



Lantmännen



SNP and DArT Diversity in European Oat Germplasm

Alf Ceplitis

AOWC, Ottawa, 2014

The Lantmännen Group

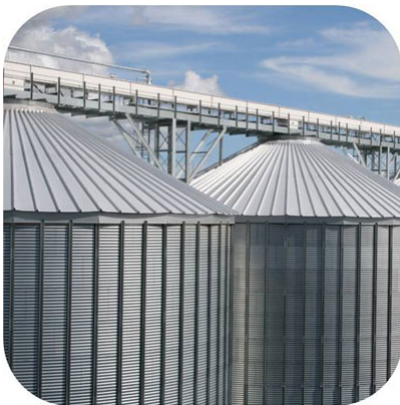
One of the largest Groups within agriculture, machinery, energy and food in the Nordic region.



Owned by more than **35,000** Swedish farmers

More than **10,000** employees

Operates in **22** countries



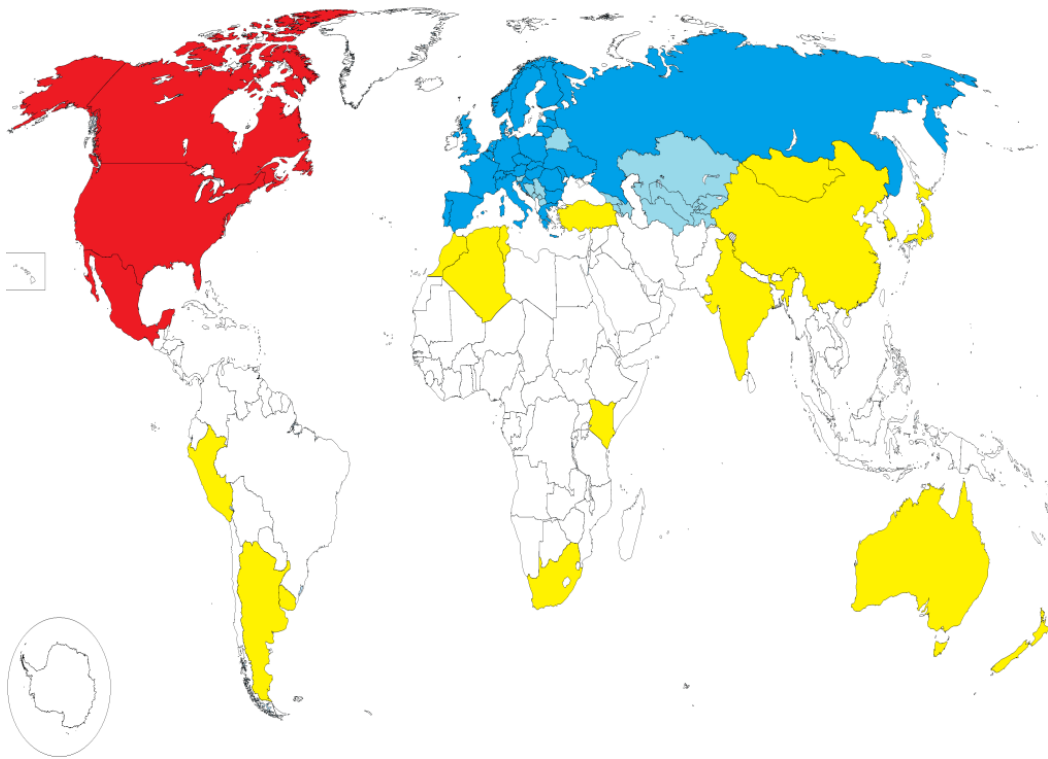
Plant Breeding at Lantmännen

Formerly Svalöf Weibull / SW Seed

- Spring oats
- Spring & winter wheat
- Spring barley
- Triticale
- Canola (rapeseed)
- Forage grasses & legumes
- Salix
- Potatoes



