frequencies over generations in a population due to random sampling
- ❖ Population size: Drift is largest in small populations

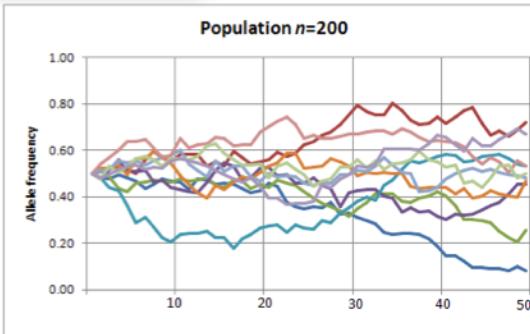


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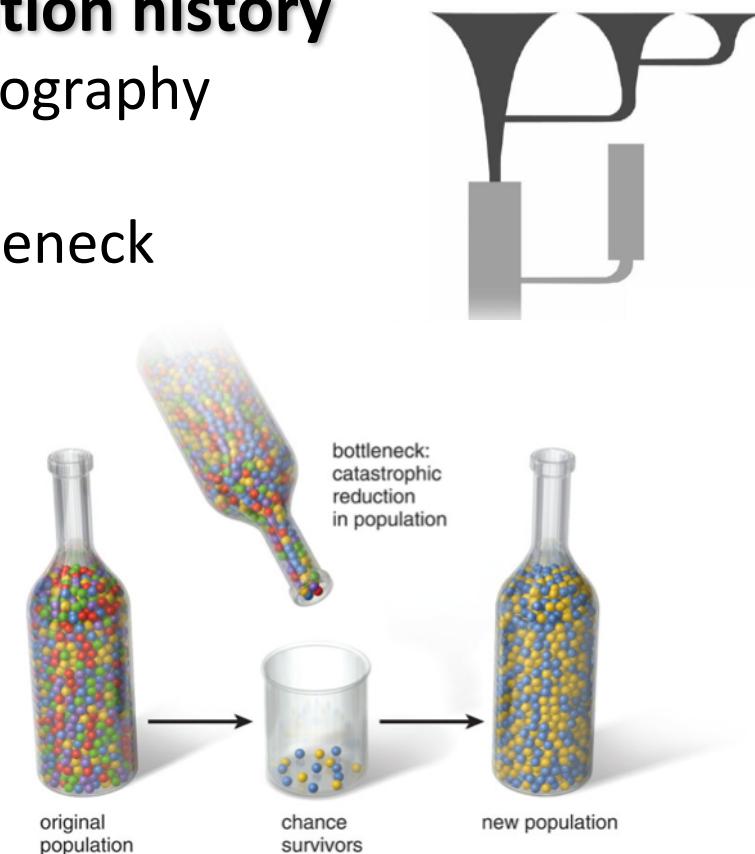


- Population history

Population history

- ❖ Demography

- ❖ Bottleneck

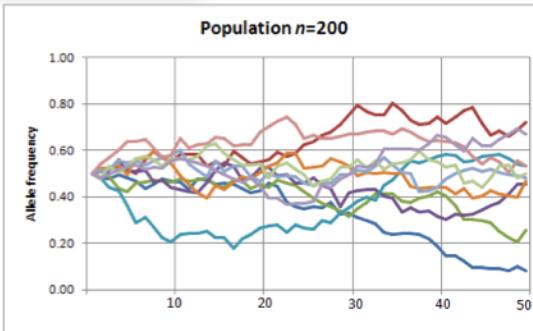


Genetic diversity

- Evolutionary changes at the molecular level are caused by...

Neutral processes

- Mutations



- Genetic drift



- Population history

Natural selection

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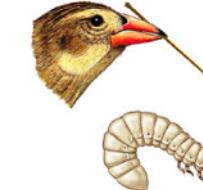
Large ground finch (seeds)



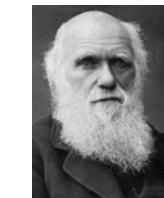
Cactus ground finch (cactus fruits and flowers)



Vegetarian finch (buds)



Woodpecker finch (insects)



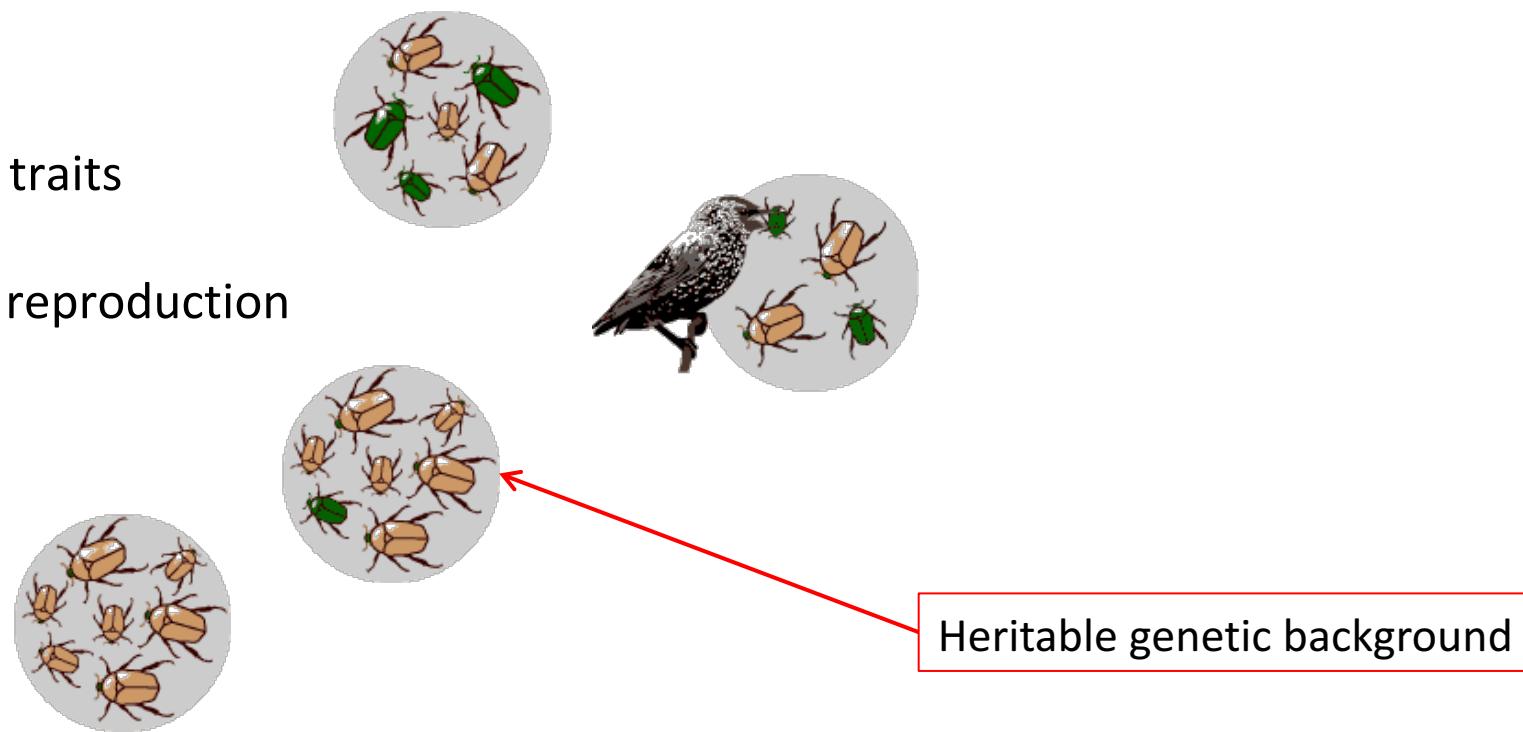
Darwin's Finches

Natural selection

Natural selection is one of the basic mechanisms of evolution

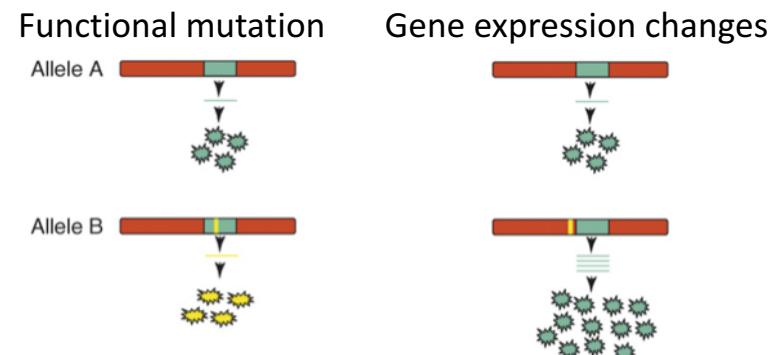
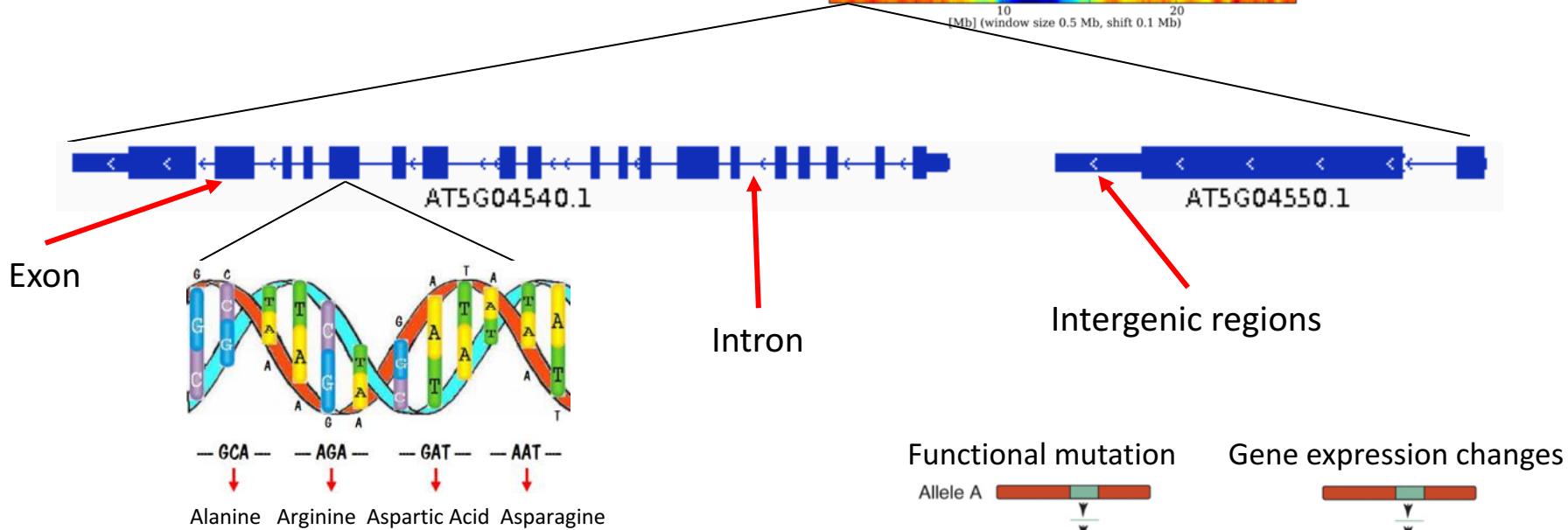
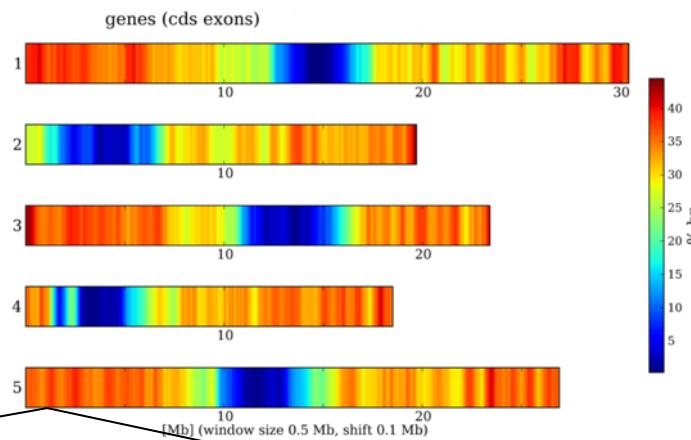
Population of beetles:

1. There is variation in traits
2. There is differential reproduction
3. There is heredity
4. End result



The genome and where selection acts

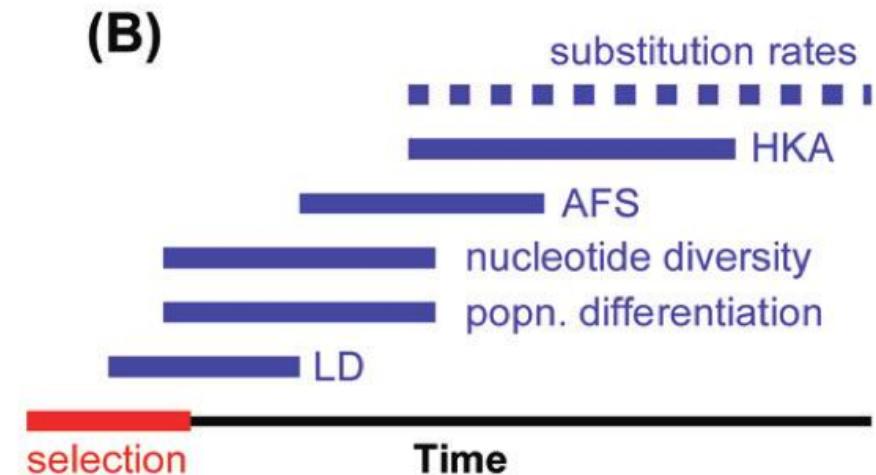
	Human	<i>A. thaliana</i>
Genome	3.165 Gb	0.157 Gb
Chromosomes	22, XY	5
Chr length	50-250 Mb	20-34 Mb
Genes	~25,000	~28,000



The genomic signature of selection

Different signals of selection:

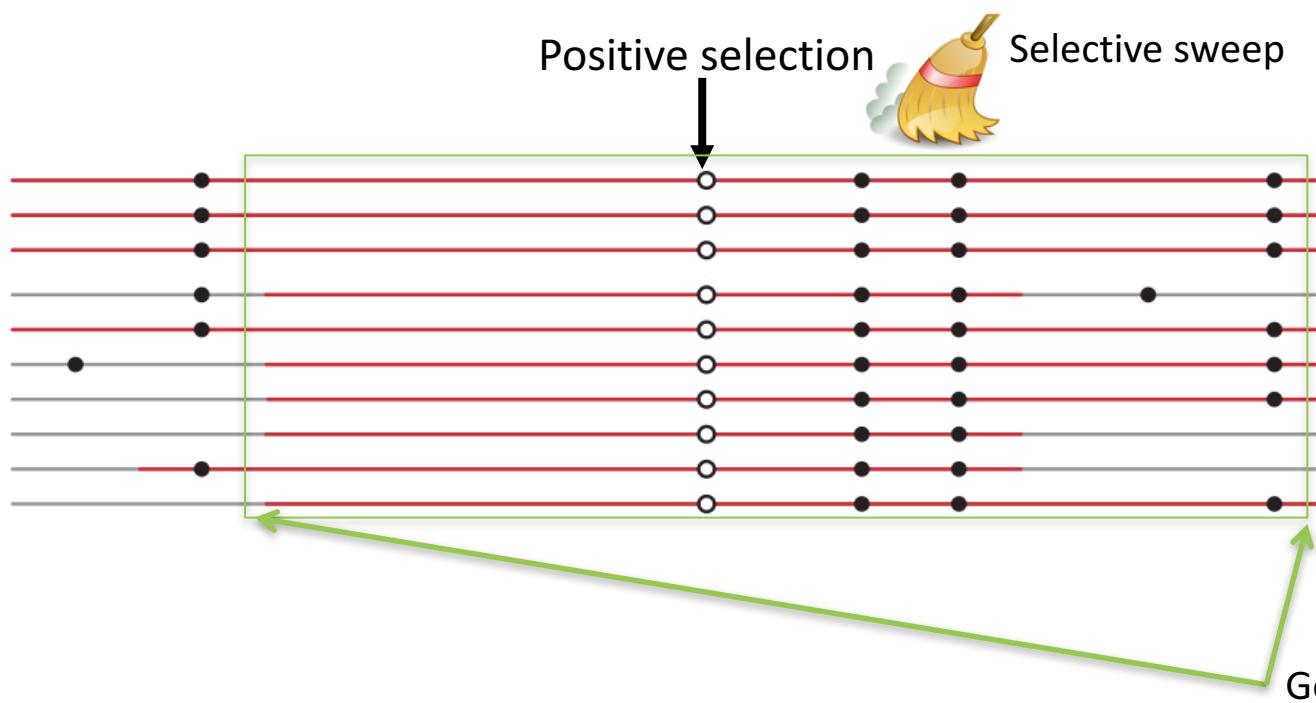
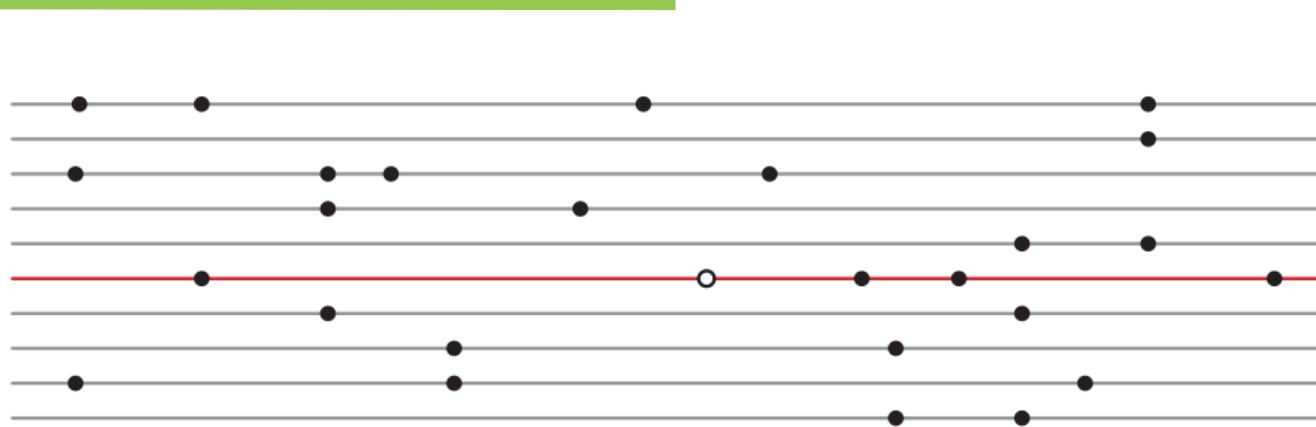
- ✧ Linkage disequilibrium (*LD*)
- ✧ Locus specific population differentiation (F_{ST} -outlier approach)
- ✧ Environmental driven locus specific signal (EAA)
- ✧ Reduced level of genetic variation (e.g. π)
- ✧ Skew of allele frequency spectra (Tajima's *D*)
- ✧ Substitution rates (e.g. dN/dS)



