The Amount and Structure of Genetic Diversity in a Global Sample of Oats

Alf Ceplitis
Lantmännen Lantbruk

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The Lantmännen Group

One of the largest Groups within agriculture, machinery, energy and food in the Nordic region.

Owned by more than 35,000 Swedish farmers

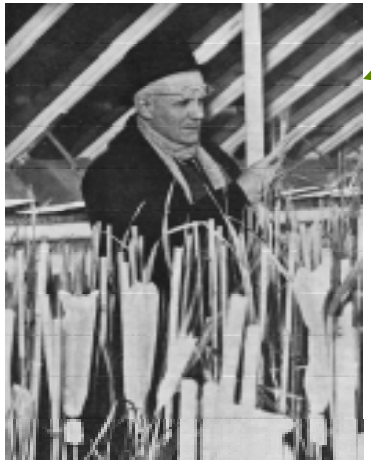
More than 10,000 employees

Operates in 22 countries

Plant Breeding at Lantmännen Lantbruk

Formerly Svalöf Weibull AB

- Based in Svalöv, Sweden
- Breeding stations in Sweden, Germany & the Netherlands
- Breeding of cereals, oil crops, forage crops, Salix
- Breeding started in 1870s, first oat in 1897



Golden Rain (1903)

Victory (1908)

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Association mapping in oats

- Global collection of 587 oat accession (mostly modern varieties)
- 53 countries from all continents represented
- Genotyping with ~2,000 DArT markers (+ ~6,000 SNP markers)
- Phenotyping of resistance, quality and performance
- Work in progress, current data set includes:
  - 498 accessions
  - 497 DArT markers
- More on this on Friday 22, 08:50 a.m., Parallel Session 1

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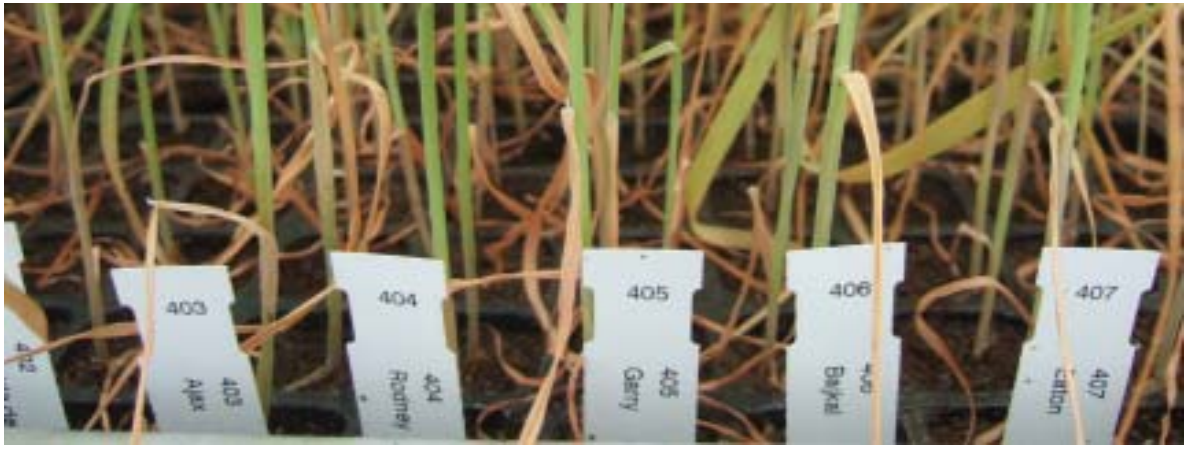
Association mapping in oats

Basic population genetics

- Overall diversity within the oat gene pool
- Population structure
- Decay of linkage disequilibrium with distance



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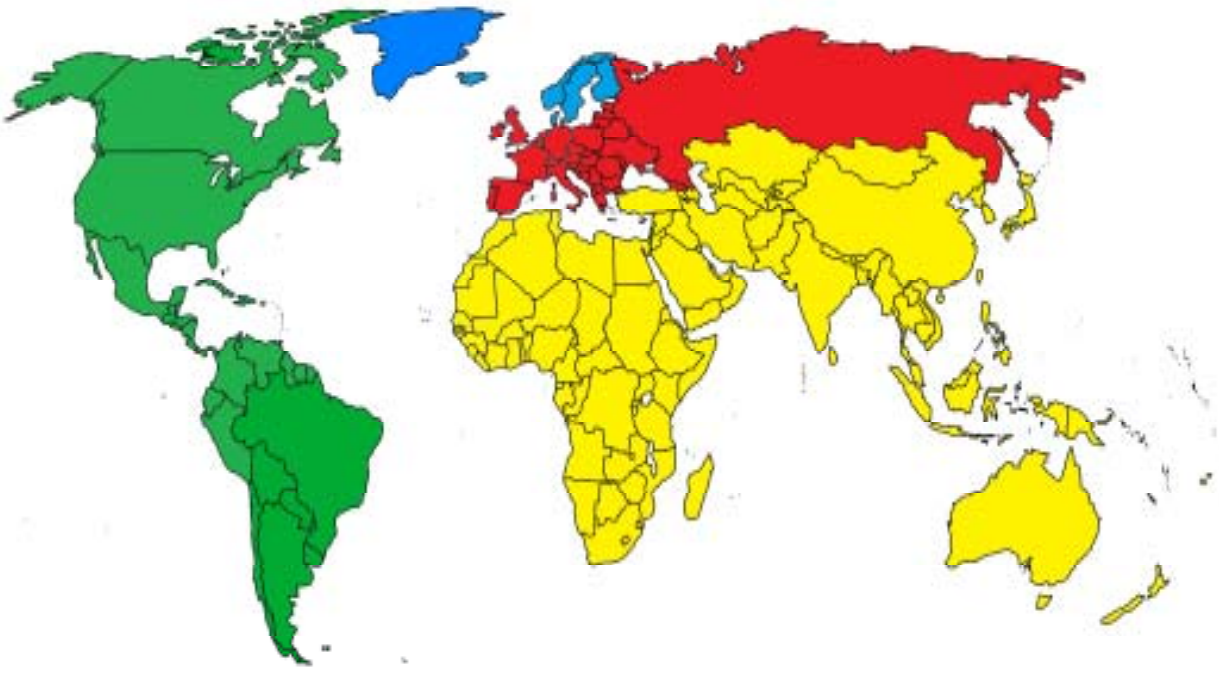
Association mapping in oats

Regions of origin of accessions included in the panel



- Nordic: 175 acc.
- Europe: 202 acc.
- Americas: 68 acc.
- Rest of world: 47 acc.
- Unknown: 6 acc.

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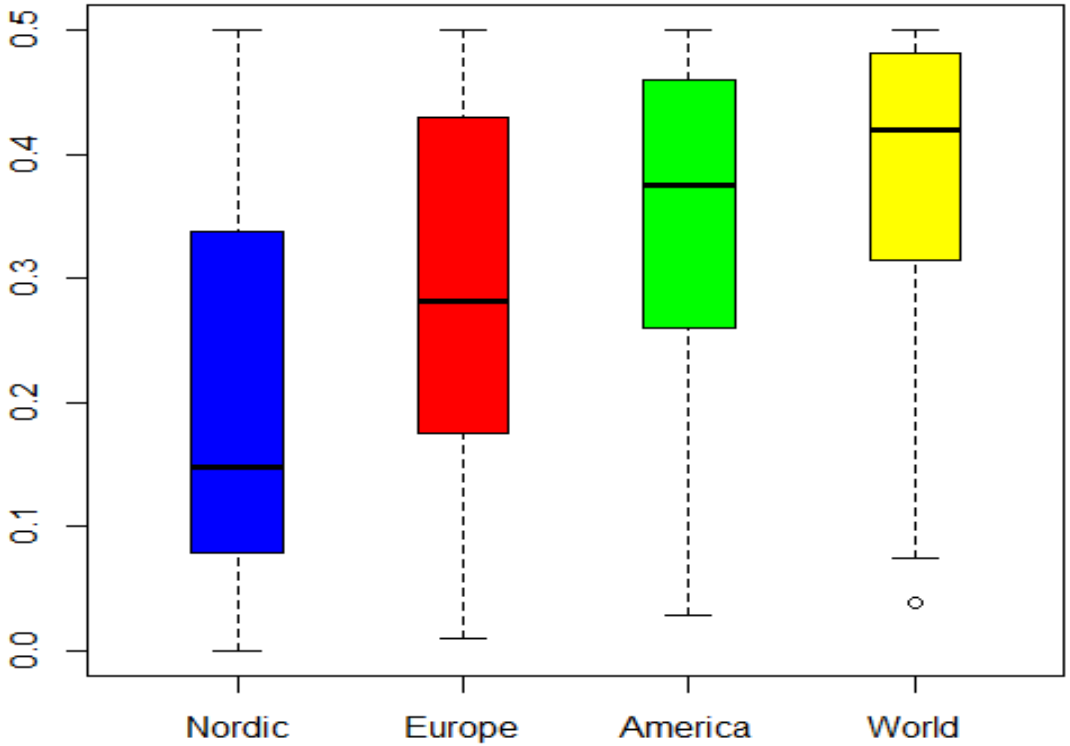
Genetic diversity in oats