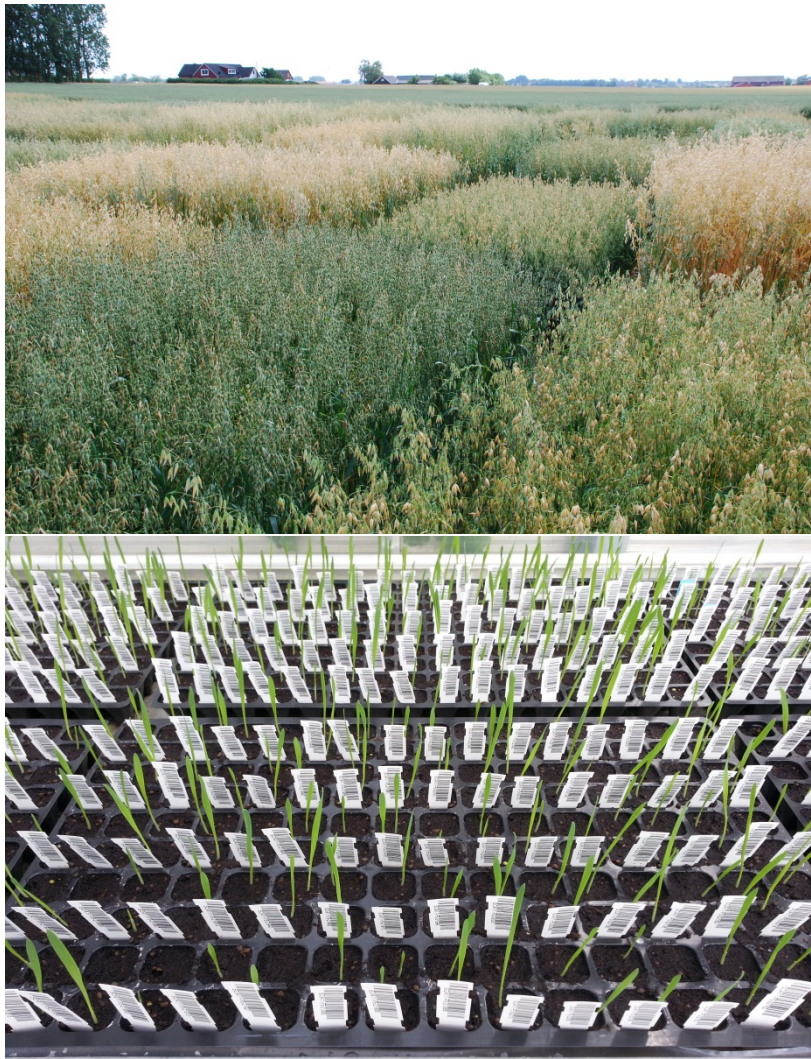
The Global Oat Diversity (GOD) Panel



Region	Accessions
Europe	410
N America	62
Rest of the world	63
Unknown	52
Total	587

- 50 countries represented
- Few winter types

Association Mapping with the GOD Panel



Phenotypic data:

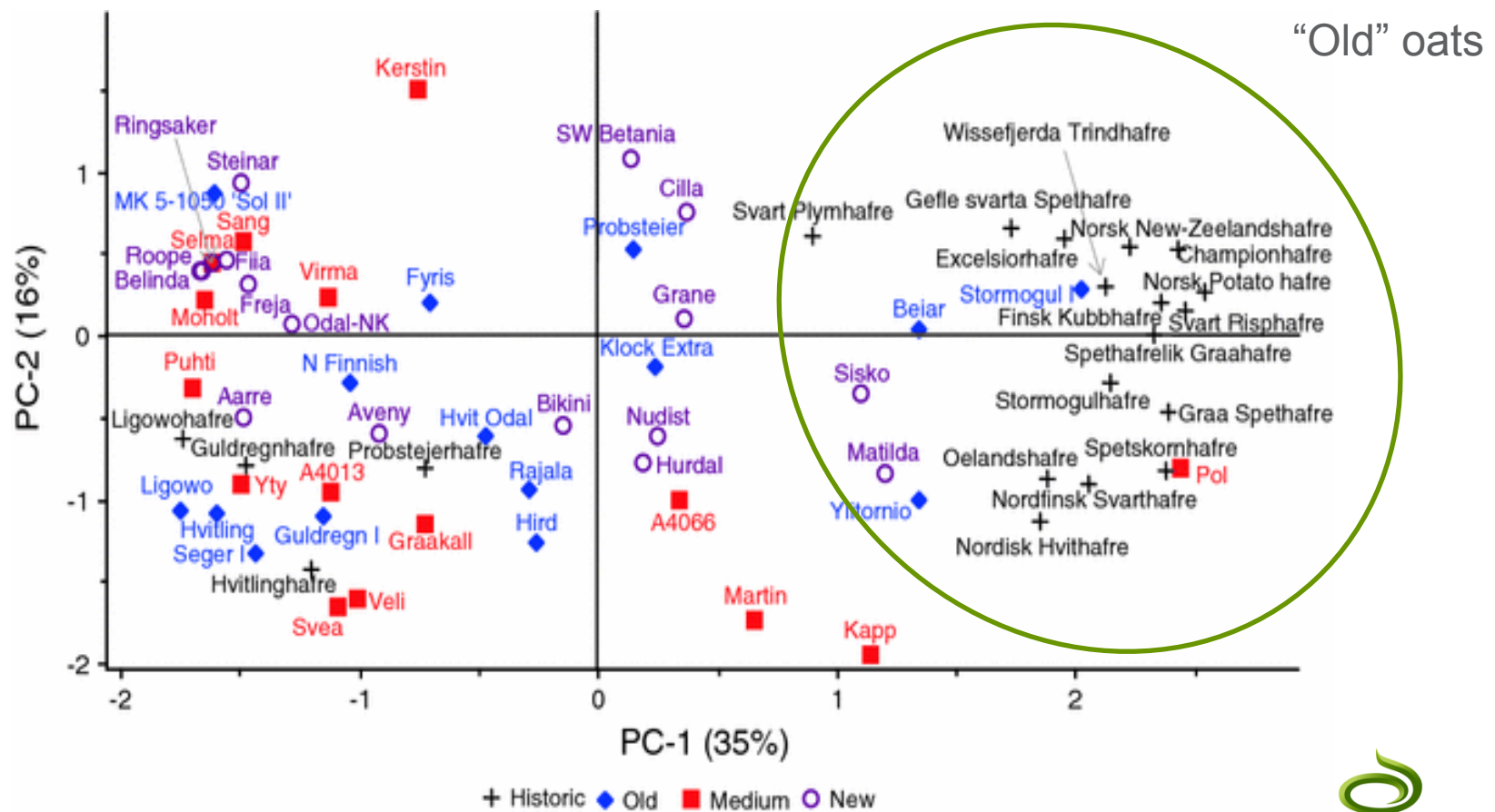
- 5 field sites from N. Sweden to S. Germany + disease nurseries
- Agronomic performance
- Disease resistance
- Kernel quality
- Biochemical composition