Comparison:

- ✧ Within a population
- ✧ Among populations
- ✧ Among species

Selective sweeps



Selective sweep:

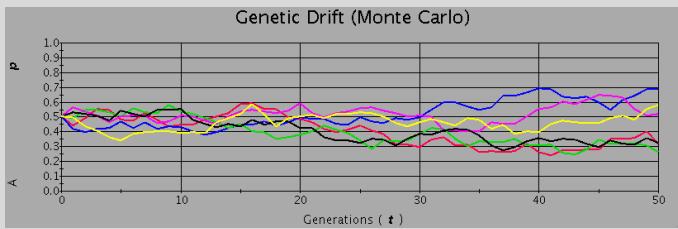
- An allele that increases fitness arises and 'sweeps' to fixation in a population

- Recombination
- Linkage disequilibrium
- Long haplotypes
- Hitchhiking

Locus under selection behaves differently

Neutral processes:

- ❖ Genetic drift
- ❖ Demographic history
- Affect all loci similarly



Selection:

- Affect only single locus

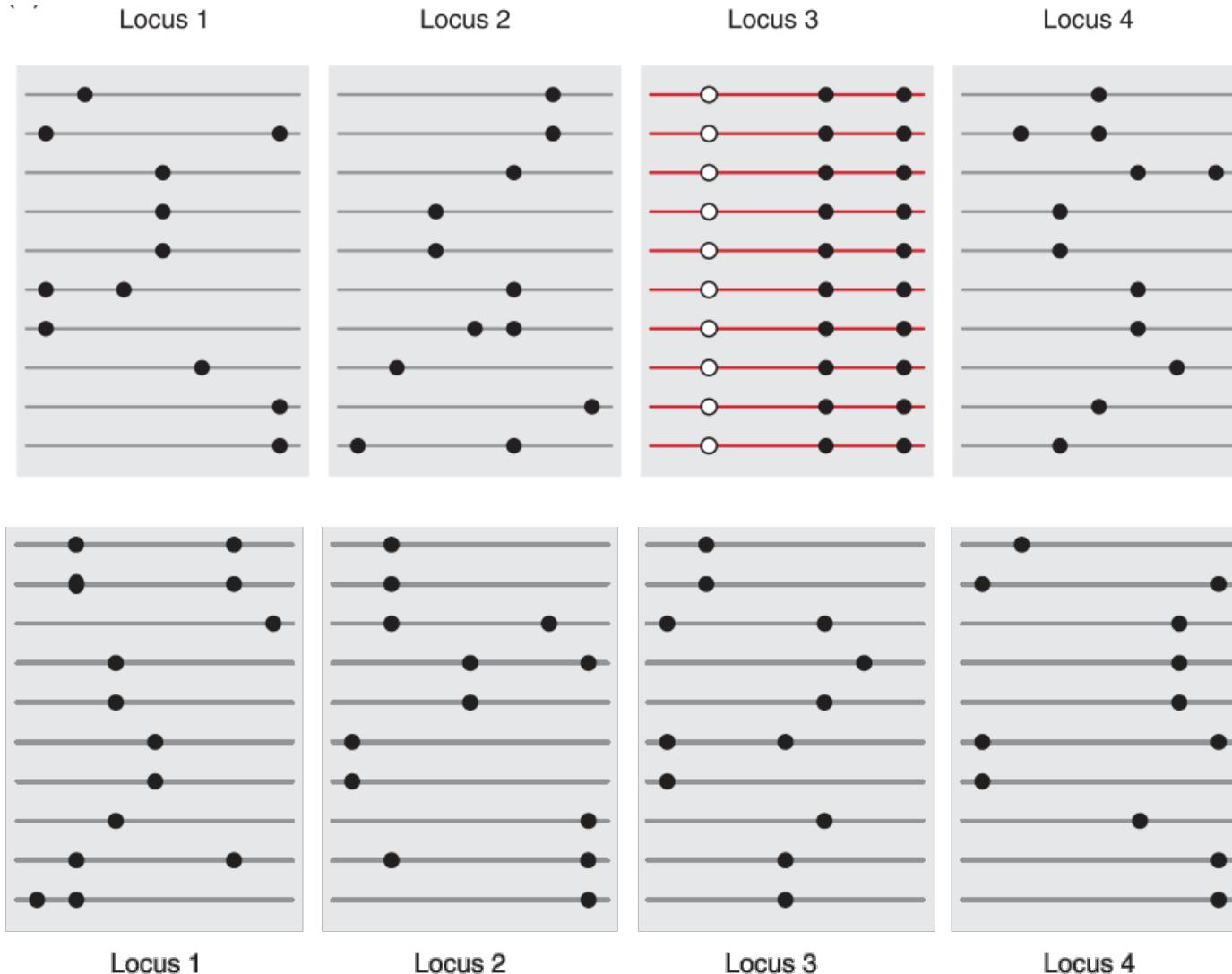


- Outlier detection



Outlier compared to the rest of the genome

Selective sweeps



Single locus is affected

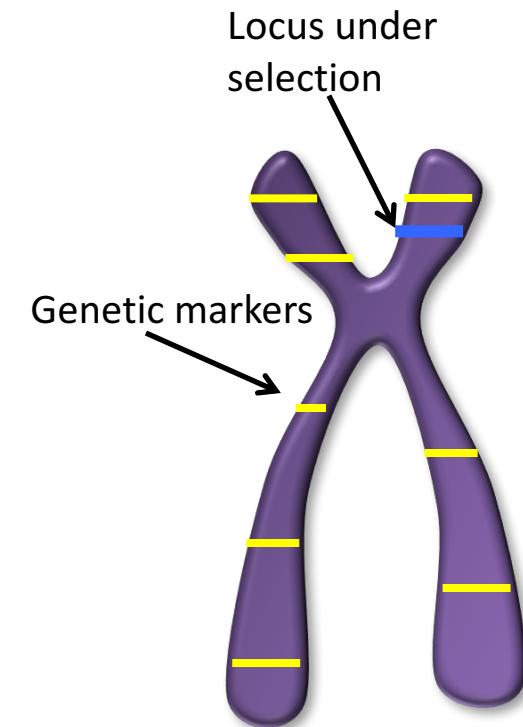
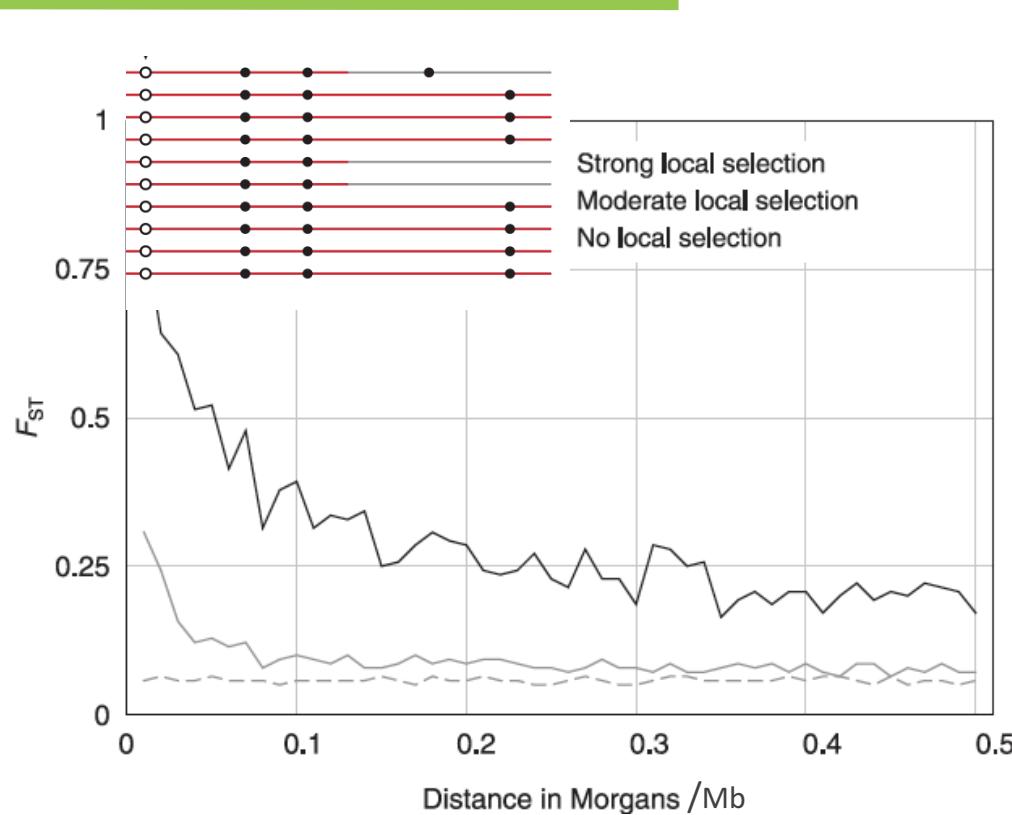
➤ Recombination

Skewed allele frequency

Reduced diversity (π, S)

Strong locus specific differentiation (F_{ST} -outlier)

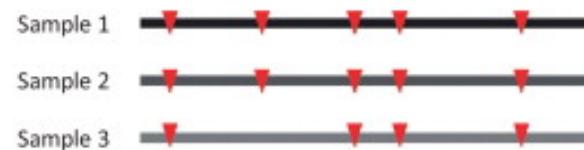
Genetic hitchhiking



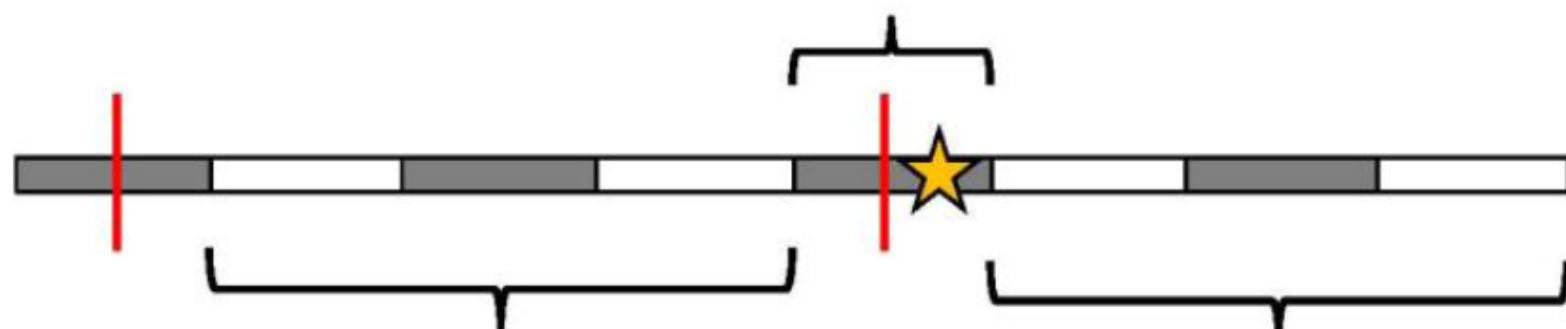
- ❖ The signature of selection decays with increasing distance from the locus under selection
=> **genetic hitchhiking**
- ❖ Recombination

Marker density

❖ E.g. Reduced representation sequencing (e.g. ddRAD-seq)

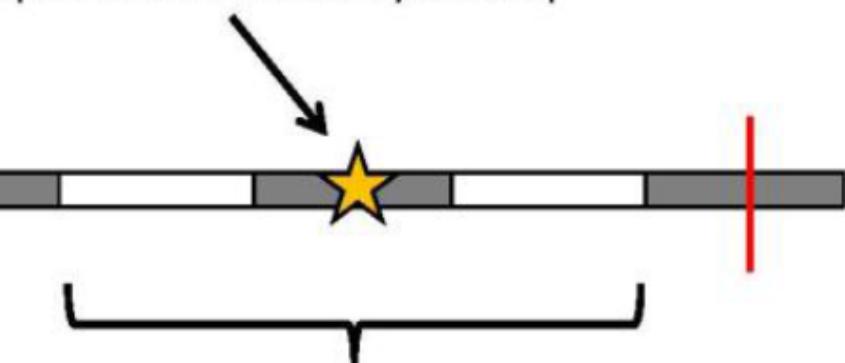


RAD-tag in LD with adaptation SNP



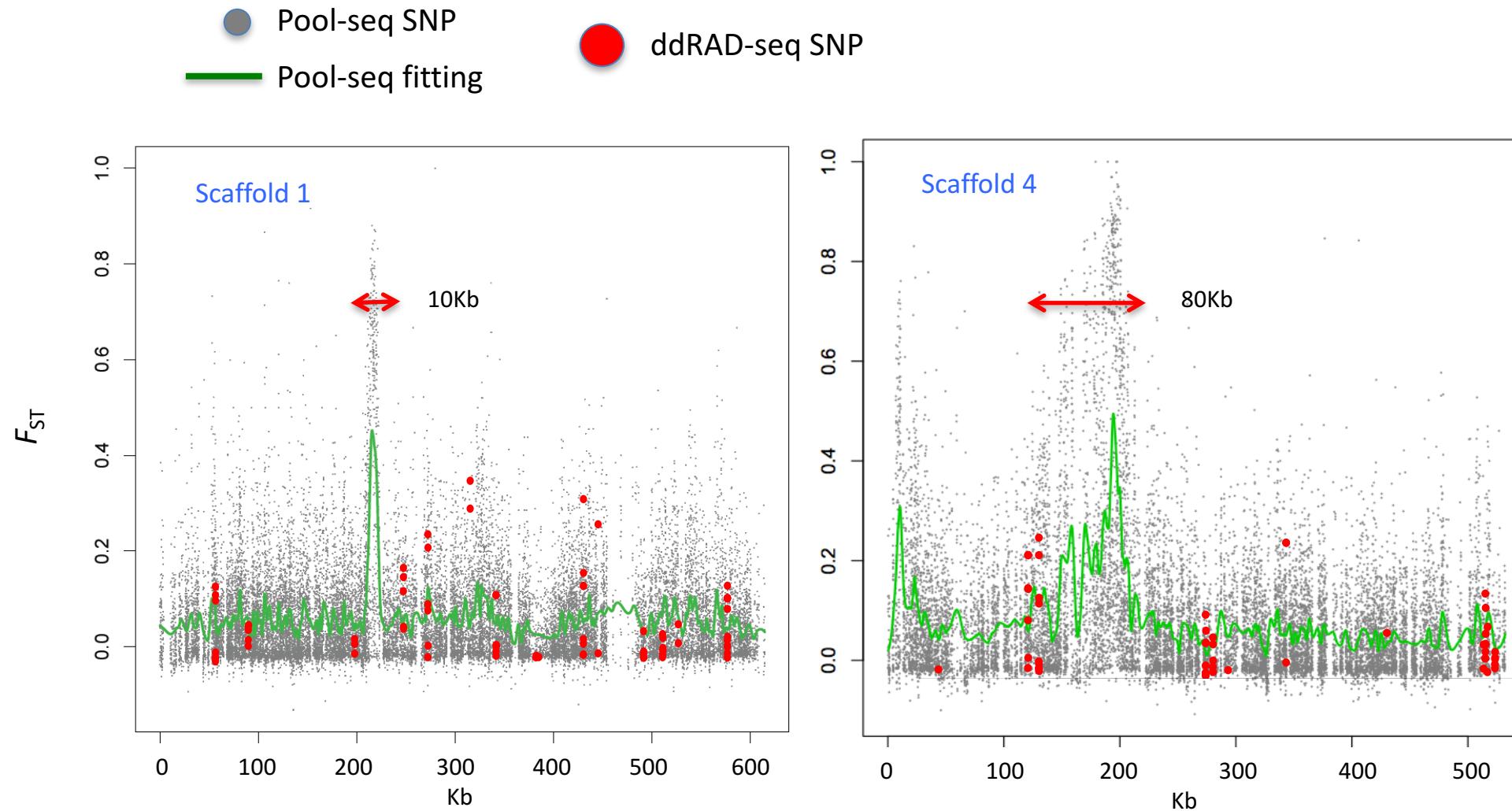
Genomic region missed by RADseq

Adaptation SNP missed by RADseq



Genomic region missed by RADseq

Marker density is important to detect outliers!

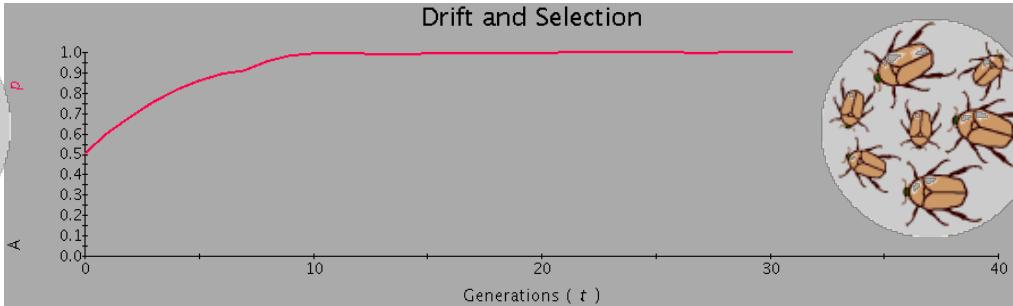
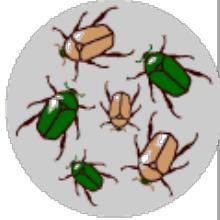


RAD-seq data can't detect most of the 'islands of selection'

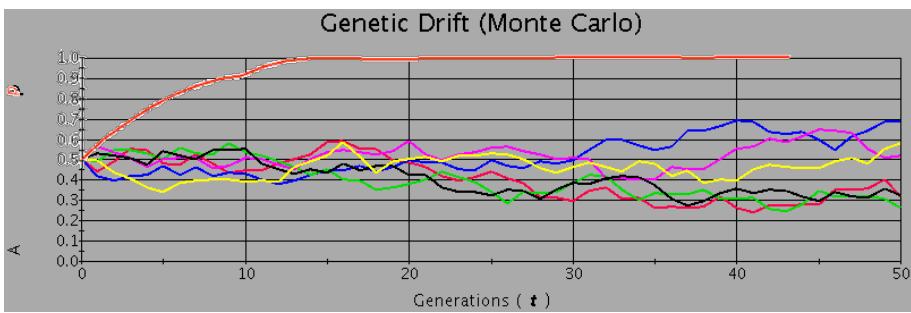


Population size matters....