Expected heterozygosity by region, 497 DArTs, 498 accessions



Whole panel *H* = 0.299

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Population structure in oats

Pairwise genetic differentiation (as F_{ST}) between regions

	Europe	Americas	World
Nordic	0.027	0.077	0.095
Europe		0.028	0.037
Americas			0.017

Overall F_{ST} = 0.068

F_{ST} = 0.292 among genbank samples of Swedish 19th century landraces (Hagenblad *et al*. 2012)

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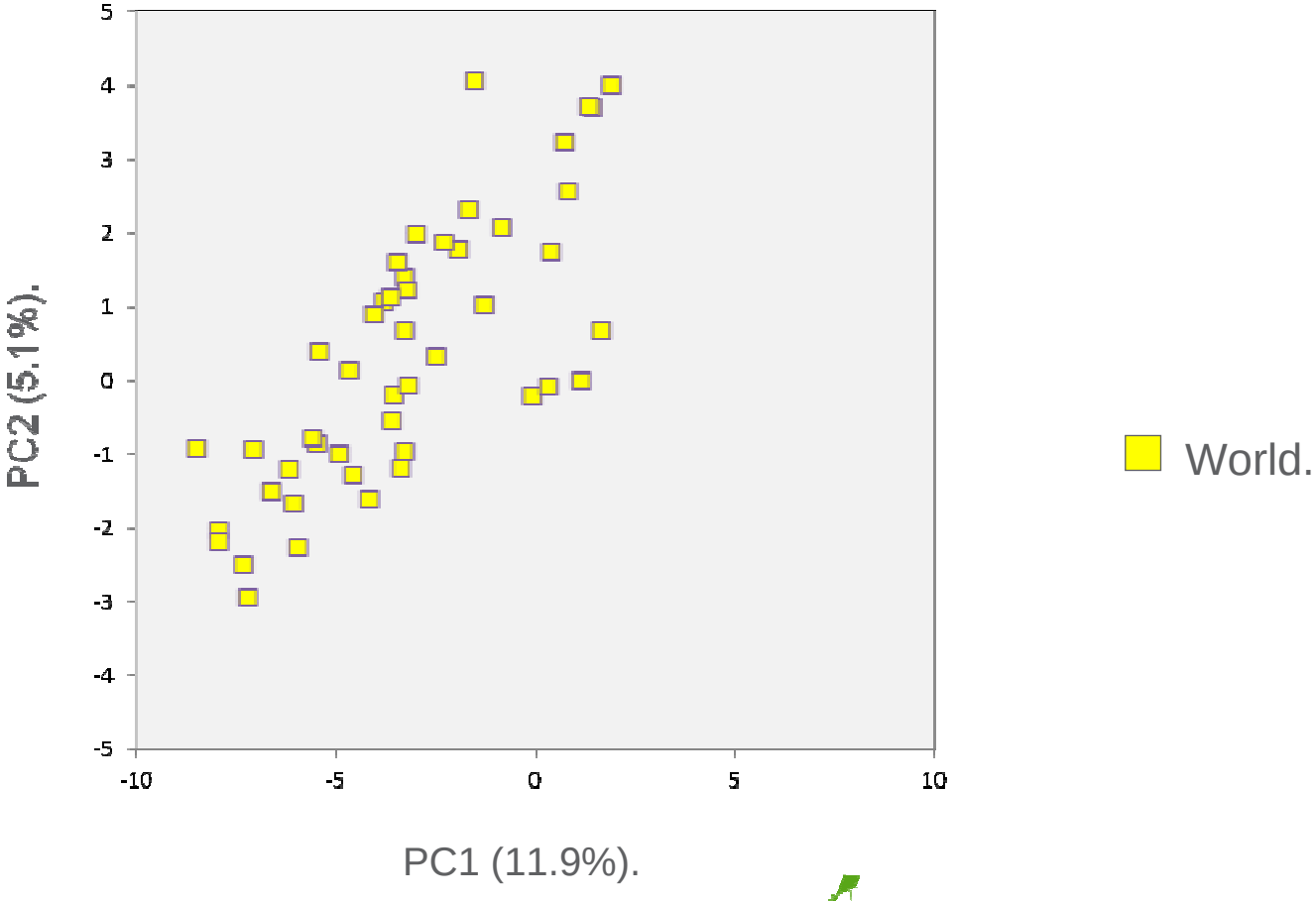
Population structure in oats

PCA based on allele frequencies



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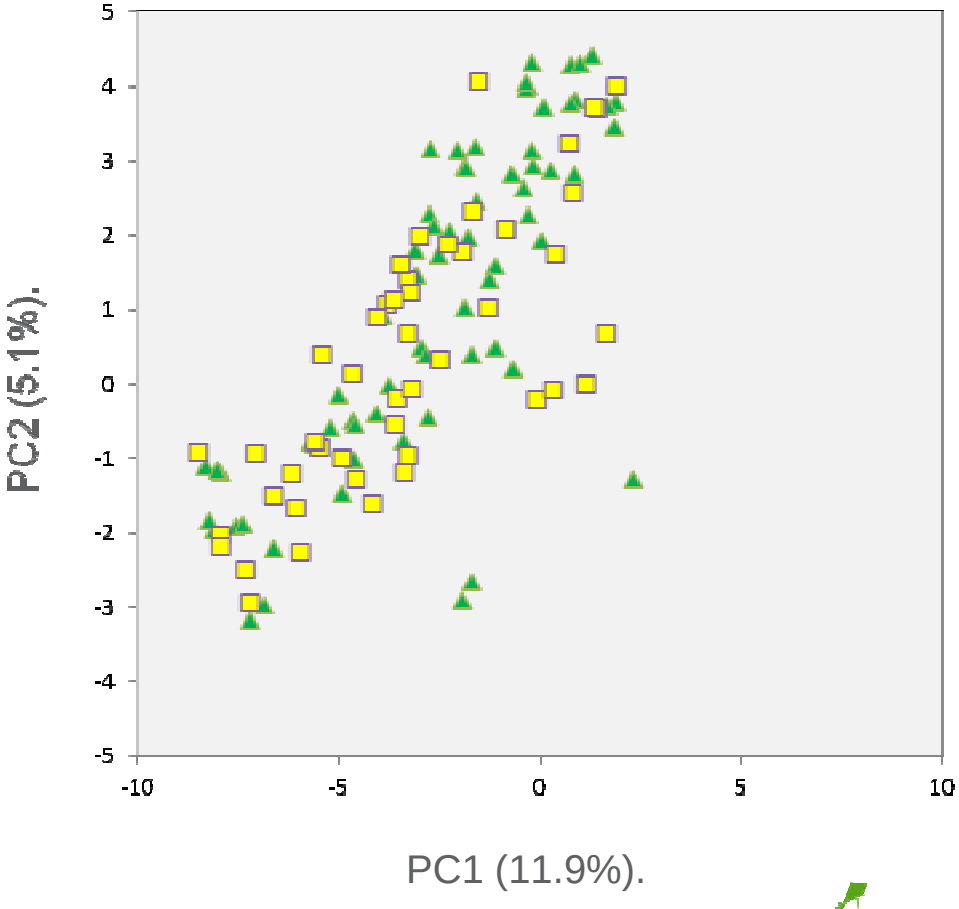
Population structure in oats

PCA based on allele frequencies



Americas

World.