Genotypic data

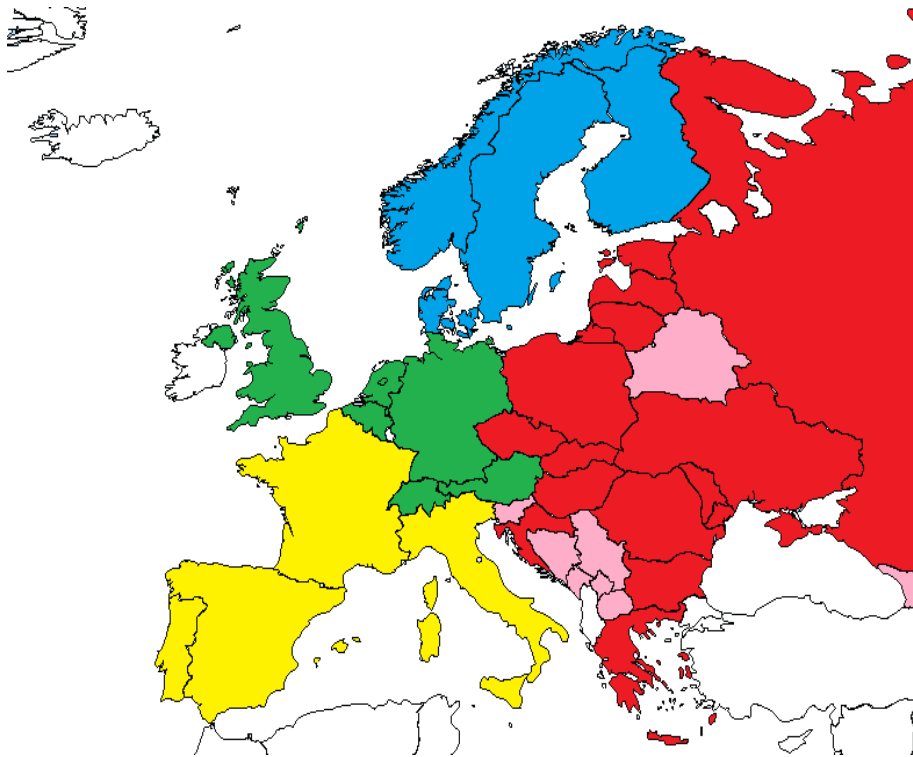
- DArT markers
- SNP markers (6k CORE chip)

Too Little Diversity in European Oats?

He & Bjørnstad 2012



GOD panel – European accessions



Number of accessions genotyped

Region	DArT.	6k SNP chip
North	185	157
East	106	43
West	85	41
South	32	20
Total	408	261

Summary SNP markers – 6k CORE chip

Feature	Number of SNP
Markers on chip	4,975
Failed	1,288
Scored	3,687
Polymorphic in European oats	2,832
MAF <1%	284 (10%)
MAF 1-5%	912 (32%)
MAF 5-10%	540 (19%)
MAF >10%	1,096 (39%)



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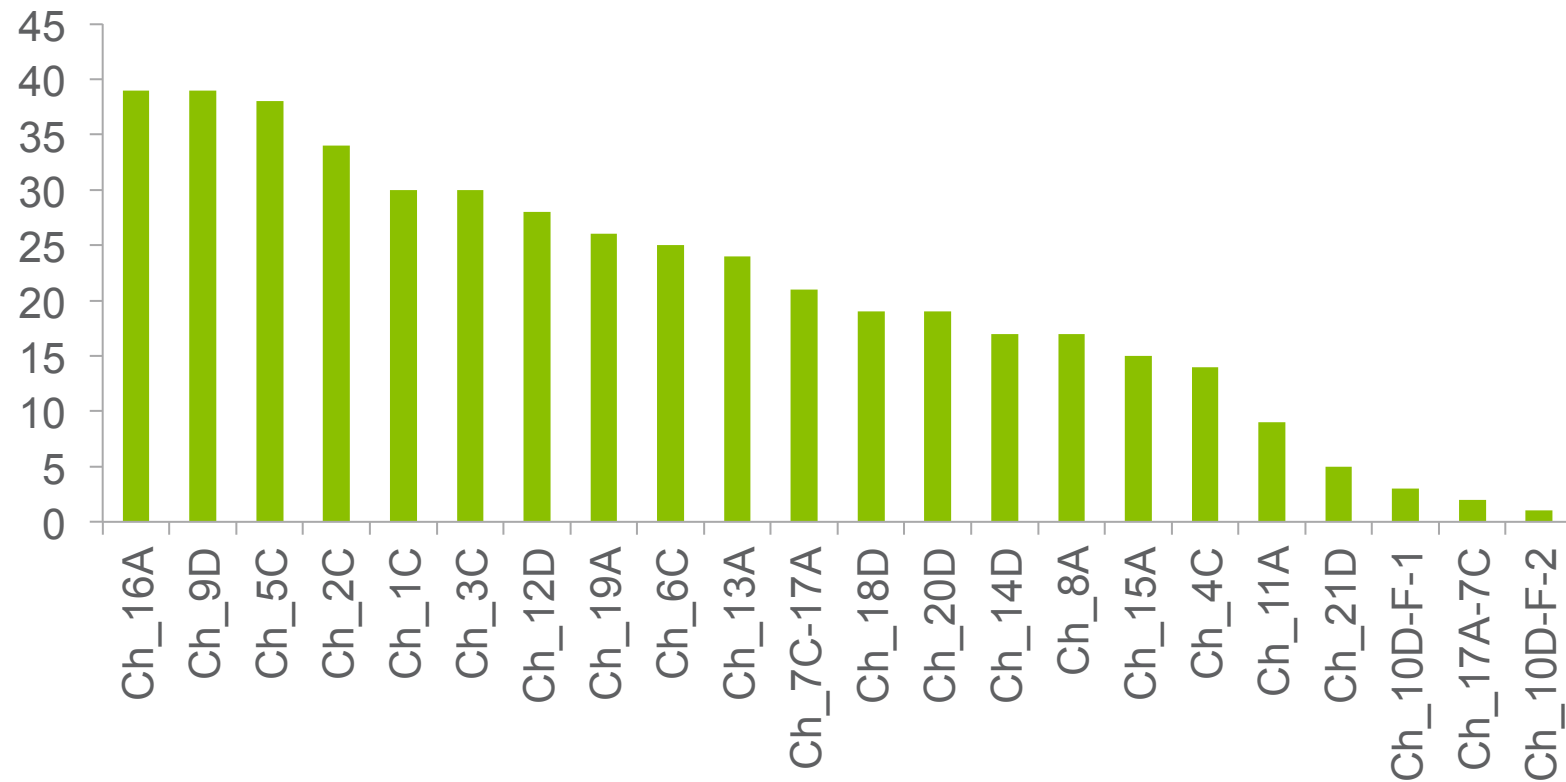
Summary SNP markers – 6k CORE chip