❖ Selection



❖ Drift



❖ Selection coefficient $s \gg (1/2N_e)$

➤ Population under selection needs to have a minimum N_e to overcome drift, or s needs to be very strong

Four flavors of selection

Positive (directional)

- 'New' (non-synonymous) mutations selected for
- Evolution of novel protein function

Diversifying

- Geographically restricted selection (e.g. due to spatial variation in climate)

Balancing

- Maintenance of multiple alleles within-population
- E.g. heterozygote advantage (sickle cell anemia), frequency dependent selection

Negative (purifying)

- New (non-synonymous) mutations selected against
- Retention of existing protein function

Case studies: Detect the genomic signature of selection

Different methods to detect selection:

- ✧ Linkage disequilibrium (*LD*)
- ✧ Locus specific population differentiation (F_{ST} -outlier approach)
- ✧ Environmental driven locus specific signal (EAA)
- ✧ Reduced level of genetic variation (e.g. π)
- ✧ Skew of allele frequency spectra (Tajima's *D*)
- ✧ Substitution rates (e.g. dN/dS)

Comparison:

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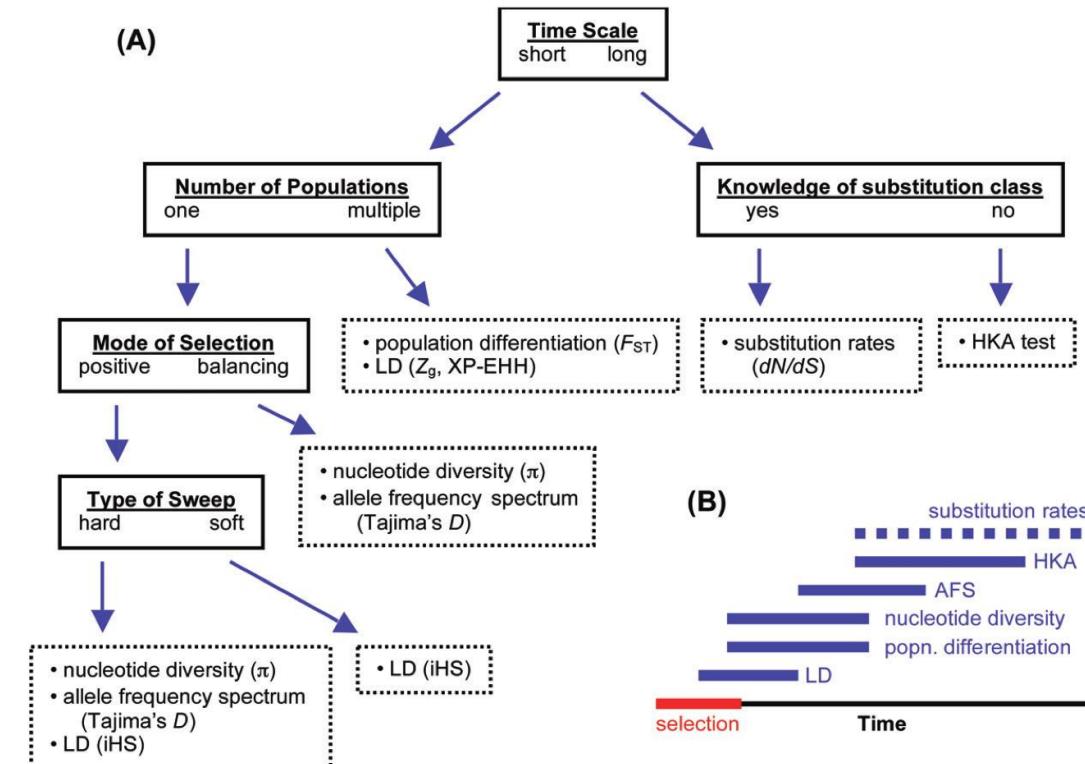
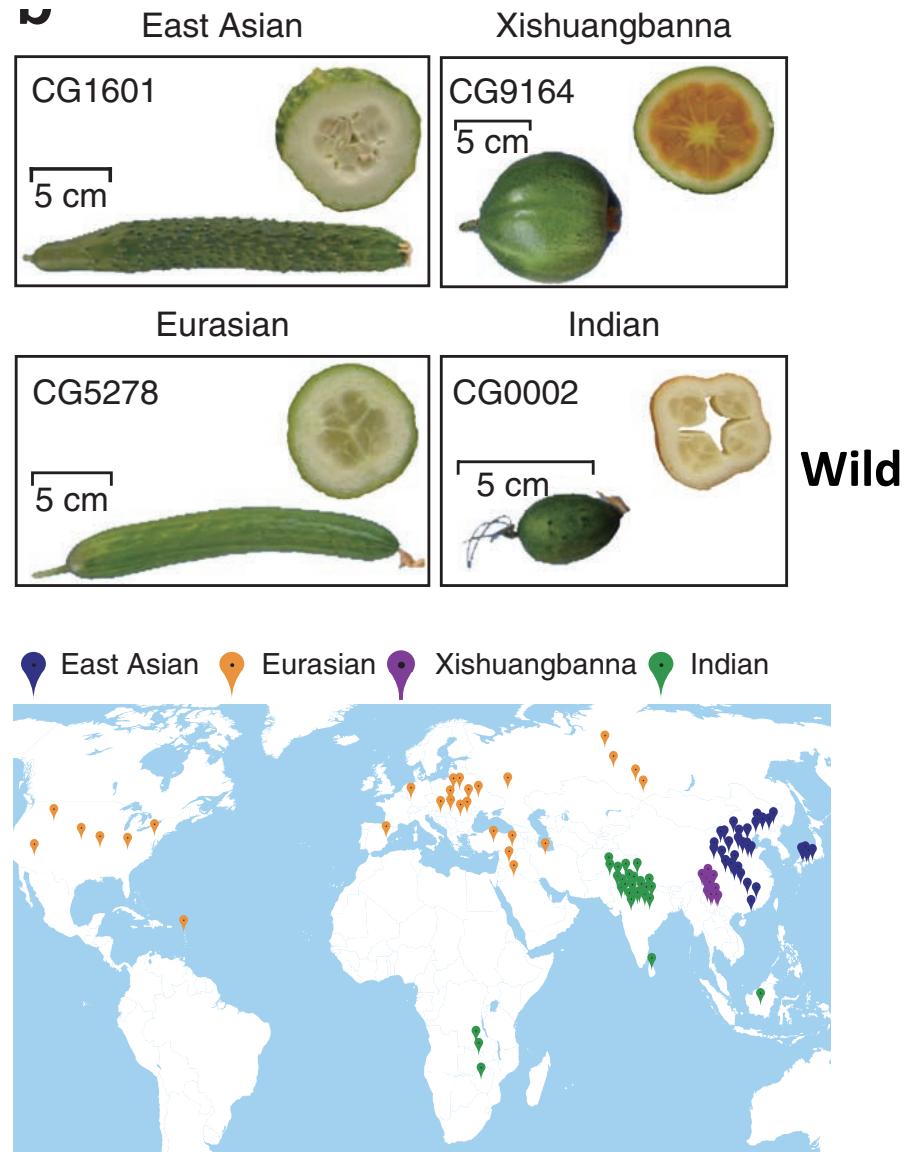


Figure 1 of Hohenlohe *et al.* (2010)

Reduced level of genetic variation (π)

Cucumber

- ❖ 3 cultivated (C) and 1 wild (W) cucumber groups
- ❖ Morphologically different
- ❖ Genome re-sequencing (n=115)
- ❖ π : nucleotide diversity
 - mean number of nucleotide substitutions per site between any two randomly selected DNA sequences in a population



Reduced level of genetic variation (π)

Domestication sweep

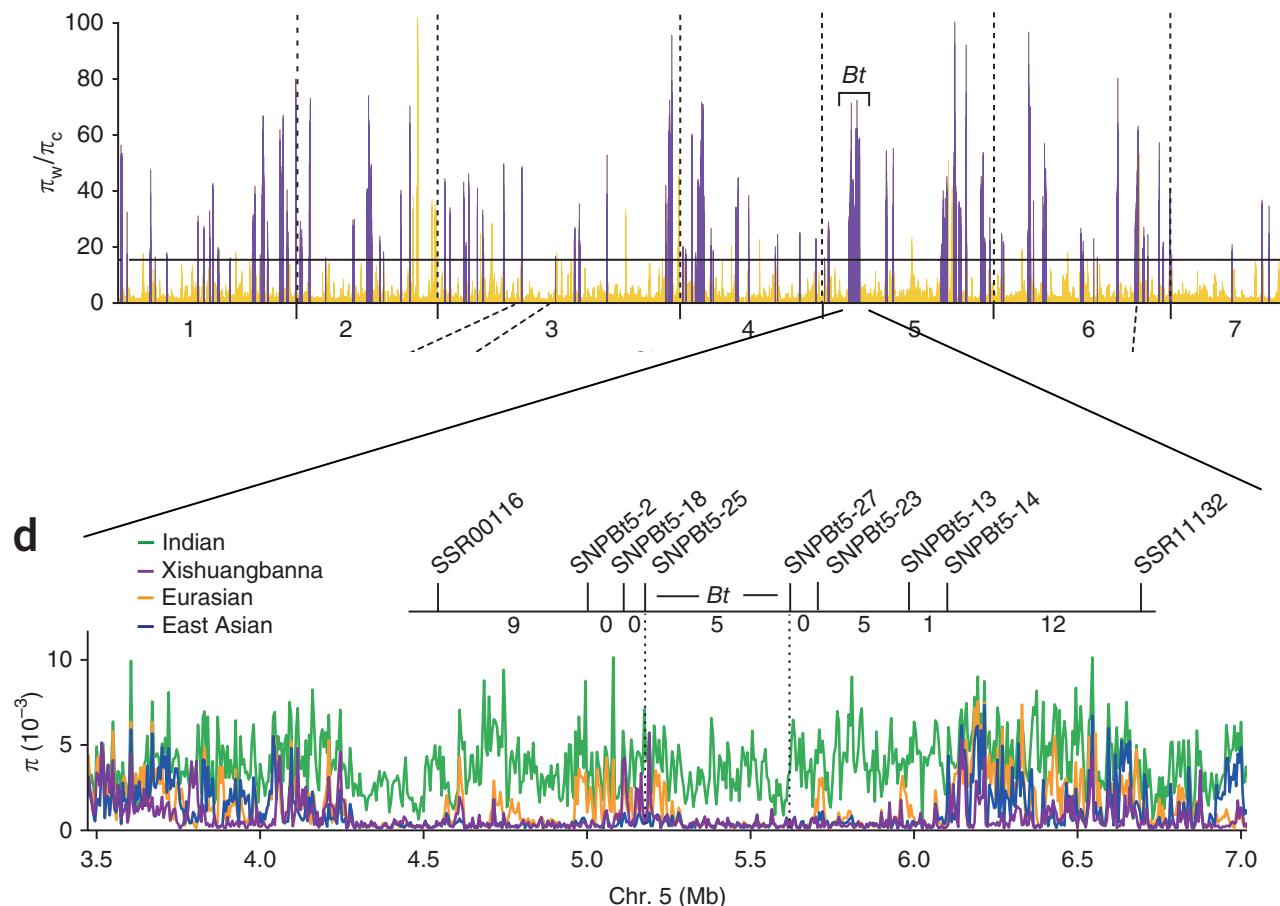
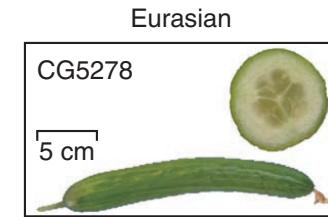
- ❖ Comparing π_w/π_c
- ❖ 112 regions detected

❖ **Bt** locus

- Fruit bitterness

❖ Reduced π in cultivated cucumbers

- ❖ 2 Mb in length (Bt: 442 kb)

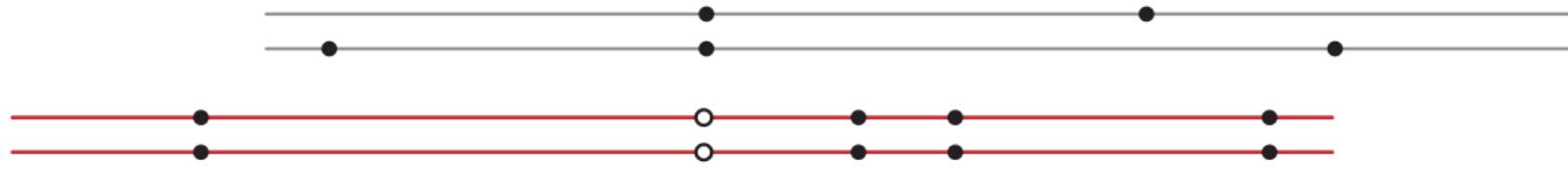


Linkage disequilibrium (LD)



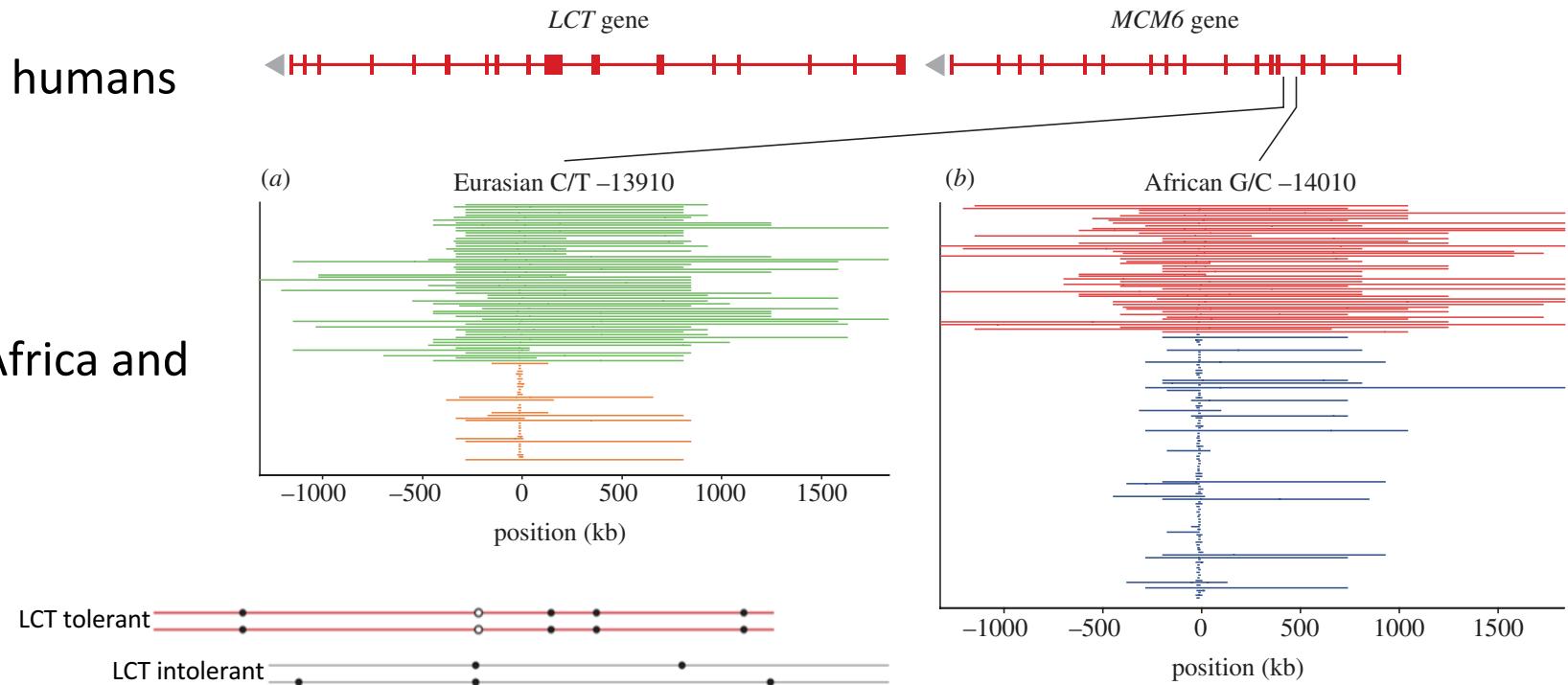
EHH: extended haplotype homozygosity

- Measures the decay of homozygosity from a 'core' SNP



LCT: lactose persistent gene in humans

- 2 Mb haplotypes
- Independent evolution in Africa and Europe



Skew of allele frequency spectra (Tajima's D)

Tajima's D

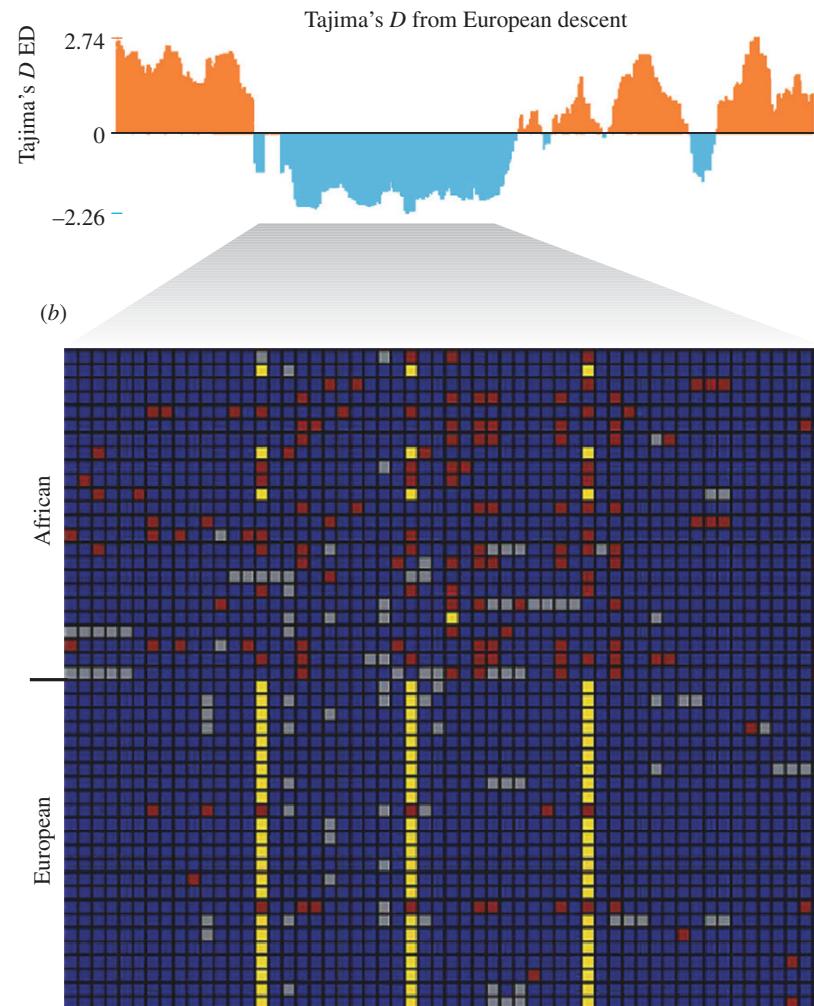
- ❖ Normalized difference between π and segregating sites (S , Θ_w)
- ❖ $d = \pi - \Theta_w$

$$D = \frac{d}{\sqrt{V(d)}}$$

- ❖ **Balancing selection**
excess intermediate-freq. SNPs:
 $\pi > \Theta_w$, $+D$