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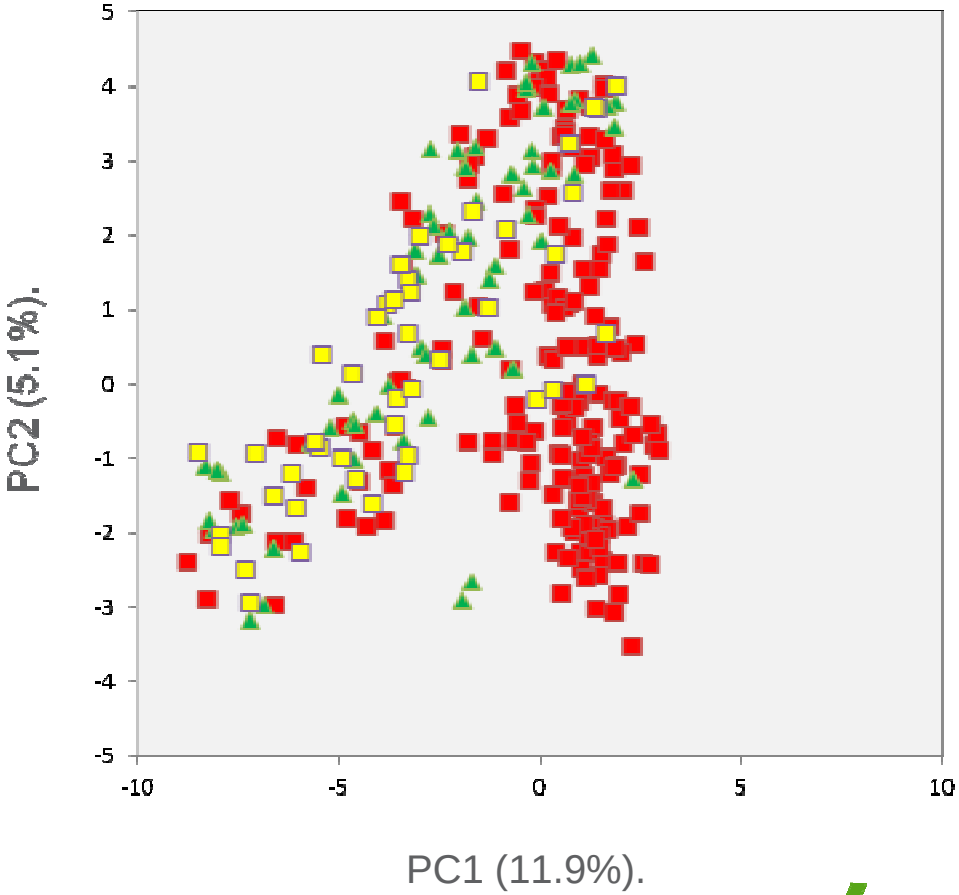
Population structure in oats

PCA based on allele frequencies



Europe

Americas

World.

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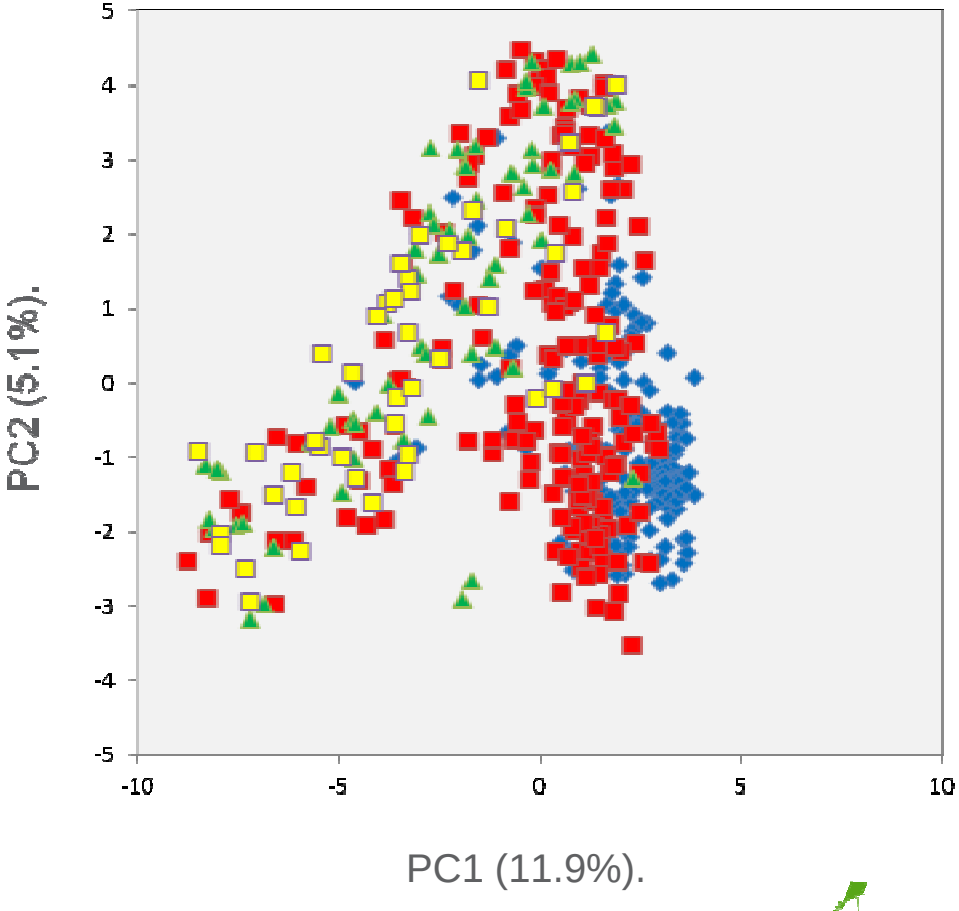
Population structure in oats

PCA based on allele frequencies



- Nordic
- Europe
- Americas
- World.

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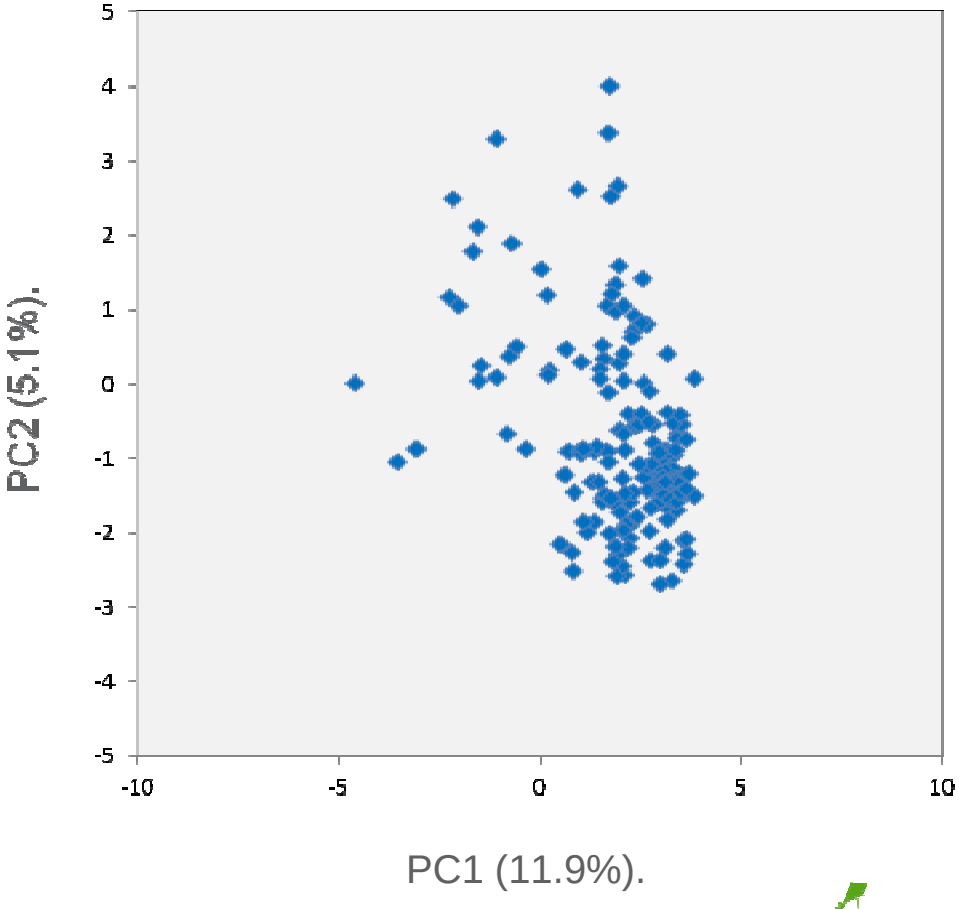
Population structure in oats