European region	Monomorphic	Polymorphic	Private	H_E
East	1,266	2,421	77	0.136
North	1,178	2,509	57	0.112
South	1,107	2,580	95	0.219
West	1,658	2,029	4	0.130
All	855	1,801		
Any	1,886	2,832		



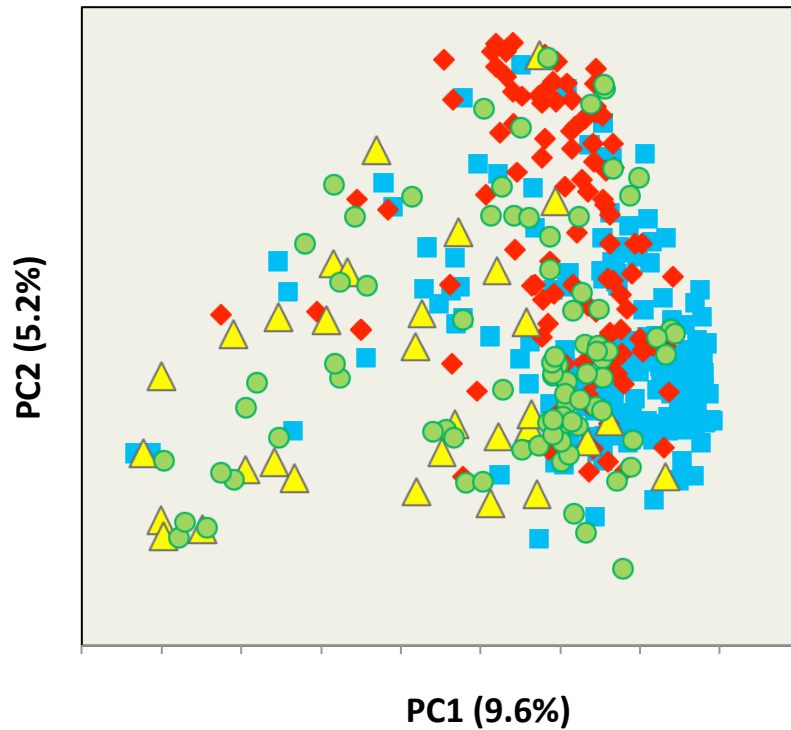
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Distribution of SNP on Chromosomes