- ❖ **Positive selection**
excess of low-frequency SNPs: 
 $\pi < \Theta_w$, $-D$

- ❖ **Correct for demographic effects**
 - Compare values against genome-wide estimates



Skew of allele frequency spectra

Human *CLSPN* gene

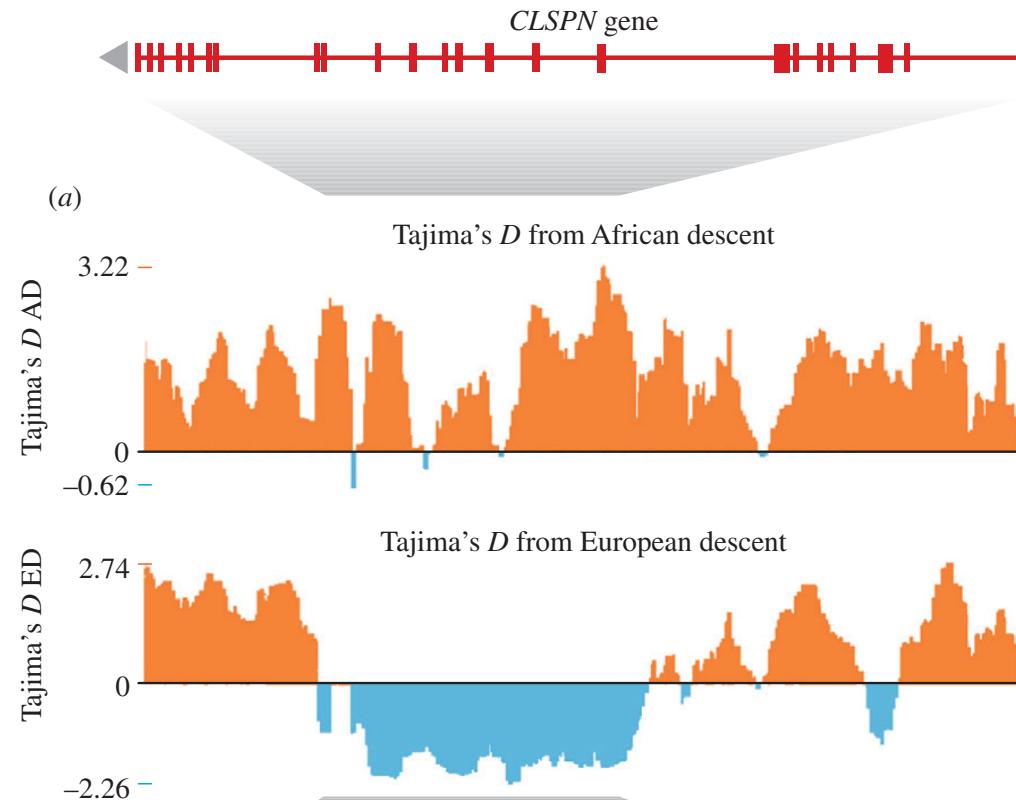
❖ Inferred from dense SNP data

❖ Tajima's *D* plot

❖ Positive selection in European ($-D$)

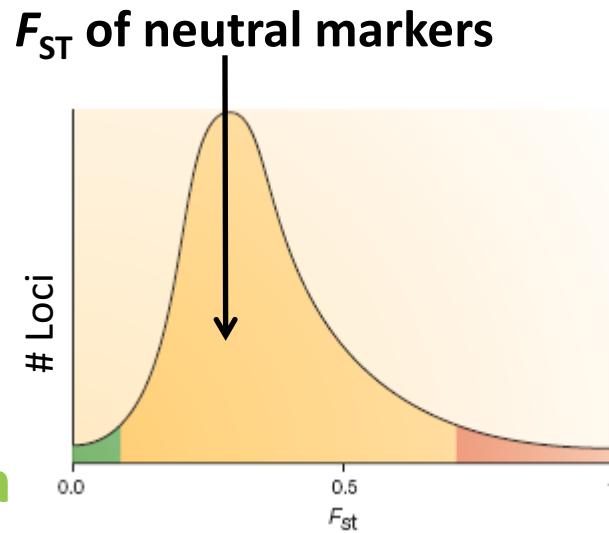
❖ 1.5 Mb

❖ Unknown function!



Model free F_{ST} -outlier approach

- >3 populations
- Screen many loci (>10,000; up to whole genome)
- **Outliers:** e.g. 95% quantile of F_{ST} distribution



Balancing selection

- relatively uniform frequencies across populations
⇒ low F_{ST} values

Fischer *et al.* 2014 PLoS One

Positive selection

- increased level of differentiation among populations
⇒ high F_{ST} values

Fischer *et al.* 2011/2013 MolEcol

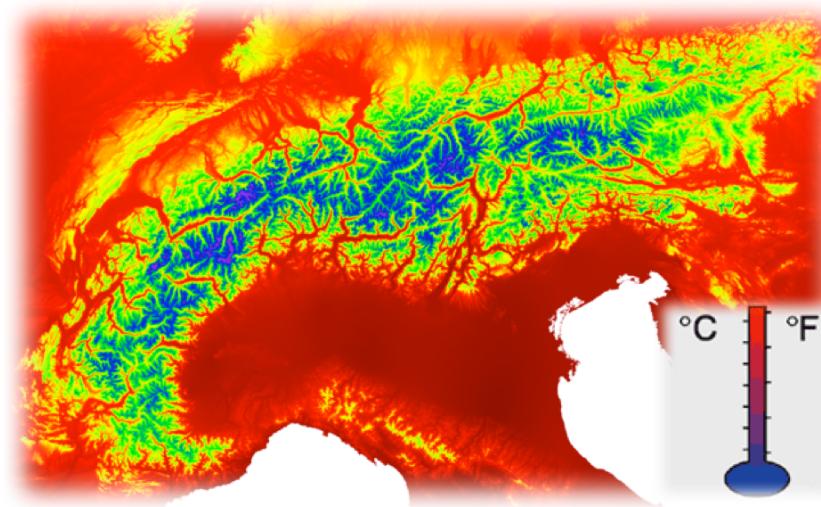
Luikart *et al.* 2003



- ❖ Highly heterogeneous
- ❖ Strong environmental gradients
- Genetic basis of adaptation

Population genomic footprints of selection and associations with climate in natural populations of *Arabidopsis halleri* from the Alps

MARTIN C. FISCHER,* CHRISTIAN RELLSTAB,† ANDREW TEDDER,‡ STEFAN ZOLLER,§
FELIX GUGERLI,† KENTARO K. SHIMIZU,‡ ROLF HOLDEREGGER*† and ALEX WIDMER*



Study organism

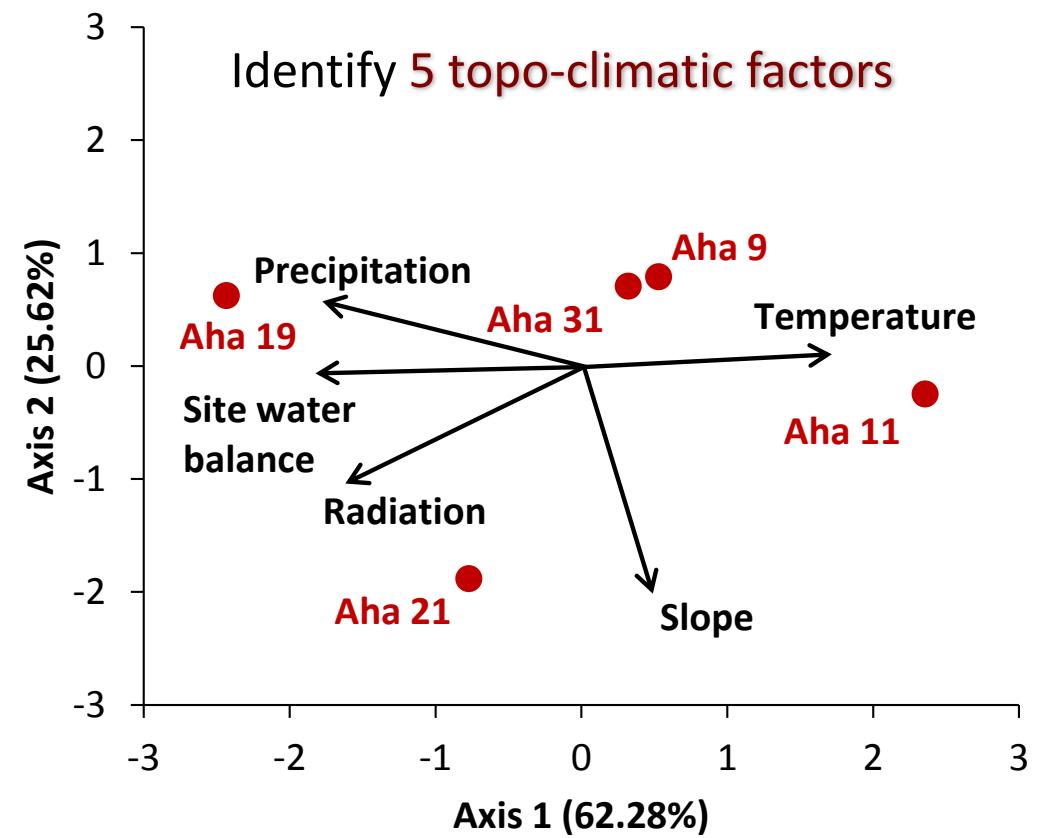
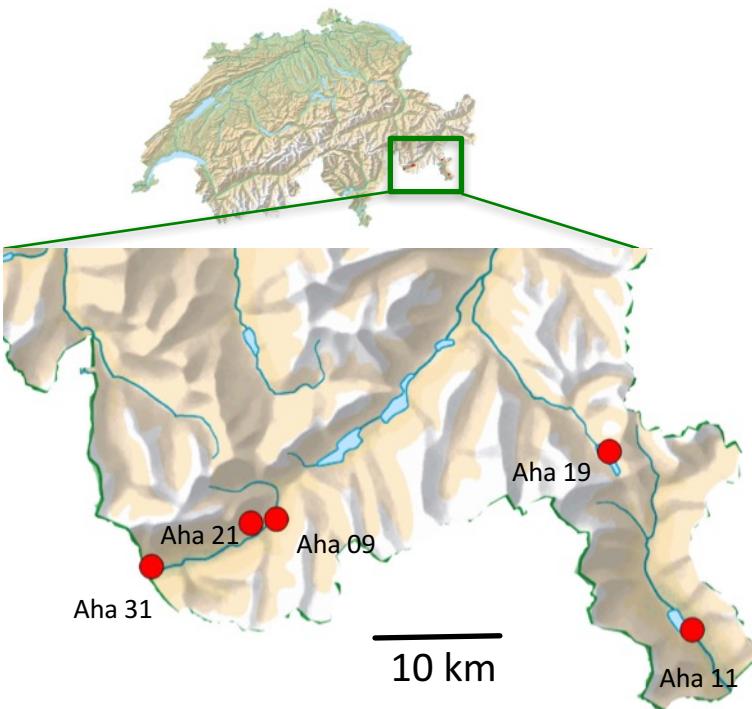
Arabidopsis halleri

- ❖ Close relative of the model organism *A. thaliana*
- ❖ Genome size 255 Mbp
- ❖ Strictly outcrossing
- ❖ 300 – 2400 m a.s.l.



Heterogeneous Alpine environments

- ❖ 5 populations in close vicinity (2 – 45 km)
- ❖ 20 individuals each
- ❖ Cover wide range of abiotic environmental condition
➤ E.g. 790 – 2308 m a.s.l.



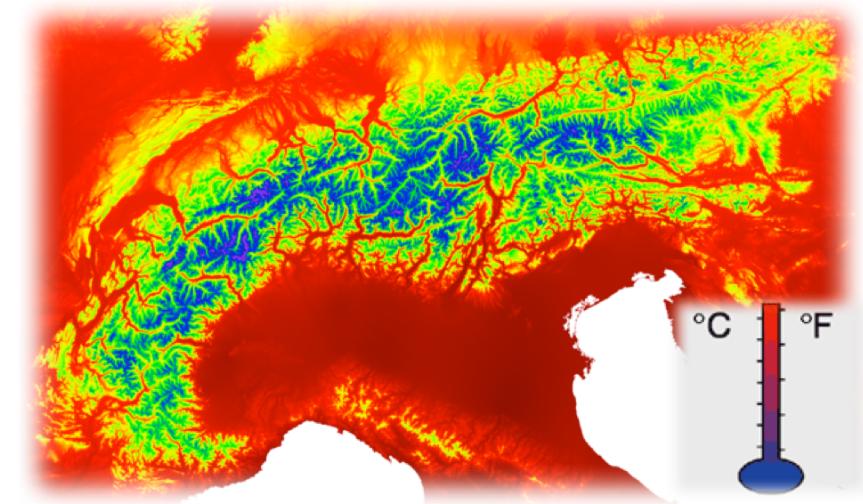
Adaptive genomics

Many abiotic factors are changing on short distance

- ❖ Expected **signature of selection?**
 - No signature of selection
 - Some genes with major effects
 - Many different genes under selection

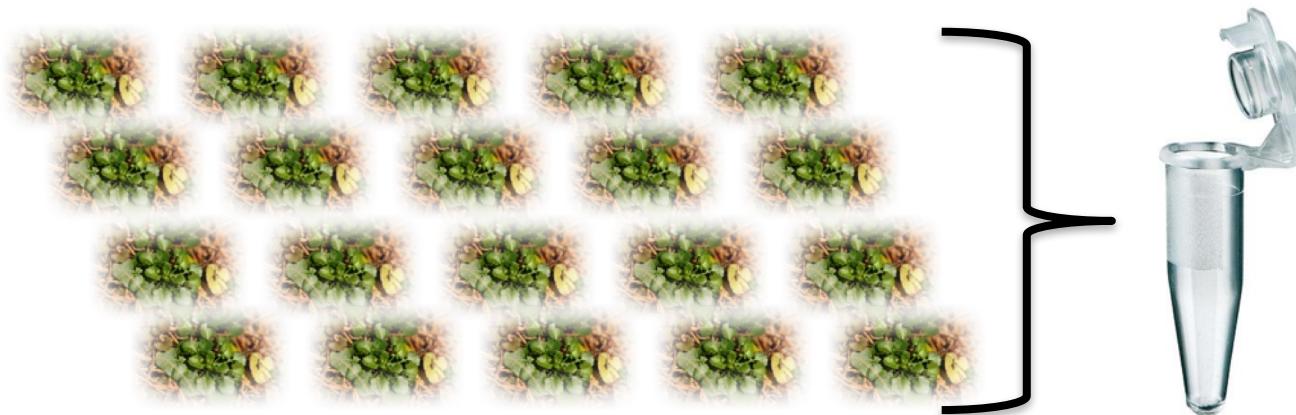
- ❖ Which **genes** are involved in **adaptation?**
 - Gene functions?
 - Abiotic factors?