PCA based on allele frequencies



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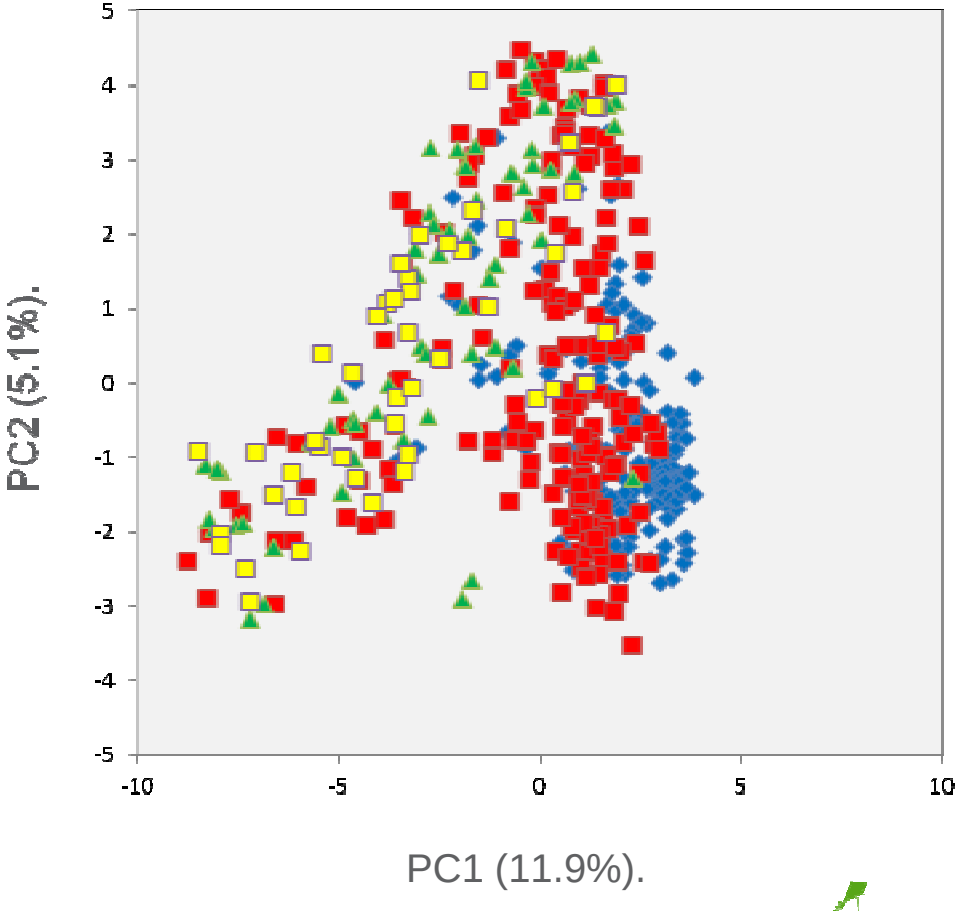
Population structure in oats

PCA based on allele frequencies



- Nordic
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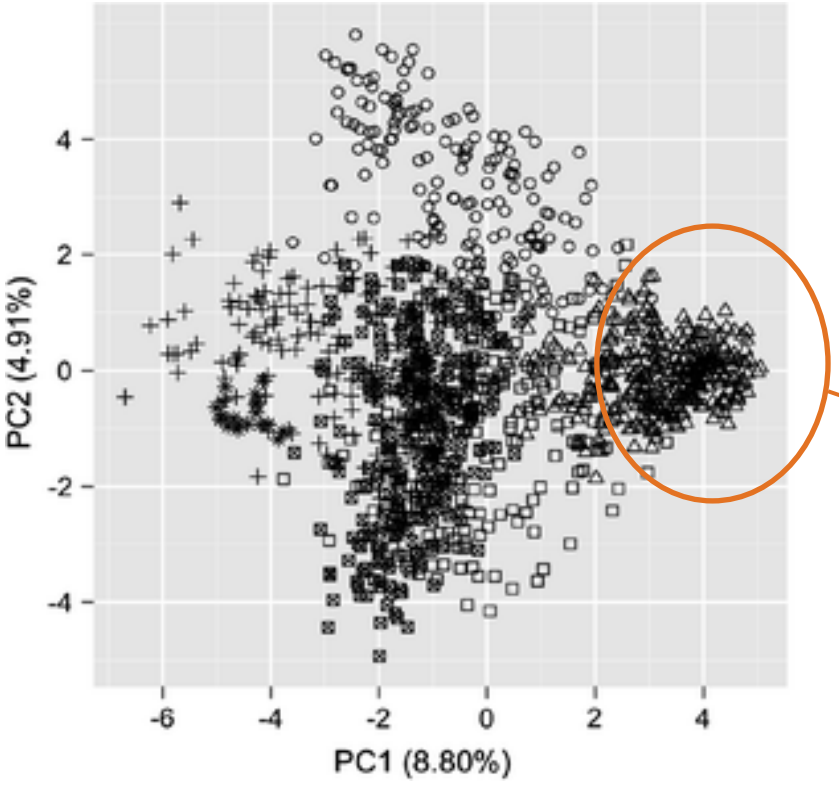
Population structure in oats



Newell et al. 2011, *TAG*

- 1,205 lines, 402 DArT markers
- 60% US & Canadian lines
- Six clusters identified

Cluster 2 contains European/Nordic varieties

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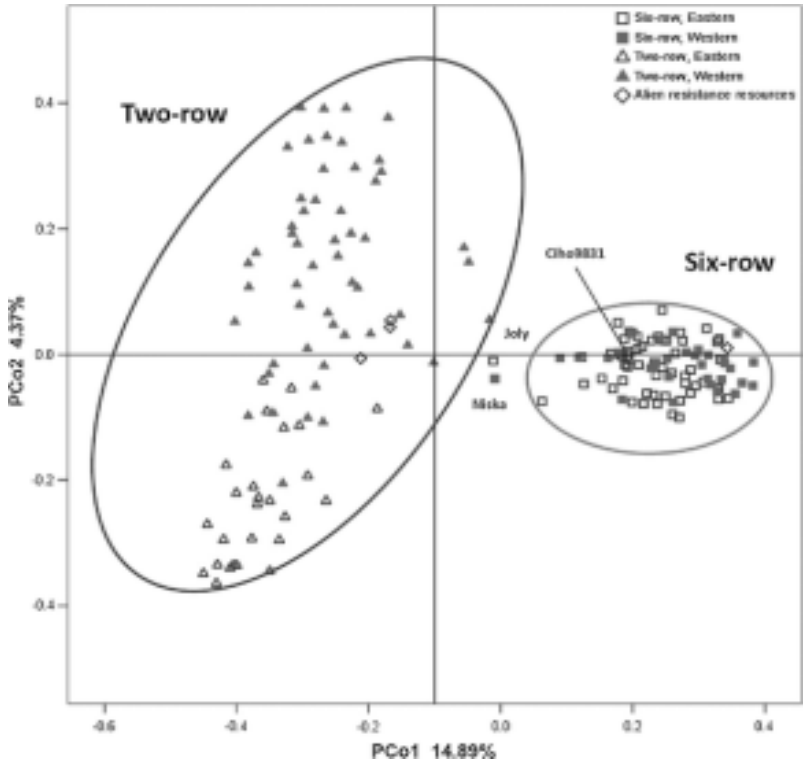
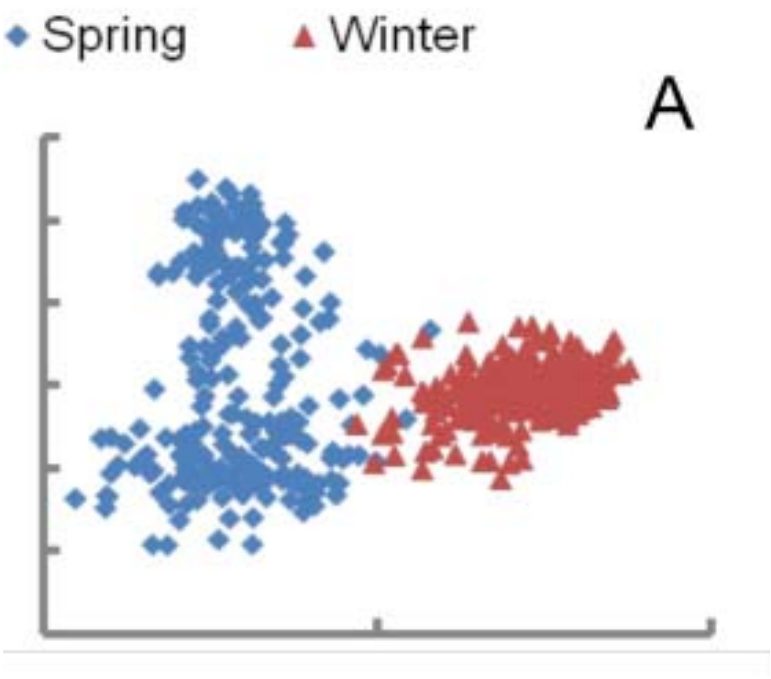
Population structure in barley & wheat