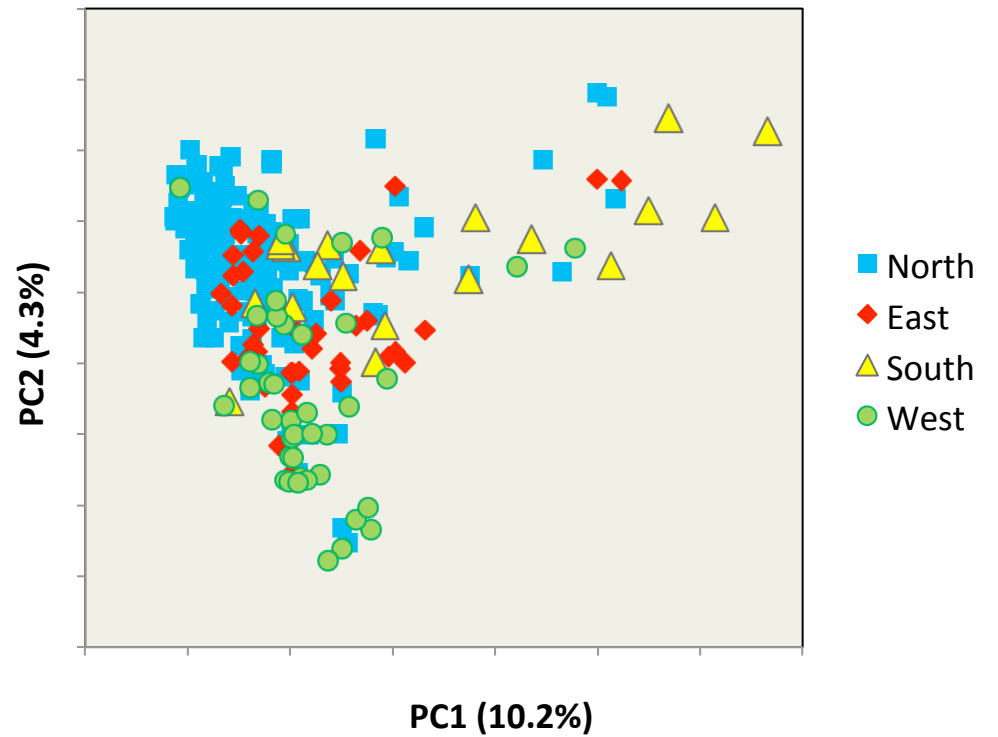


European oats – DArT vs SNP markers

DArT - 747 polymorphic markers



6k chip – 2,832 polymorphic markers



Linkage Disequilibrium (LD) Decay

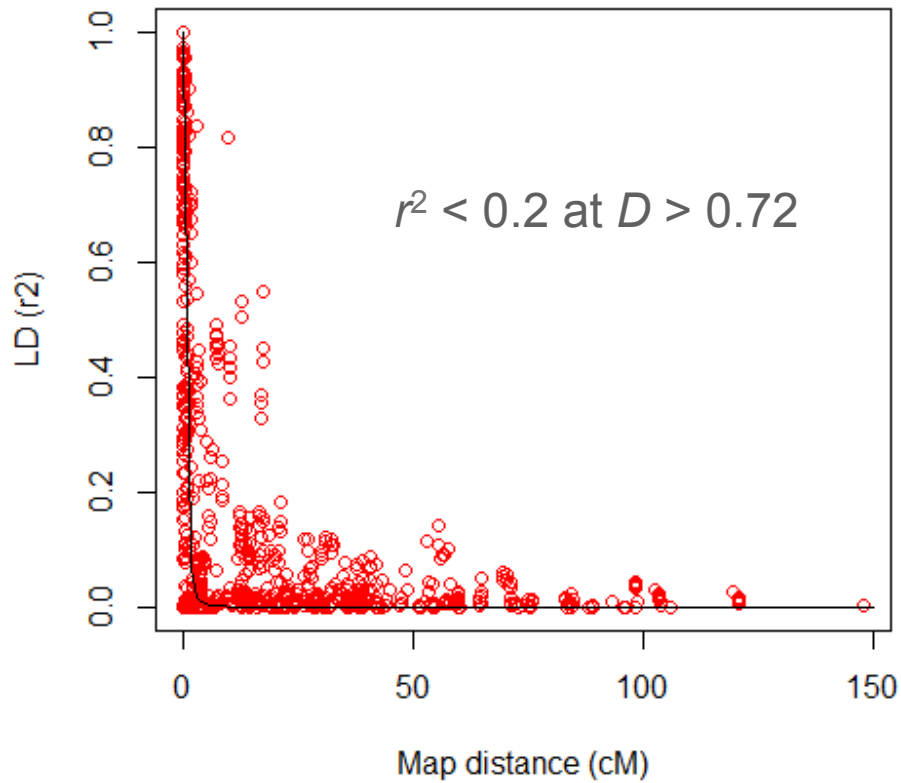
DArT vs. SNP markers

- 180 DArT markers with map positions from Kanota x Ogle (Tinker *et al.* 2009)