- Population genomic approach



Whole genome re-sequencing

- No bias from insufficient marker density or distribution
- ❖ **Pool-Seq**; pooled population approach
 - Cost effective => 5 libraries
 - Reduces amount of DNA required
- ❖ 20 diploid genomes pooled per population



Accuracy of Pool-Seq approach

OPEN  ACCESS Freely available online

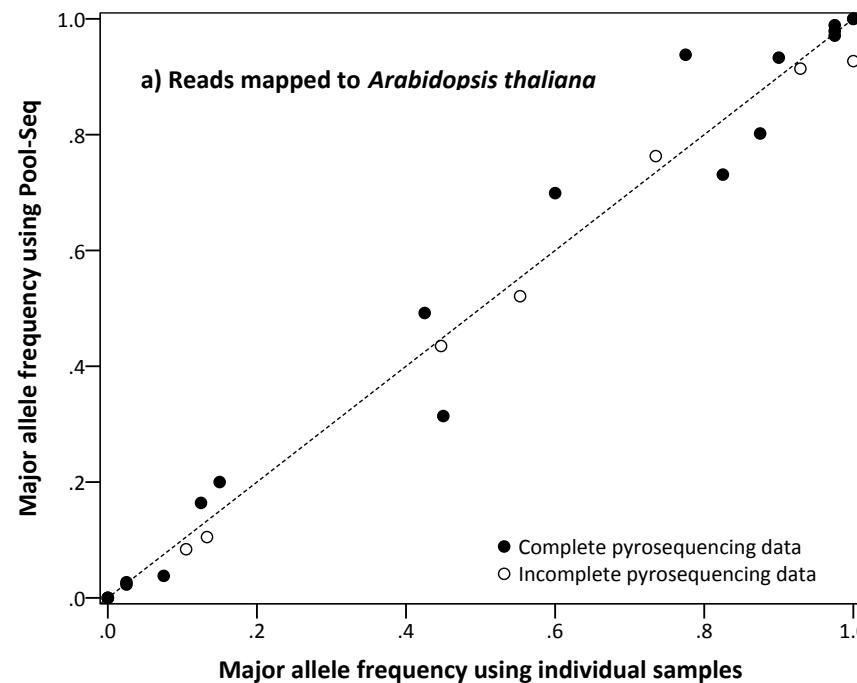


Validation of SNP Allele Frequencies Determined by Pooled Next-Generation Sequencing in Natural Populations of a Non-Model Plant Species

Christian Rellstab¹, Stefan Zoller², Andrew Tedder³, Felix Gugerli¹, Martin C. Fischer^{4*}

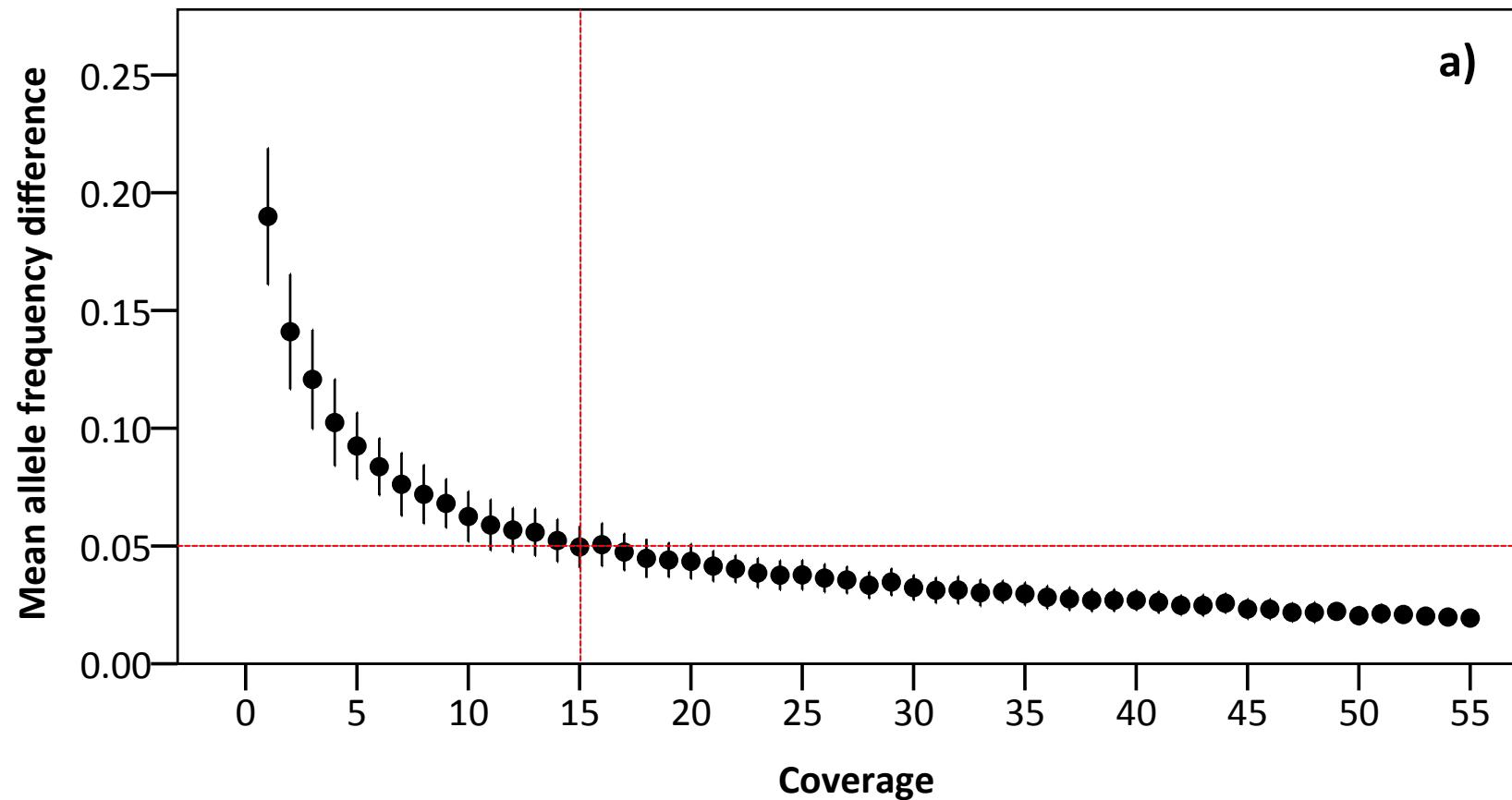
1 Biodiversity and Conservation Biology, Swiss Federal Research Institute WSL, Birmensdorf, Switzerland, **2** Genetic Diversity Centre, ETH Zürich, Zürich, Switzerland, **3** Institute of Evolutionary Biology and Environmental Studies and Institute of Plant Biology, University of Zürich, Zürich, Switzerland, **4** Institute of Integrative Biology, ETH Zürich, Zürich, Switzerland

- ❖ Individual SNP genotyping
- ❖ 3 populations
- ❖ 9 SNPs validated
- ❖ PyroMark
- ❖ $R^2 = 0.98$



Accuracy of Pool-Seq approach

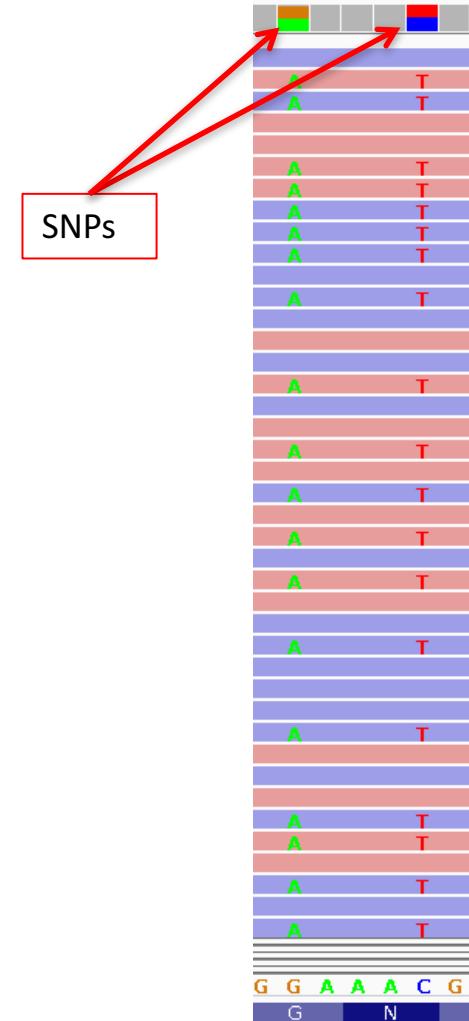
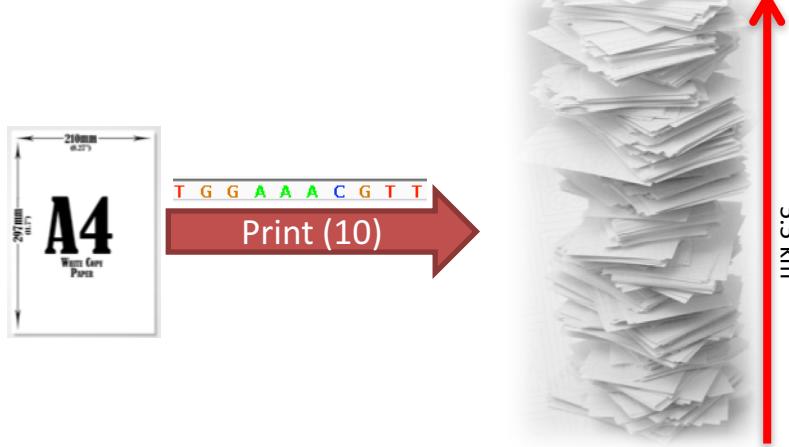
❖ Influence of the coverage for Pool-Seq



Population genomics

❖ Mapping of reads onto *A. thaliana* ref. genome

- BWA (Li & Durbin 2009)
- ~60x coverage
- >120 billion bases



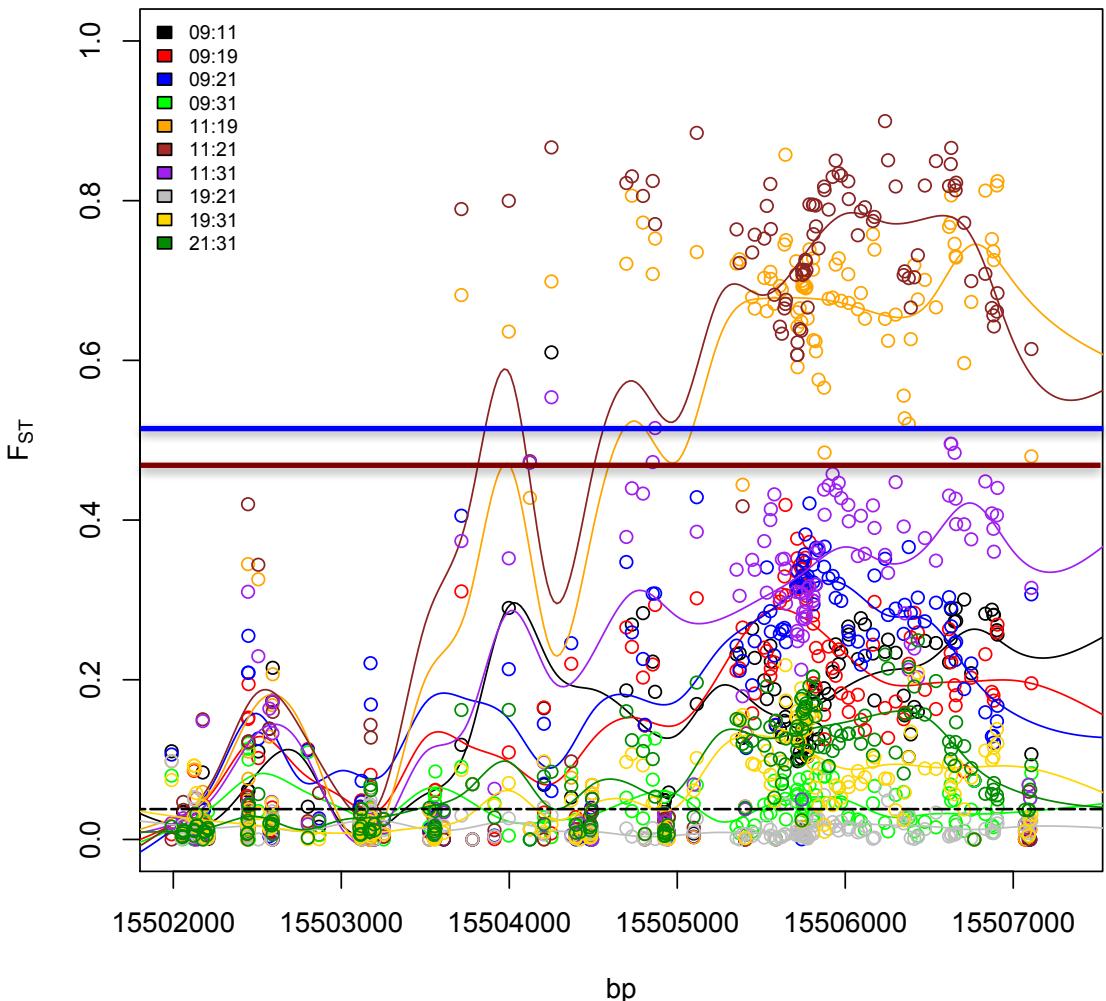
❖ PoPopulation2 (Kofler *et al.* 2011)

- Identified **2,091,957 SNPs**
- 25,764 genes covered
- Genome-wide pairwise F_{ST}
 - Mean: 0.038

F_{ST} -outlier detection

3 step model free approach:

- ❖ 0.1% of highest F_{ST} regions: $F_{ST} > 0.47$
 - F_{ST} sliding windows approach of 500 bp
- ❖ 0.1% of highest F_{ST} SNPs: $F_{ST} > 0.54$
 - Corrected for population structure
- Fisher's exact test
 - $p < 2.39 \times 10^{-9}$
 - Strong allele frequency differences
 - Corrects for coverage

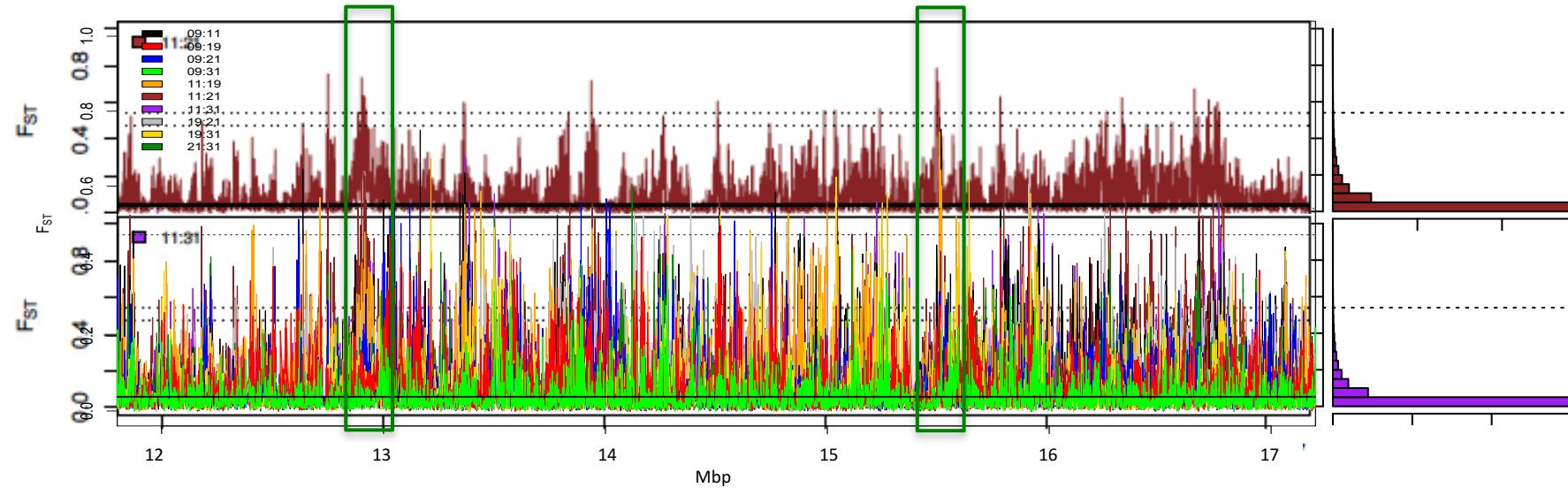


Genomic Signature of Selection

❖ 4282 strong outlier SNPs

➤ 0.2% of all SNPs

❖ 571 outlier genes



Gene functions

❖ 571 outlier genes

➤ 139 genes (24%) unknown function

Gene Ontology Terms (Biological process)

Defense response to bacterium

Aging

Cell surface receptor signaling pathway

Seed coat development

Protein autophosphorylation

Anion transport

Salicylic acid mediated signaling pathway

Transmembrane transport

Cofactor catabolic process

Chromatin modification

Recognition of pollen

Gibberellic acid mediated signaling pathway

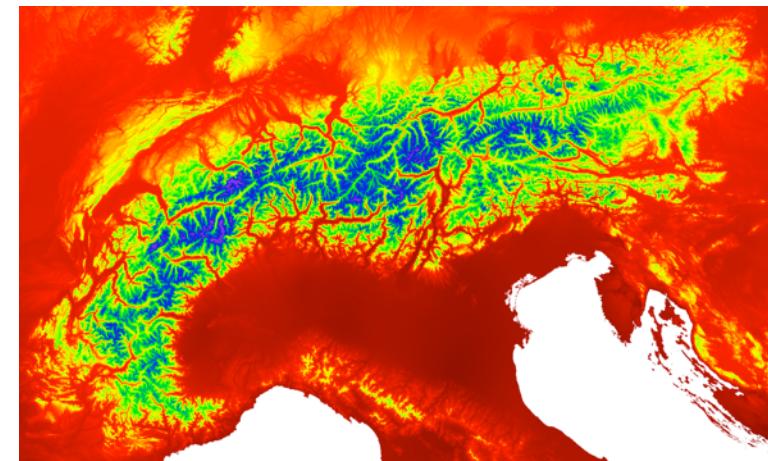
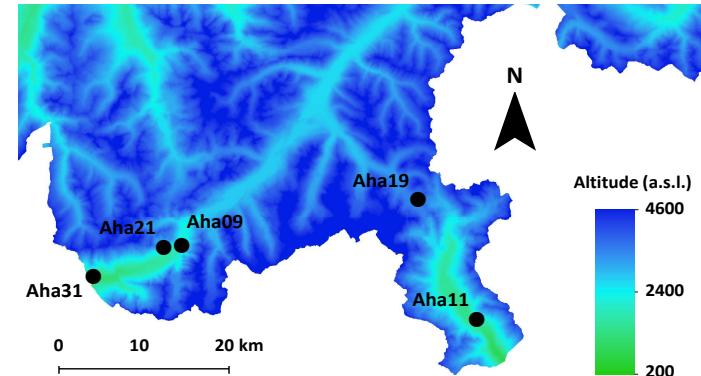
DNA methylation

Chromatin silencing

Regulation of root development

Protein N-linked glycosylation

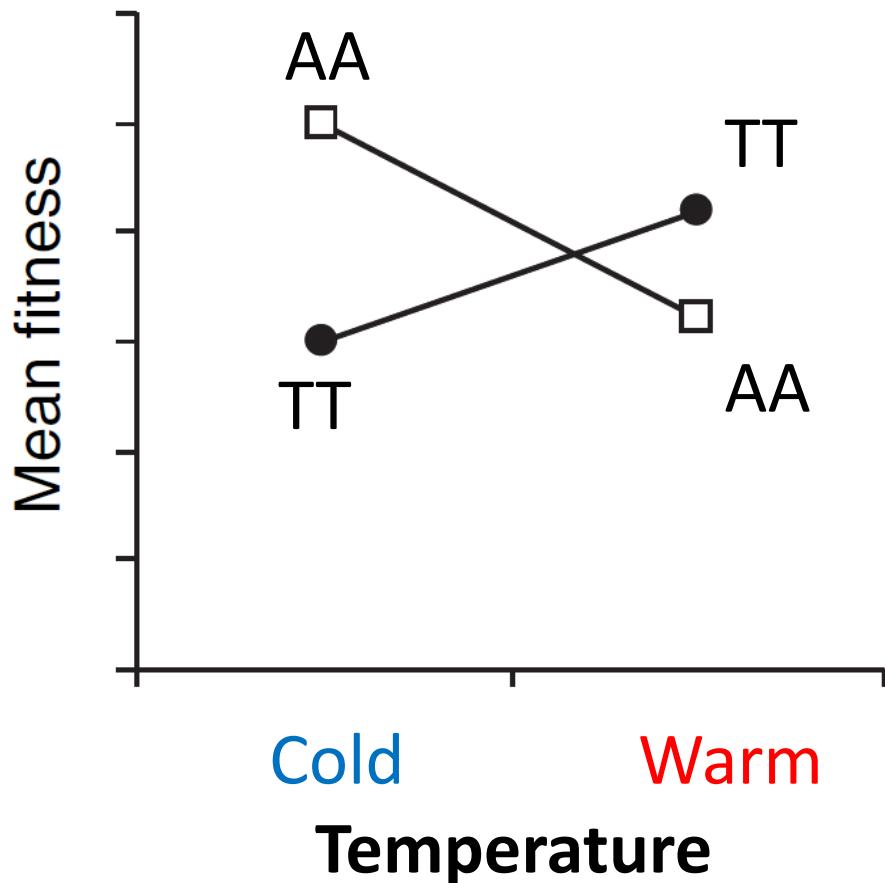
Identify genes involved in environmental adaptation