Canadian barley, Zhang et al. 2009



US wheat, Chao et al. 2010

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Population structure in oats

Probabilistic assignment of accessions to clusters with genetic equilibrium

- STRUCTURE algorithm (Pritchard et al. 2000)
- Admixture model, correlated allele frequencies
- K = 1 – 6 (clusters tested)
- Region-of-origin as prior
- 40K burn-in, 200K iterations, 2 runs per K
- Output: posterior probability of K clusters given data (and priors)

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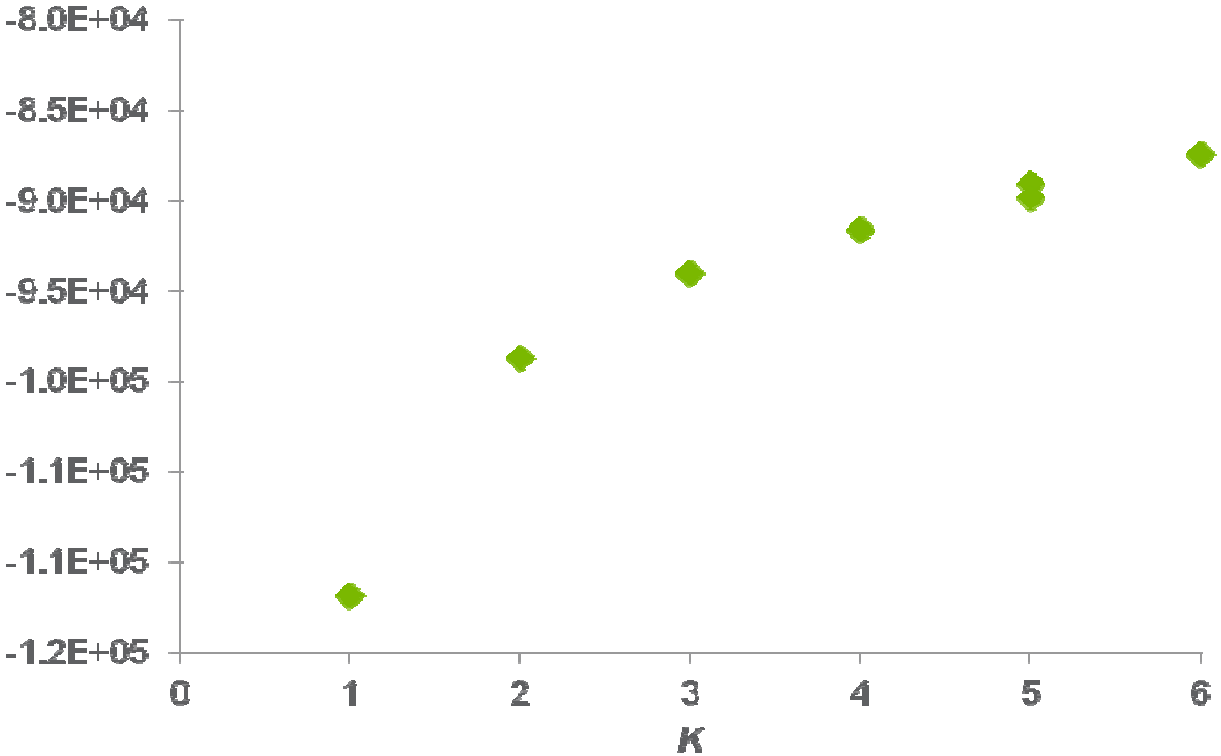
Population structure in oats

Posterior probability of different number of populations (*K*)



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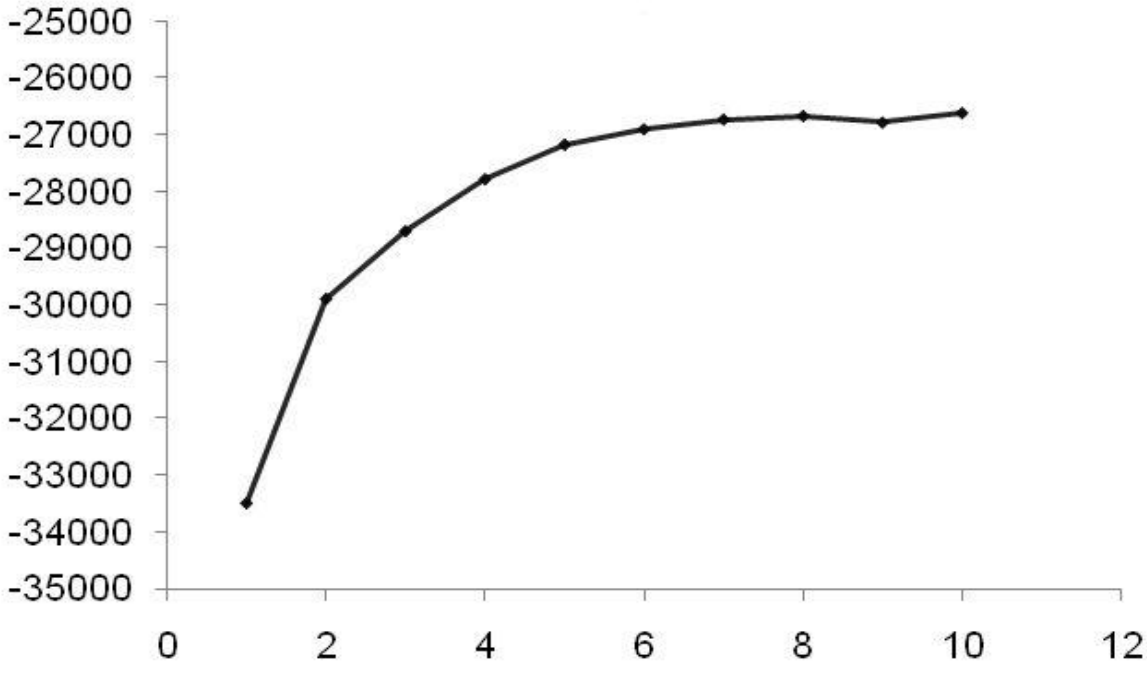
Population structure in barley