- 454 SNP markers with map positions from Oliver *et al.* (2013) consensus map
- LD (r^2) plotted against genetic distance (cM) for all pairs of markers
- Rate of LD decay quantified by fitting the function $L=1/(D+1)^{\theta}$ and estimating θ

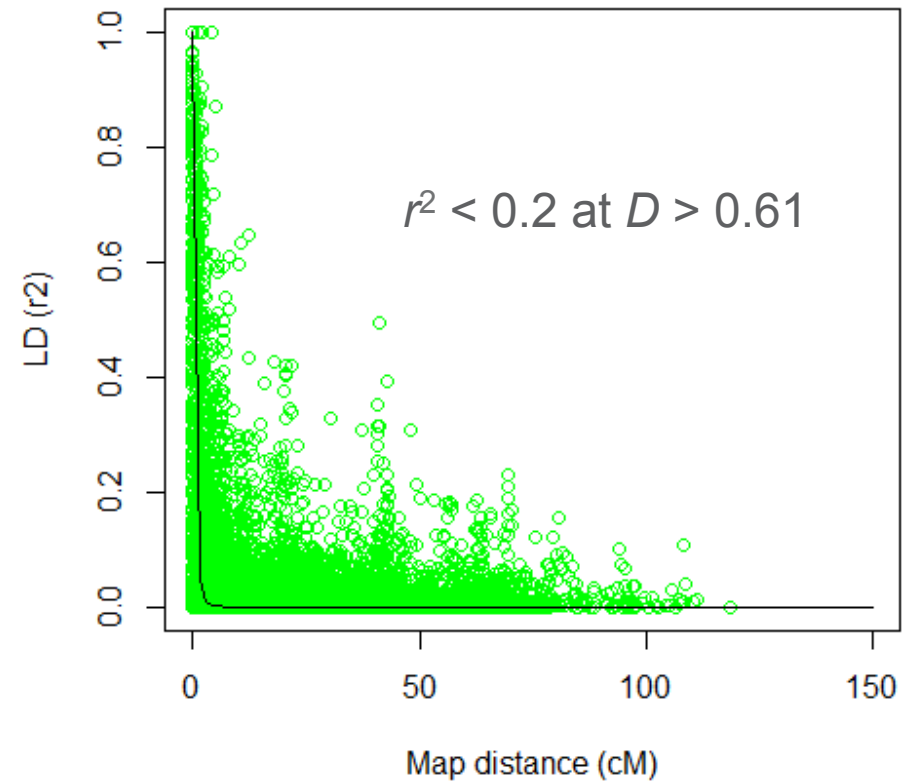


LD Decay for DArT & SNP markers

DArT



SNP





Thank you!