Genes with a signature of selection are involved in diversity of biological processes

Environmental association analyses (EAA): Local adaptation

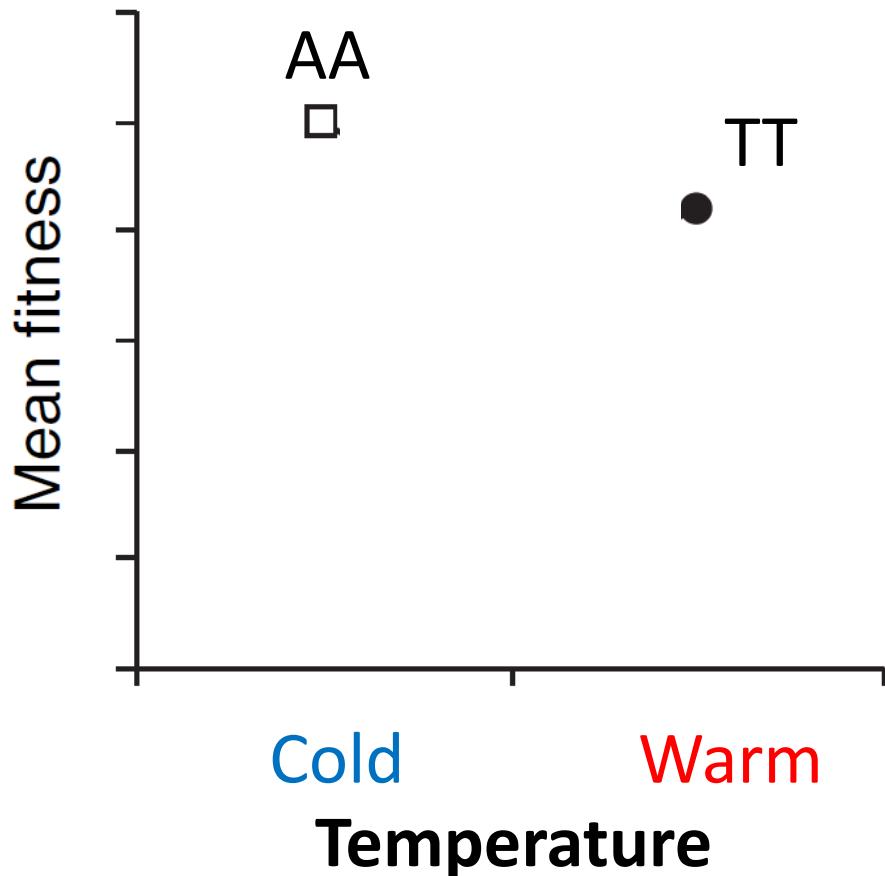
- Population from cold habitat
- Population from warm habitat



Fitness difference is genetically controlled (by a single SNP locus)

Environmental association analyses: Local adaptation

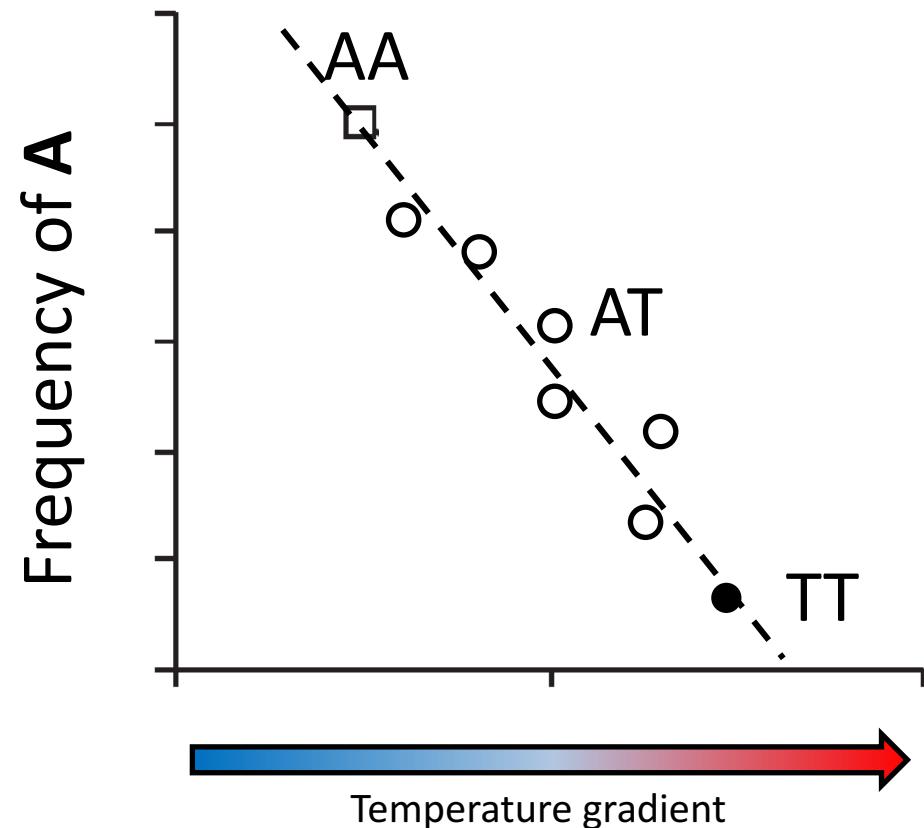
- Population from cold habitat
- Population from warm habitat



All populations are adapted to their local environmental conditions

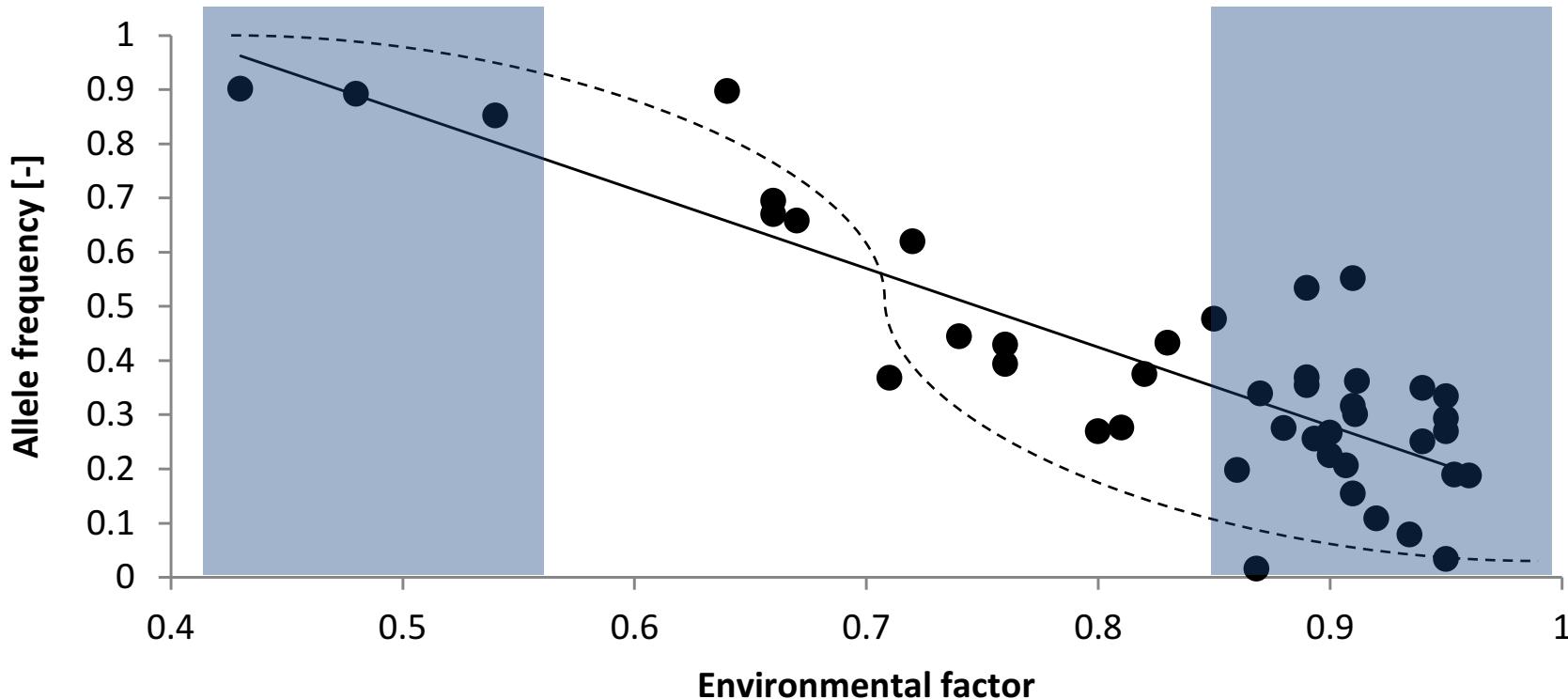
Environmental association analyses: Local adaptation

- Population from cold habitat
- Population from warm habitat



Additive genetic effects

Environmental association analyses



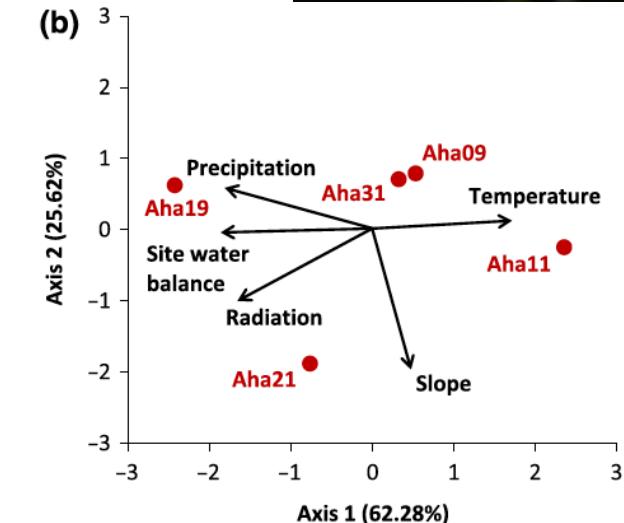
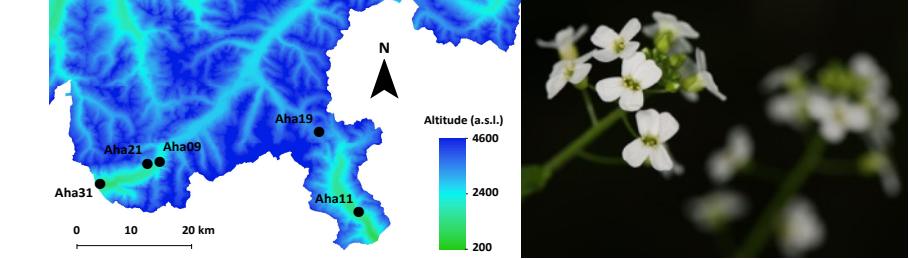
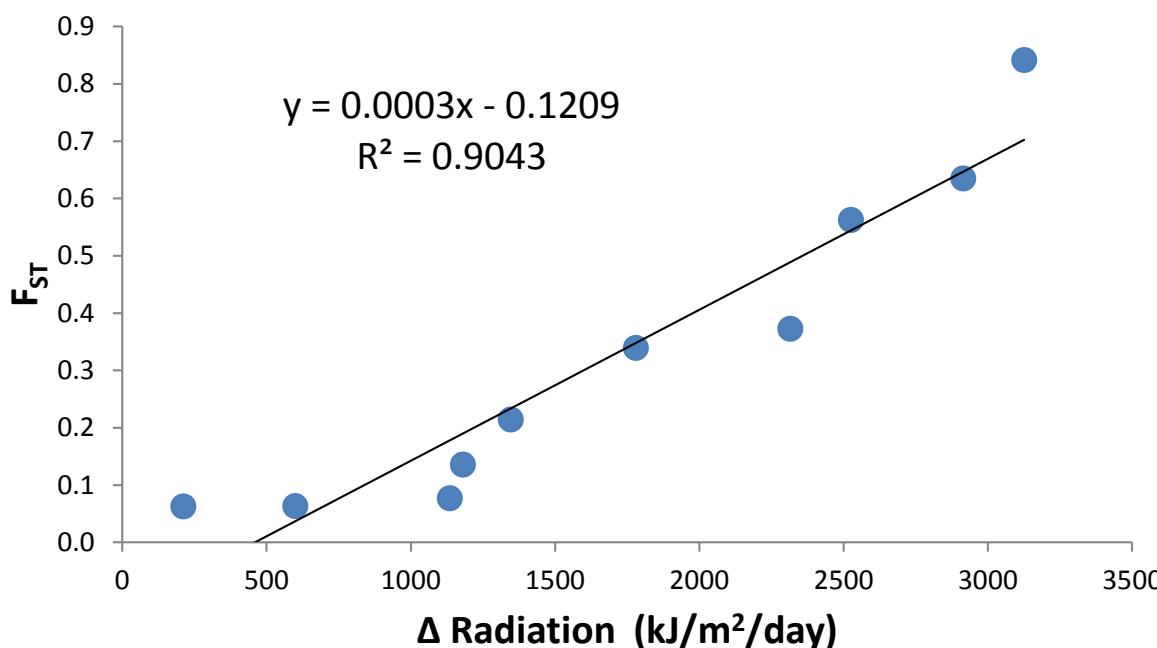
- ❖ Identify alleles, SNPs, or genes associated with particular environmental factors
- ❖ Identify environmental factors that drive local adaptation
- Partial Mantel test, LFMM (latent factor mixed models), BayEnv,....

Environmental Associations

Partial Mantel tests

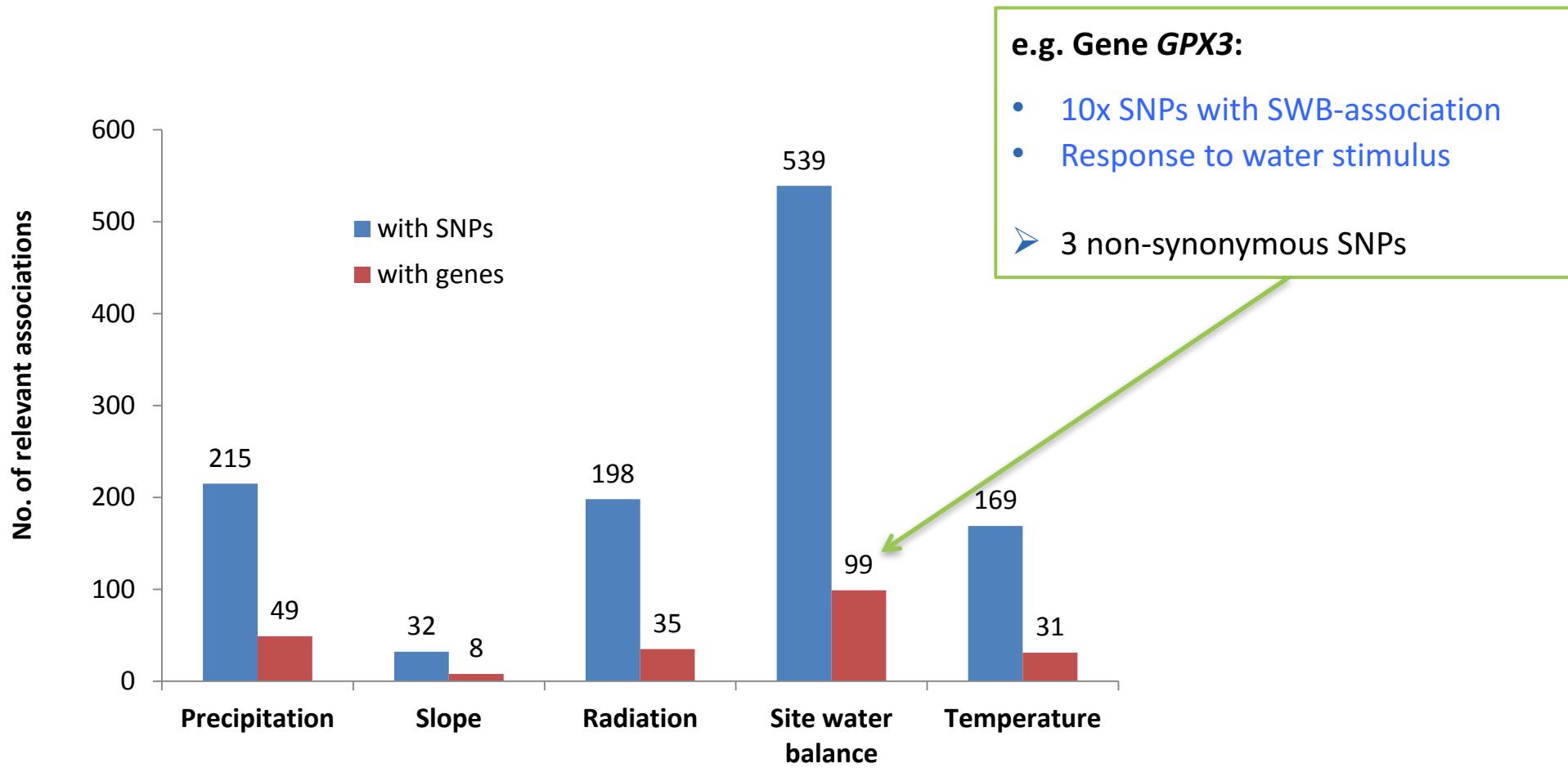
- ❖ Correlates two distance matrices:
 - Pairwise **genetic** distance of **outlier SNPs**
 - Pairwise **climatic** distance of **environmental factors**

- ❖ Controlling for population structure



Abiotic environmental associations

❖ 175 genes with environmental associations (**30.6%**; out of 571 genes)



Last glacial maximum (18,000 years)

- ❖ F_{ST} -outlier approached detect recent selection
- ❖ Selective signals mostly found in low elevation populations
- ❖ Alpine plants are already adapted to harsh environments
- ❖ Adaptation to warm and dry environments



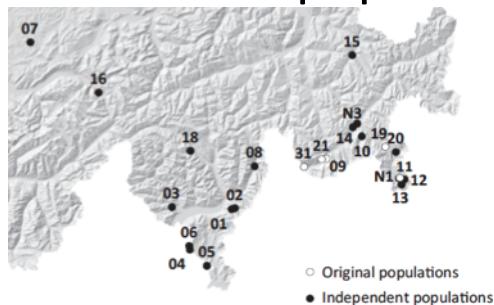
Local remains local... ... in a highly heterogeneous environment