Based on 1088 DArTs scored in 224 accessions of the Gatersleben Core Collection



Pasam et al. 2012, *BMC Biology*

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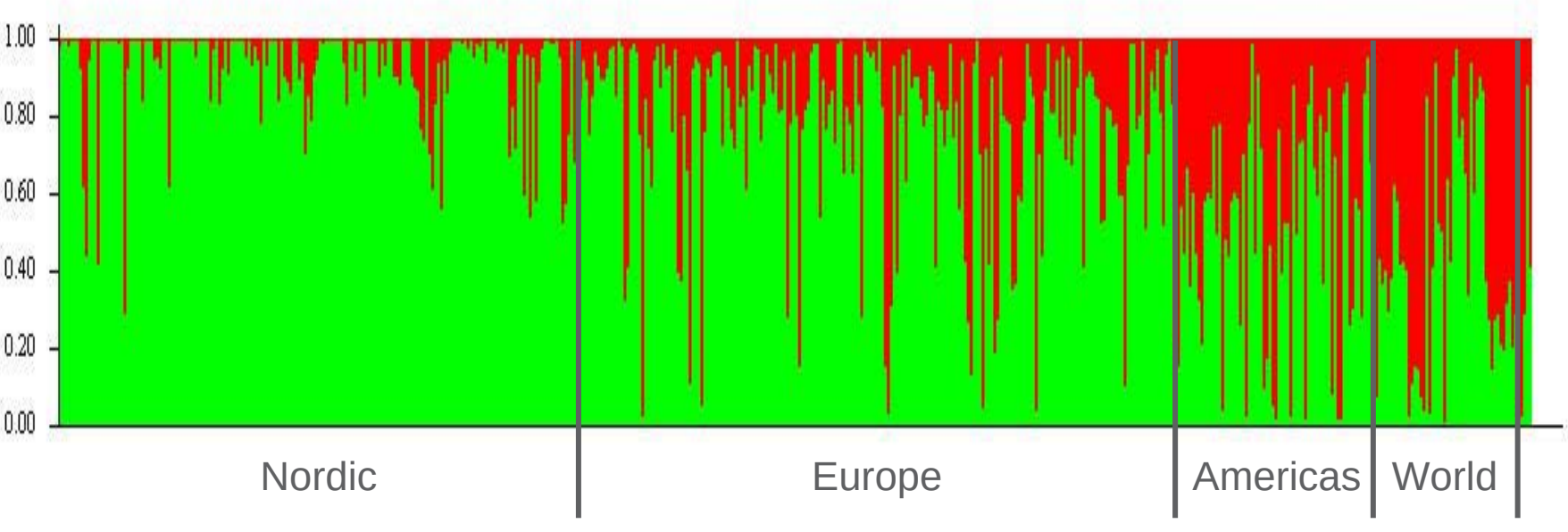
Population structure in oats

Proportion of *K* inferred clusters in each accession



K = 2

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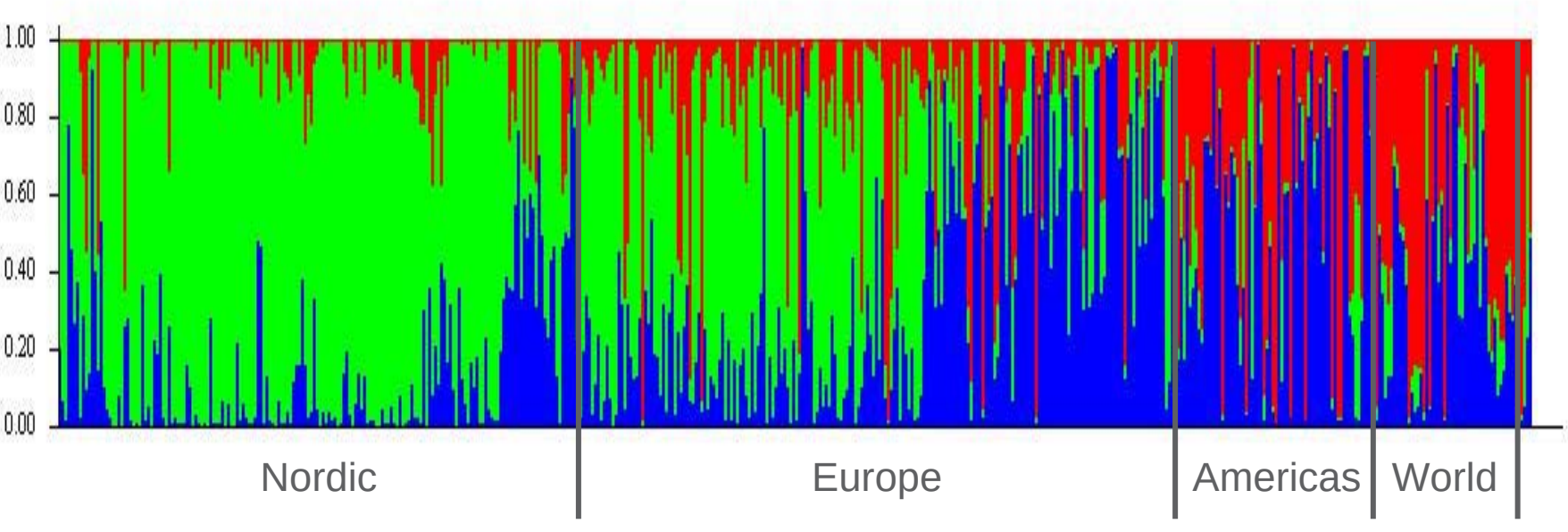
Population structure in oats

Proportion of *K* inferred clusters in each accession



K = 3

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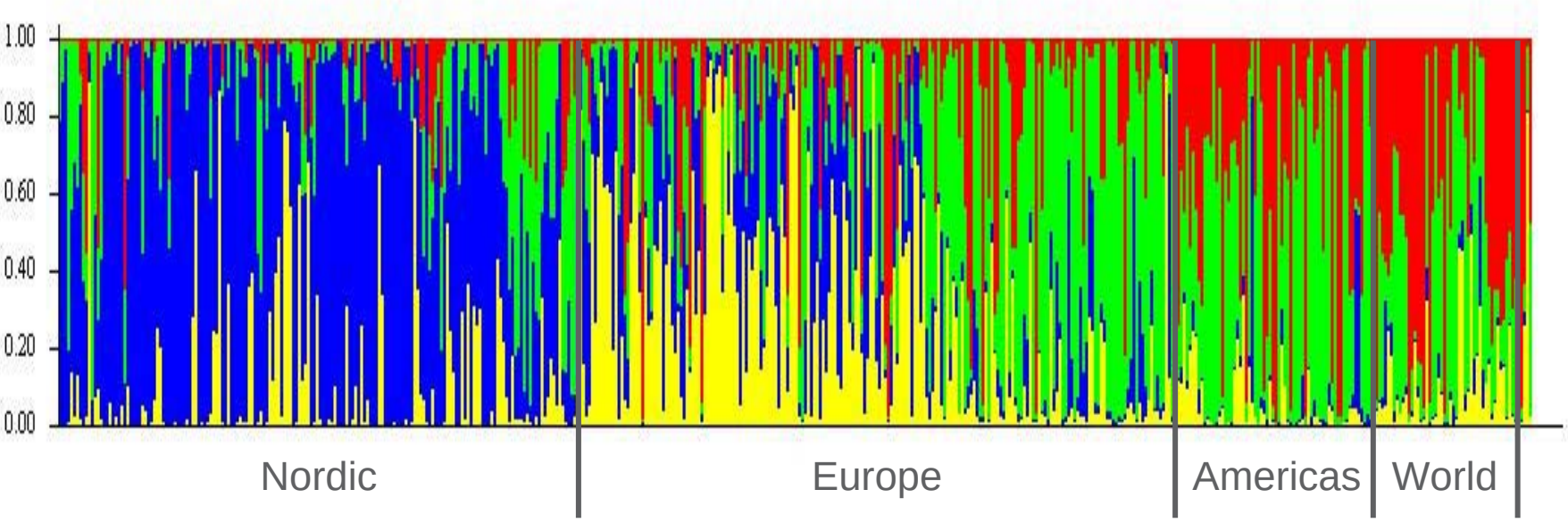
Population structure in oats