ORIGINAL ARTICLE

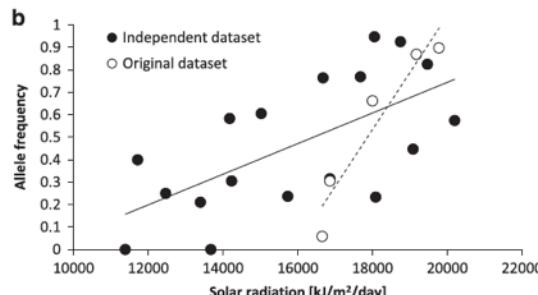
Local adaptation (mostly) remains local: reassessing environmental associations of climate-related candidate SNPs in *Arabidopsis halleri*

C Rellstab¹, MC Fischer², S Zoller³, R Graf¹, A Tedder⁴, KK Shimizu⁴, A Widmer², R Holderegger^{1,2} and F Gugerli¹

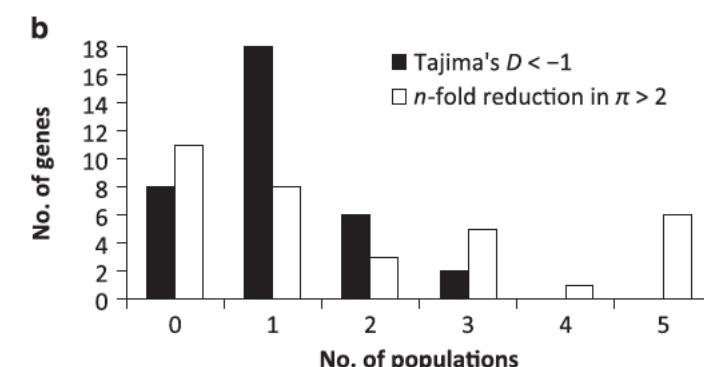
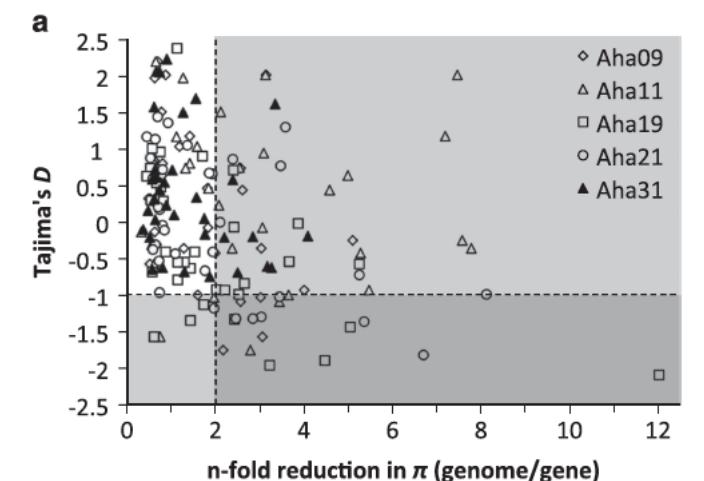
- ❖ 74 candidate SNPs tested for EAA on a large geographic scale
- ❖ 444 individuals in 23 populations



- ❖ LFMM and partial Mantel Test
- ❖ 31% of the genes revealed the same association

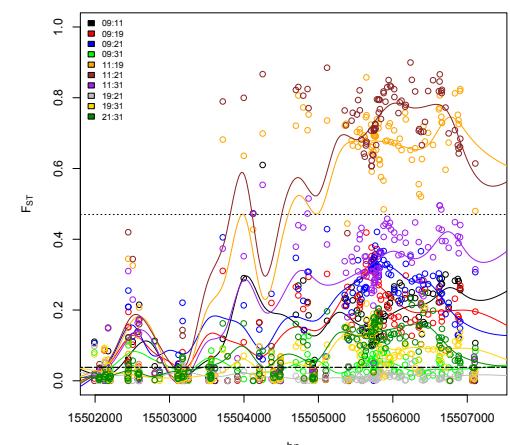
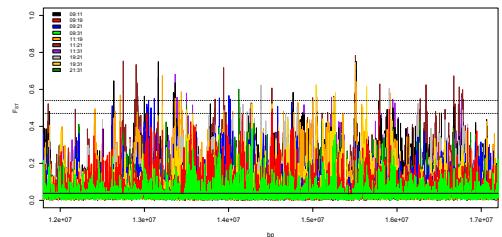
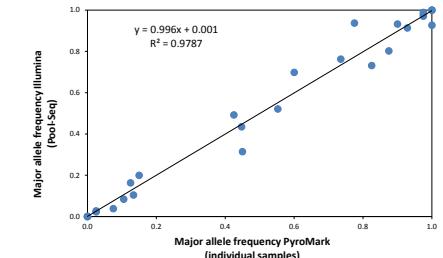


- ❖ Signature of selection was mainly found in single populations



Conclusions

- Population genomic analyses of **non-model** species using a **Pool-Seq** approach are:
 - Feasible and provide accurate SNP estimates
 - Reveal evidence for selection across the genome
- ❖ The molecular signature of adaptation in Alpine populations of *A. halleri* is **highly complex**
- ❖ Many genes showing interesting patterns of variation have unknown functions – need for **ecological gene annotation**
- ❖ Local adaptation remains local, in a highly heterogeneous environments



Model based F_{ST} -outlier approach



Estimates probability of each locus to be under selection (Island model)

❖ **BayeScan**

➤ Bayesian model comparison

$$PO = \frac{\Pr(M_1 | Data)}{\Pr(M_2 | Data)}$$

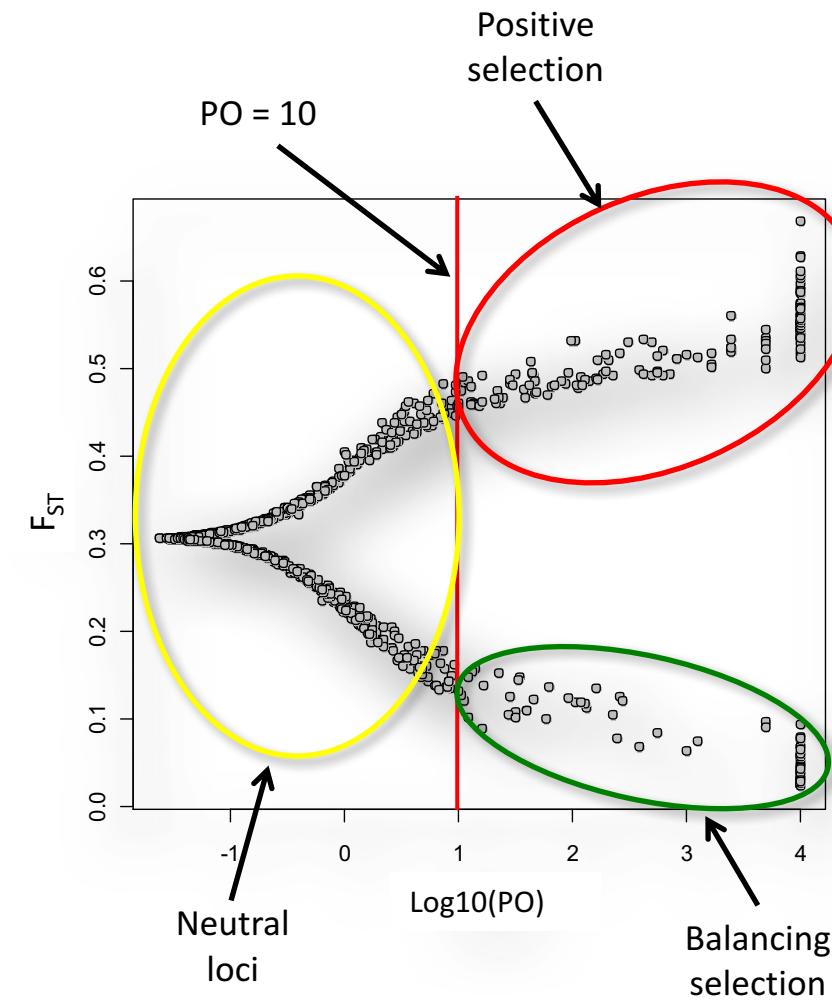
Posterior odds

Model with selection

Neutral model

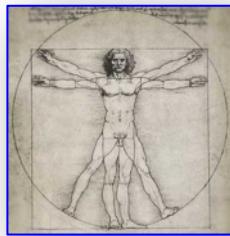
A mathematical equation for Posterior Odds (PO) comparing two models. The numerator is the probability of Model 1 given the data, and the denominator is the probability of Model 2 given the data. Arrows point from the labels to the respective terms in the equation.

❖ **PO > 10** strong evidence for accepting a model
(Jeffreys 1961)



Substitution rates (e.g. dN/dS)

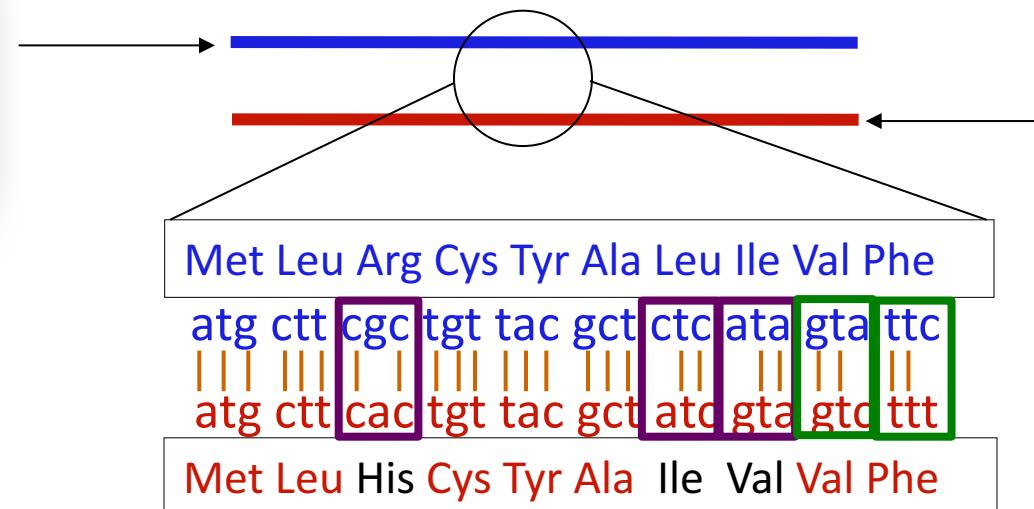
- ❖ Human-chimpanzee divergence 5 million years
- ❖ 13,731 orthologous genes compared



Human



Chimpanzee



Non-synonymous substitution
Fitness effects

Synonymous substitution
No fitness effects

dN = number of non-synonymous substitutions / number of non-synonymous sites

dS = number of synonymous substitutions / number of synonymous sites

Substitution rates (e.g. dN/dS)

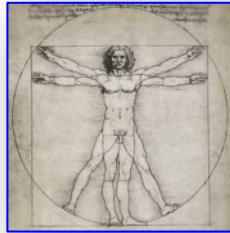
❖ Universal genetic code

		Second letter					
		U	C	A	G		
First letter	U	UUU UUC UUA UUG } Phe	UCU UCC UCA UCG } Ser	UAU UAC UAA UAG } Tyr Stop Stop	UGU UGC UGA UGG } Cys Stop Trp	U C A G	
	C	CUU CUC CUA CUG } Leu	CCU CCC CCA CCG } Pro	CAU CAC CAA CAG } His Gln	CGU CGC CGA CGG } Arg	U C A G	
	A	AUU AUC AUA AUG } Ile Met	ACU ACC ACA ACG } Thr	AAU AAC AAA AAG } Asn Lys	AGU AGC AGA AGG } Ser Arg	U C A G	Third letter
	G	GUU GUC GUA GUG } Val	GCU GCC GCA GCG } Ala	GAU GAC GAA GAG } Asp Glu	GGU GGC GGA GGG } Gly	U C A G	

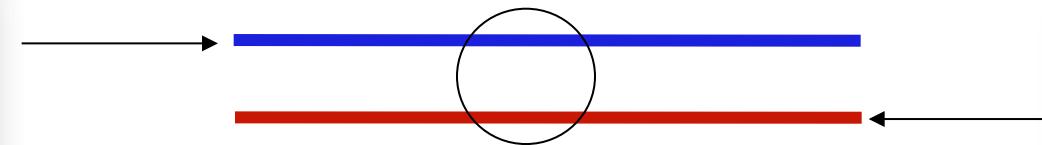
Substitution rates (e.g. dN/dS)

❖ Human-chimpanzee divergence 5 million years

❖ 13,731 orthologous genes compared



Human



Chimpanzee

- $dN/dS > 1 \Rightarrow$ Positive selection \Rightarrow 733 genes
- $dN/dS < 1 \Rightarrow$ Purifying selection
- Sensory perception or **immune defenses genes** detected
- Selection over long time scale
- Requires multiple amino acid substitutions

The genomic signature of selection

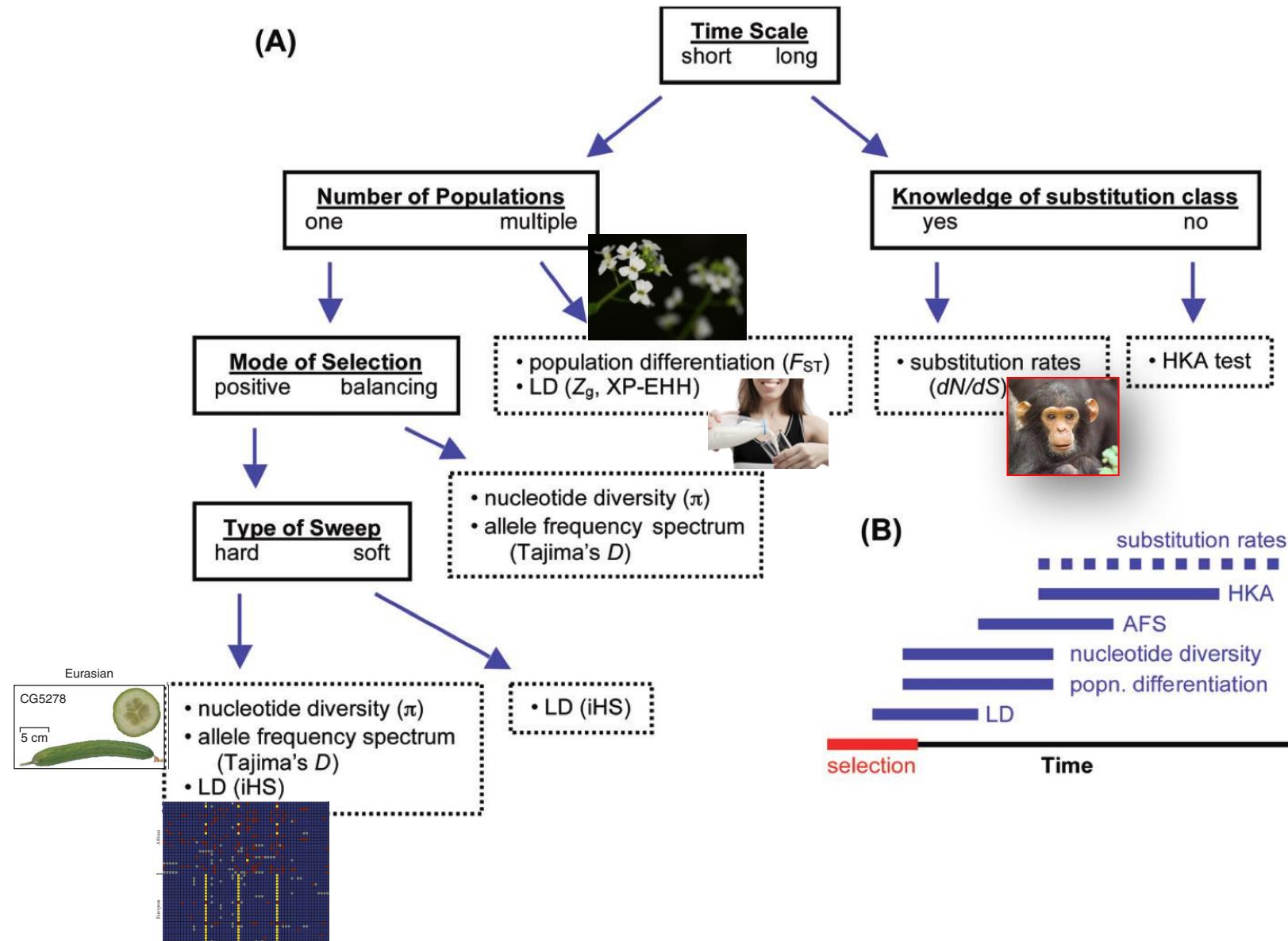


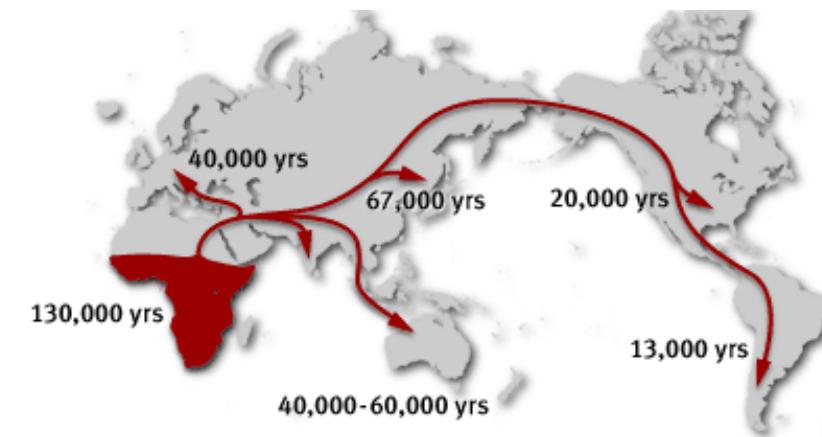
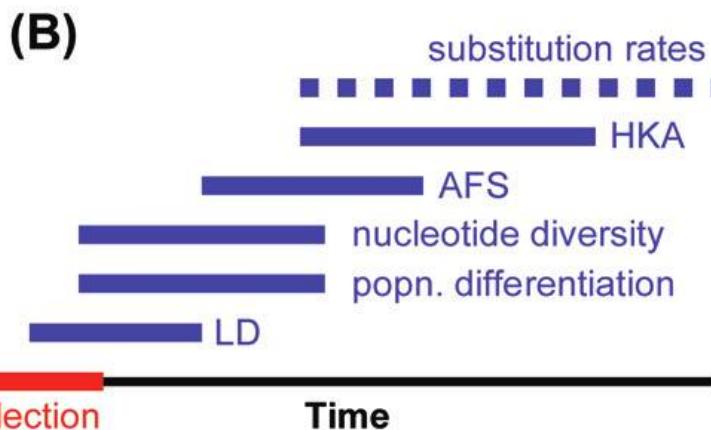
Figure 1 of Hohenlohe et al. 2010

Different time scale of selection tests

Example in humans

- ❖ Substitution rates (dN/dS)
- ❖ Skew of allele frequency spectra
- ❖ Reduced level of genetic variation (π)
- ❖ Population differentiation (F_{ST} -outlier)
- ❖ Linkage disequilibrium (LD)

>1'000'000 years
<200'000 years
<200'000 years
<80'000 years
<30'000 years



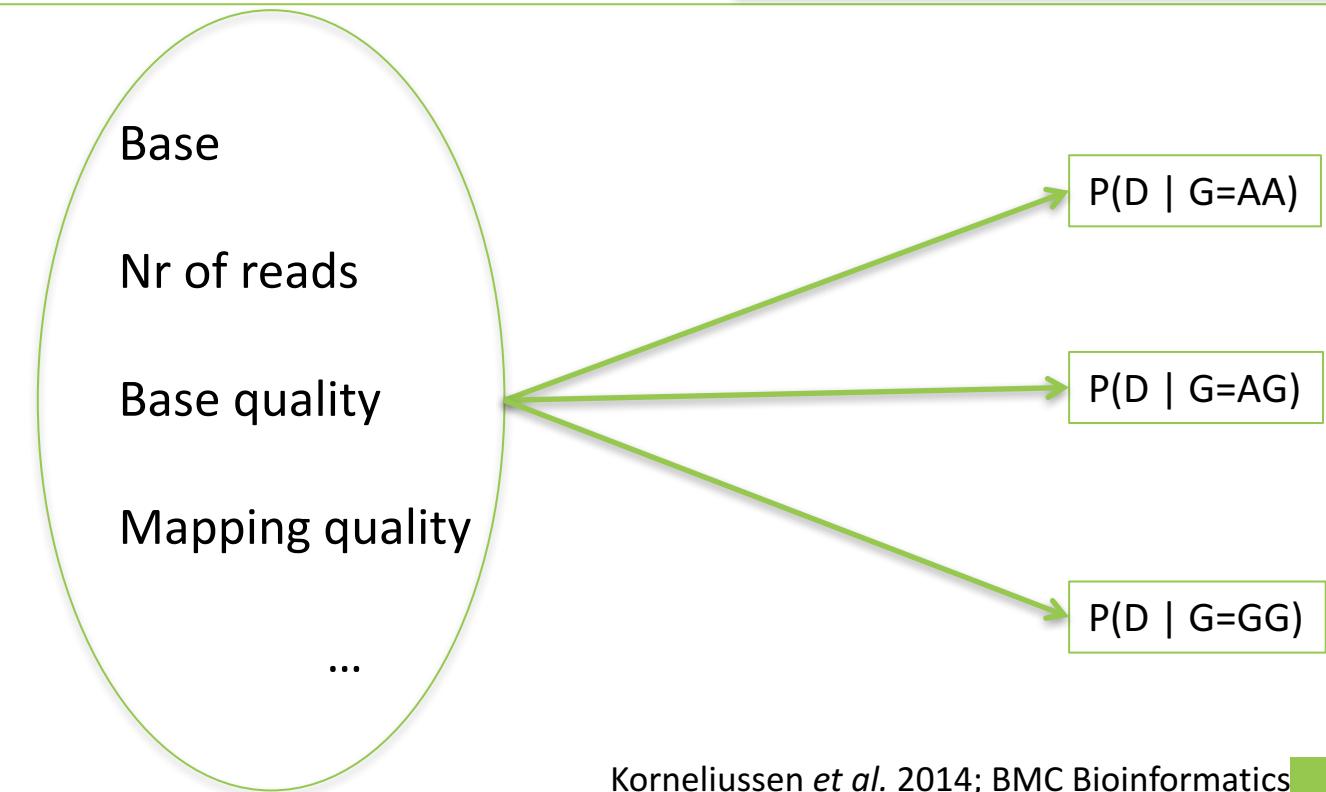
Genotype likelihoods (ANGSD)

- Low coverage individual sequencing: ~2x
- Sequencing many individuals!
- Cheap library preparation, ~5.- CHF (Therkildsen & Palumbi 2017)

- SFS
- Demographic inferences
- Outlier detection
- GWAS
-

Base quality in Phred scale

Chrom1 272 A 24 AAAAAGGAGAGGTAAG <<<+;<<<<<<<=<;7<&



It is time to go big.....

Fischer et al. BMC Genomics (2017) 18:69
DOI 10.1186/s12864-016-3459-7

BMC Genomics

RESEARCH ARTICLE

Open Access

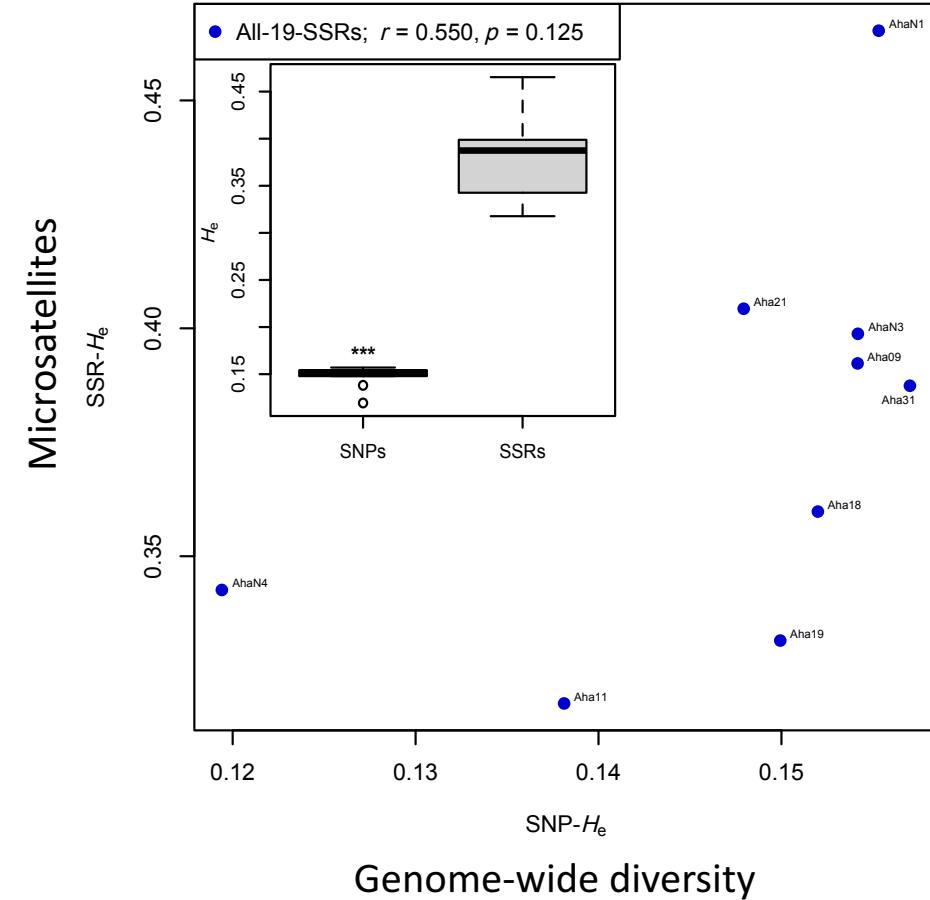


Estimating genomic diversity and population differentiation – an empirical comparison of microsatellite and SNP variation in *Arabidopsis halleri*

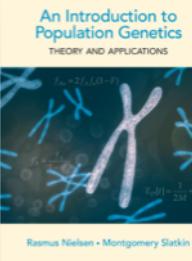
Martin C. Fischer^{1*}, Christian Rellstab², Marianne Leuzinger¹, Marie Roumet¹, Felix Gugerli², Kentaro K. Shimizu³, Rolf Holderegger^{1,2} and Alex Widmer¹

- ❖ Make use of the new NGS tools!
- ❖ E.g. Microsatellite (SSR) data are unreliable estimate of genome-wide diversity

➤ ~4000 random SNPs are required to get $\text{SNP-}H_e$ estimate of an accuracy of ± 0.005



Further Reading



Nielsen R & Slatkin M (2013) An Introduction to Population Genetics: Theory and applications. *Sinauer*

Cutter AD, Payseur BA (2013) Genomic signatures of selection at linked sites: unifying the disparity among species. *Nature Reviews Genetics* **14**, 262-274.

Fischer MC, Rellstab C, Leuzinger M, et al. (2017) Estimating genomic diversity and population differentiation – an empirical comparison of microsatellite and SNP variation in *Arabidopsis halleri*. *BMC Genomics* **18**, 69.

Fischer MC, Foll M, Heckel G, Excoffier L (2014) Continental-scale footprint of balancing and positive selection in a small rodent (*Microtus arvalis*). *PLoS One* **9**, e112332.

Fischer MC, Rellstab C, Tedder A, et al. (2013) Population genomic footprints of selection and associations with climate in natural populations of *Arabidopsis halleri* from the Alps. *Molecular Ecology* **22**, 5594-5607.

Fischer MC, Foll M, Excoffier L, Heckel G (2011) Enhanced AFLP genome scans detect local adaptation in high-altitude populations of a small rodent (*Microtus arvalis*). *Molecular Ecology* **20**, 1450-1462.

Hohenlohe PA, Phillips PC, Cresko WA (2010) Using population genomics to detect selection in natural populations: key concepts and methodological considerations. *International Journal of Plant Sciences* **171**, 1059-1071.

Oleksyk TK, Smith MW, O'Brien SJ (2010) Genome-wide scans for footprints of natural selection. *Philosophical Transactions of the Royal Society B: Biological Sciences* **365**, 185-205.

Storz JF (2005) Using genome scans of DNA polymorphism to infer adaptive population divergence. *Molecular Ecology* **14**, 671-688.

Rellstab C, Fischer MC, Zoller S, et al. (2017) Local adaptation (mostly) remains local: reassessing environmental associations of climate-related candidate SNPs in *Arabidopsis halleri*. *Heredity* **118**, 193-201.

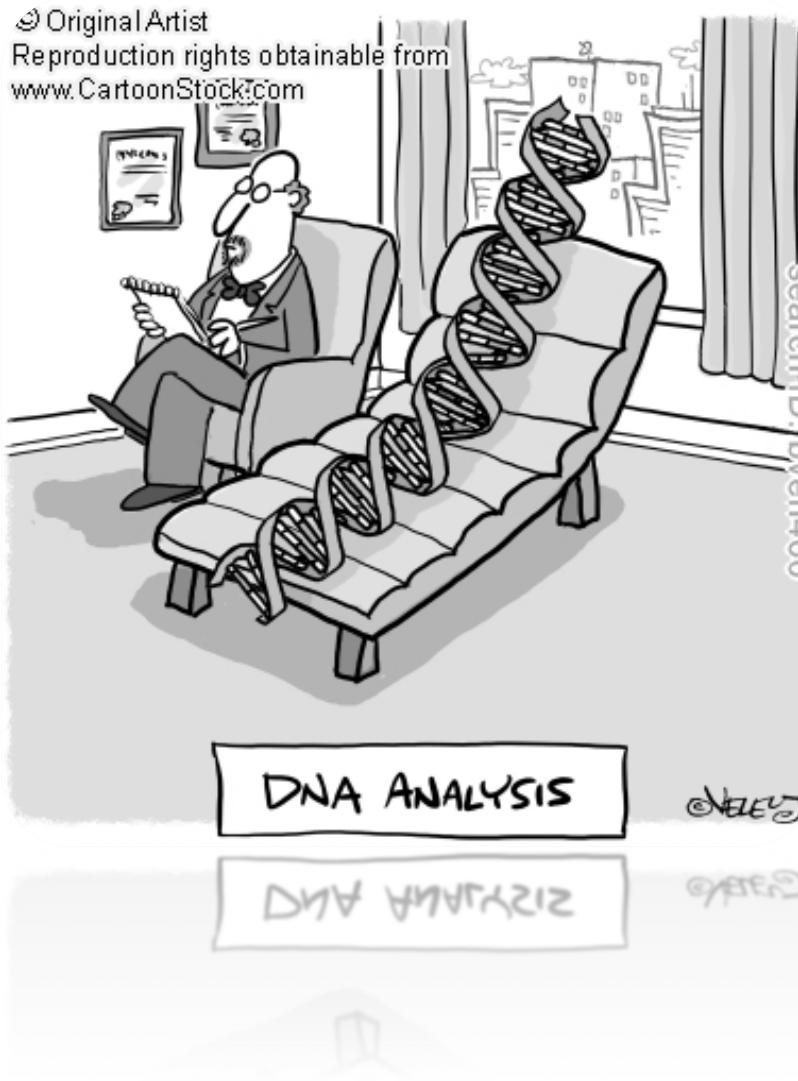
Rellstab C, Zoller S, Tedder A, Gugerli F, Fischer MC (2013) Validation of SNP allele frequencies determined by pooled next-generation sequencing in natural populations of a non-model plant species. *PLoS One* **8**, e80422.

Rellstab C, Gugerli F, Eckert AJ, Hancock AM, Holderegger R (2015) A practical guide to environmental association analysis in landscape genomics. *Molecular Ecology* **24**, 4348-4370.

Winter School: Bioinformatics for Adaption Genomics (B@G): <http://www.adaptation.ethz.ch/education/winter-school-2017.html>

➤ Bioinformatics resources: <http://www.adaptation.ethz.ch/education/winter-school-2017/teaching-resources.html>

Thanks!



Box 1**Critical Population Genetic Concepts and Statistical Measures Used to Detect Selection in Population Genomics**

Allele frequency spectrum (AFS): The distribution of frequencies across alleles in a sample. Tests based on AFS using DNA sequence data rely on a few related statistics, all of which are comparisons between estimates of the population genetic parameter $\theta = 4N\mu$. The statistics are calculated as the difference of two such estimates, normalized by the expected variance of the difference under a neutral model, so that values below -2 or greater than 2 roughly exceed the 95% confidence limits about the neutral expectation of 0. However, the actual mean may frequently deviate from 0 (Thornton 2005; Wares 2010). Simonsen *et al.* (1995) compared three measures and found Tajima's D to have the most statistical power:

Tajima's D : Normalized difference between π and S , the number of segregating sites (Tajima 1989).

Fu and Li's D^* : Normalized difference between S and the number of singletons η (alleles observed only once in a sample; Fu and Li 1993).

F^* : Normalized difference between π and η (Fu and Li 1993).

Background selection: Ongoing selection against deleterious mutations that can result in the loss of linked neutral variation (Charlesworth *et al.* 1993).

Balancing selection: Here we define balancing selection broadly as the class of selective forces that maintain polymorphism over time. This can include, for example, frequency-dependent selection or heterozygote advantage (Charlesworth 2006).

Coalescent theory: A theoretical framework for understanding genetic variation based on the retrospective pattern of shared ancestry among alleles in a sample (Wakeley 2009).

Divergent selection: Positive selection acting differentially between separate populations.

dN/dS : Ratio of nonsynonymous (amino acid-changing) to synonymous substitutions in a nucleotide sequence. Testing for selection based on this ratio typically uses aligned sequence data among populations or taxa and can detect selection over long timescales, although it requires multiple amino acid substitutions (i.e., recurrent selective sweeps).

F_{ST} : A statistic describing the partitioning of allelic variance within versus among populations; F_{ST} ranges from 0 (no population differentiation) to 1 (complete population differentiation). There are multiple ways of calculating F_{ST} that can occasionally have substantial effects on its value but rarely its relative magnitude among loci (Charlesworth 1998; Holsinger and Weir 2009). Commonly used population genomic tests for selection based on identifying outliers in F_{ST} are as follows:

LOSITAN (Antao *et al.* 2008) computer software implements the method of Beaumont and Nichols (1996) to identify F_{ST} outliers based on heterozygosity, which affects the predicted neutral distribution of F_{ST} .

ARLEQUIN (Excoffier *et al.* 2009) software performs the same analysis, accounting for hierarchical population structure.

BAYESFST (Beaumont and Balding 2004) assesses the significance of a locus-specific parameter that indicates selection in a model of F_{ST} .

BAYESCAN (Foll and Gaggiotti 2008) modifies the approach of Beaumont and Balding (2004) to estimate the posterior probability of a locus being subject to selection.

DETSEL (Vitalis *et al.* 2003) uses coalescent simulations in a simple two-population model to identify F_{ST} outliers.

Genetic draft: The loss of genetic diversity and changes in AFS at loci linked to a selected locus during a selective sweep (Gillespie 2000).

HKA test: A test of the neutral prediction for the relationship between within-population diversity and among-population divergence (Hudson *et al.* 1987).

Linkage disequilibrium (LD): The correlation between alleles across loci. Traditionally, LD has been calculated as a function of a pair of loci, regardless of their physical position (Slackin 2008). This aspect of LD can be partitioned among populations in the statistic Z_g as a test of selection (Storz and Kelly 2008). Genome scans for selection also apply several of the following statistics that describe the decay of LD as a function of physical distance, also known as haplotype structure:

Extended haplotype homozygosity (EHH) measures the probability that any two randomly chosen haplotypes are identical over a given distance from a focal site (Sabeti *et al.* 2002).

Integrated haplotype score (iHS) integrates the area under the EHH curve (Voight *et al.* 2006). Huff *et al.* (2010) found this measure to have greater statistical power and to be more robust to complex demographics than two related alternatives.

Cross-population extended haplotype homozygosity (XP-EHH) compares EHH between two populations to test for interpopulation differences in the extent of LD (Sabeti *et al.* 2007).

π : A measure of nucleotide diversity, calculated as the proportion of pairwise differences in a sample; π can be estimated either within or between populations and is directly used in some calculations of F_{ST} (Charlesworth 1998).

Positive (directional) selection: Selection in which one or a class of alleles is favored.

Selective sweeps: The increase in frequency of one or a class of alleles favored by selection. Hard sweeps result from selection on a single allele, typically a new mutation that is favored immediately on its appearance in a population. Soft sweeps are selection on standing genetic variation or on variants supplied by recurrent mutation or migration during the selective phase, so that a number of different alleles are collectively favored and increase in frequency. These alleles are typically considered to be neutral or even deleterious before a shift in selective regime (Hermisson and Pennings 2005).