Proportion of *K* inferred clusters in each accession



K = 4

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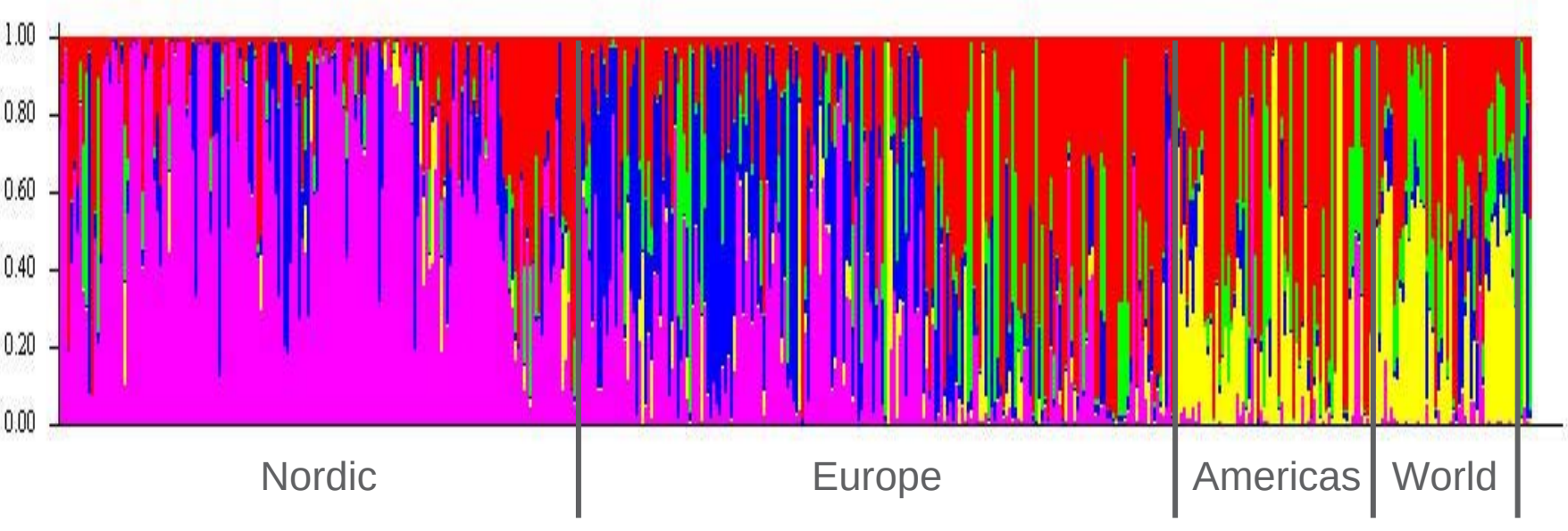
Population structure in oats

Proportion of *K* inferred clusters in each accession



$K = 5$

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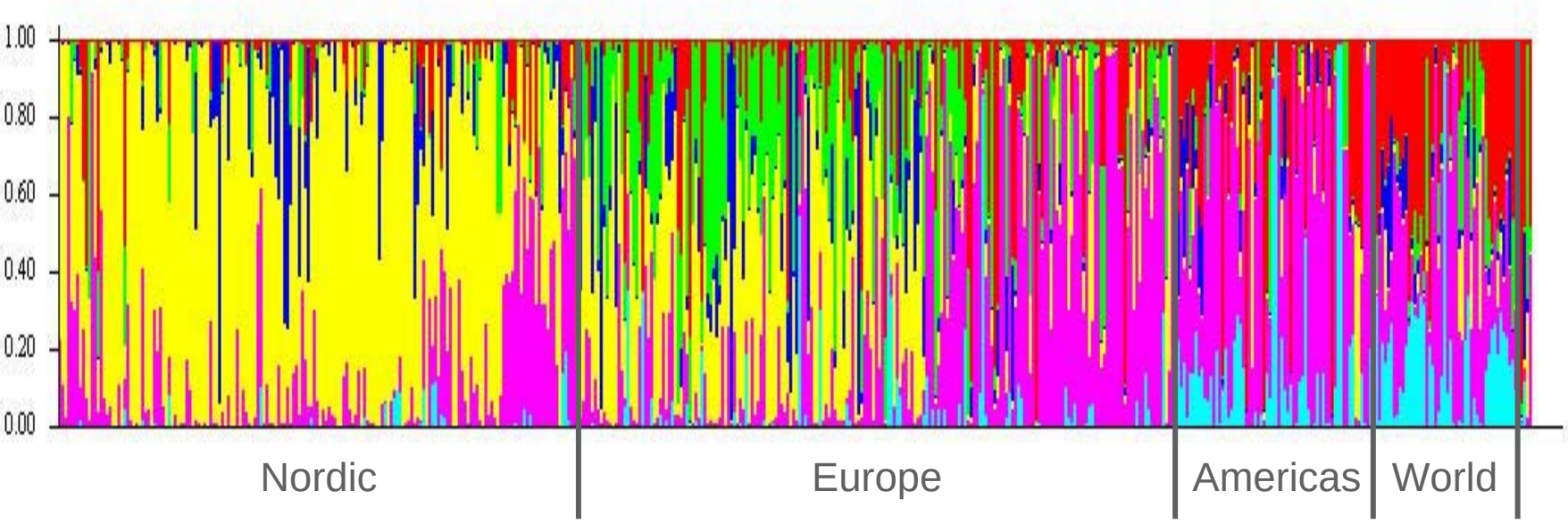
Population structure in oats

Proportion of *K* inferred clusters in each accession



K = 6

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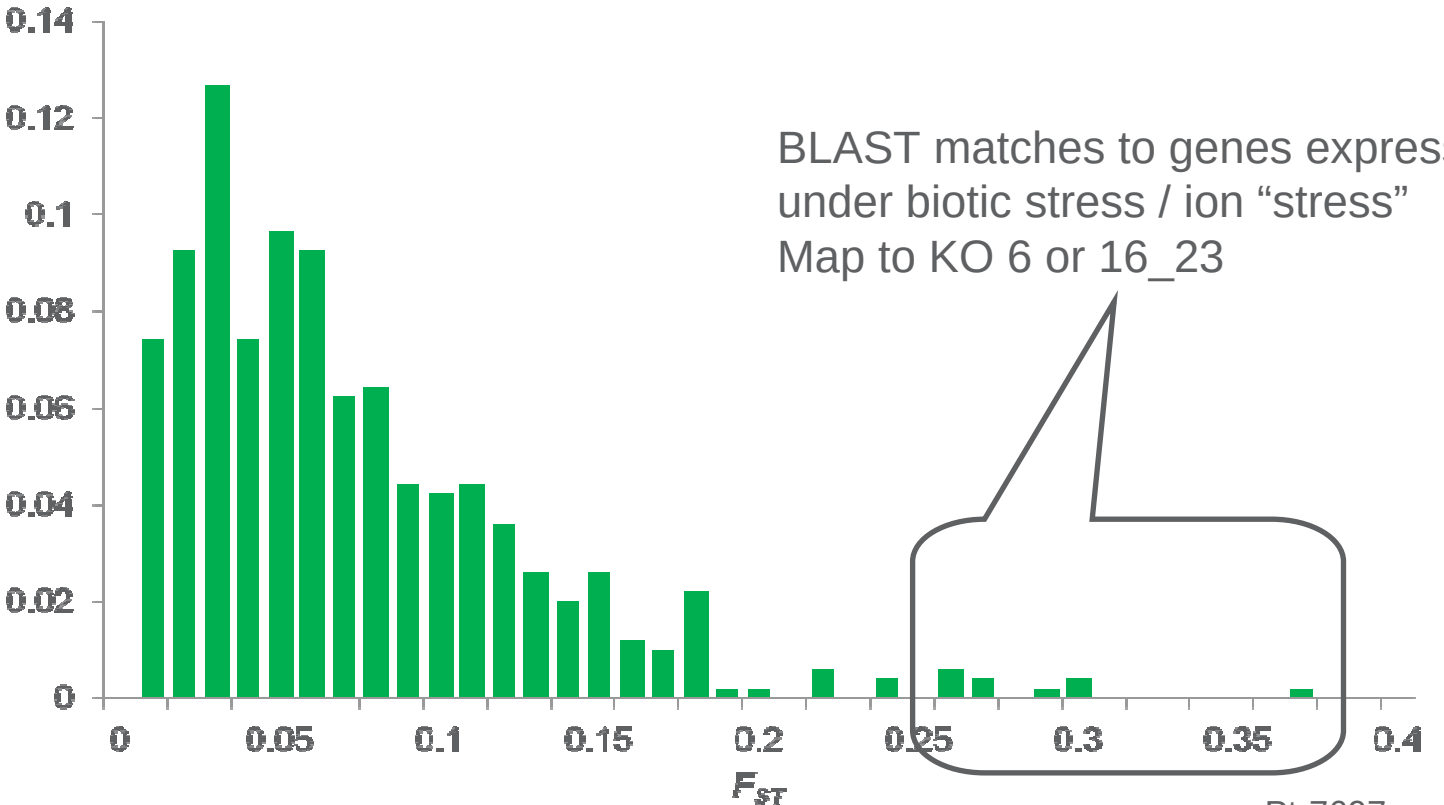
Population structure in oats

Per-locus F_{ST} among regions



BLAST matches to genes expressed under biotic stress / ion “stress”
Map to KO 6 or 16_23

oPt-7697

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Linkage disequilibrium *vs*. distance

Rate of decay of LD estimated from two different genetic maps

Parameter	Kanota x Ogle (KO)	Firth x SW Betania (FB)
Population type	RIL	RIL
Population size	80	184
Number of markers	1010+287	366
Map length	2028 cM	693 cM
Linkage groups	34	39
F_1 translocation het.	Yes	No

Decay curve fitted by non-linear least-square regression $L = \frac{1}{(d+1)^{\theta}}$

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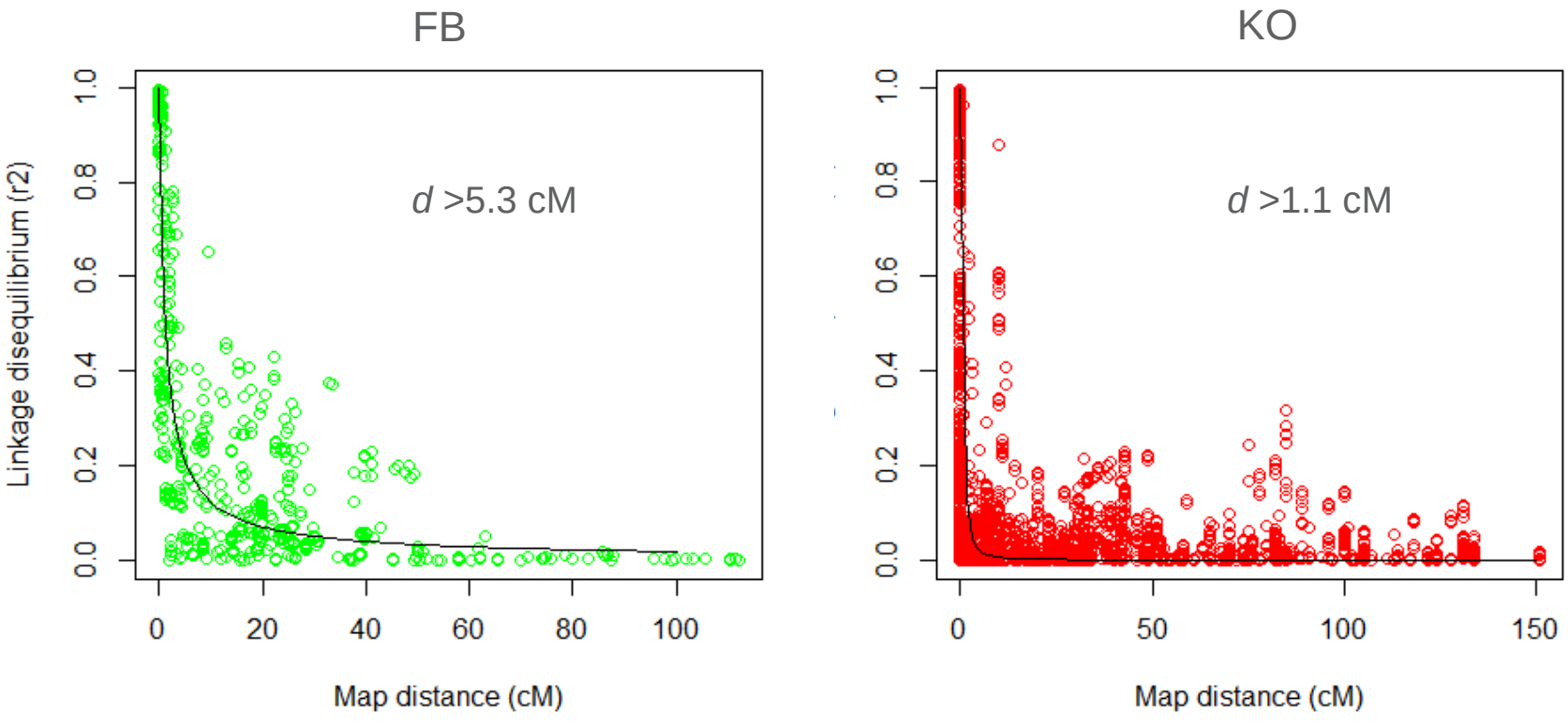
Linkage disequilibrium *vs*. distance

At which distance is $r^2 < 0.2$?



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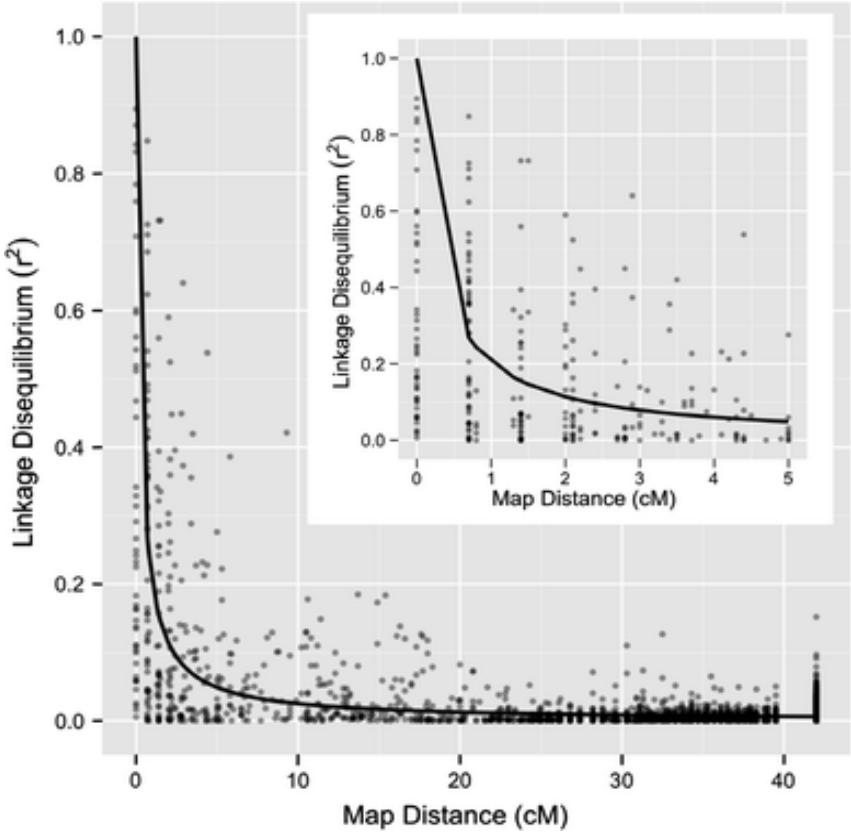
Linkage disequilibrium vs. distance



Newell et al. 2011, *TAG*

$r^2 < 0.2$ at distances >1.0 cM

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Thanks to…

Swedish Farmers' Foundation for Agricultural Research

- The Swedish Farmers' Foundation of Agricultural Research
- The CORE team
- Dr Ren Changzhong
- Dr Keith Armstrong
- Dr John Stevens
- Special thanks to Andy Hay & crew, Plant & Food Research, NZ

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"…you are bloody lucky you are sitting on the other side of the world while we are attempting to get these out of the field!!!!!"