Multivariate associations between climate and genome-wide methylation in European Arabidopsis panels

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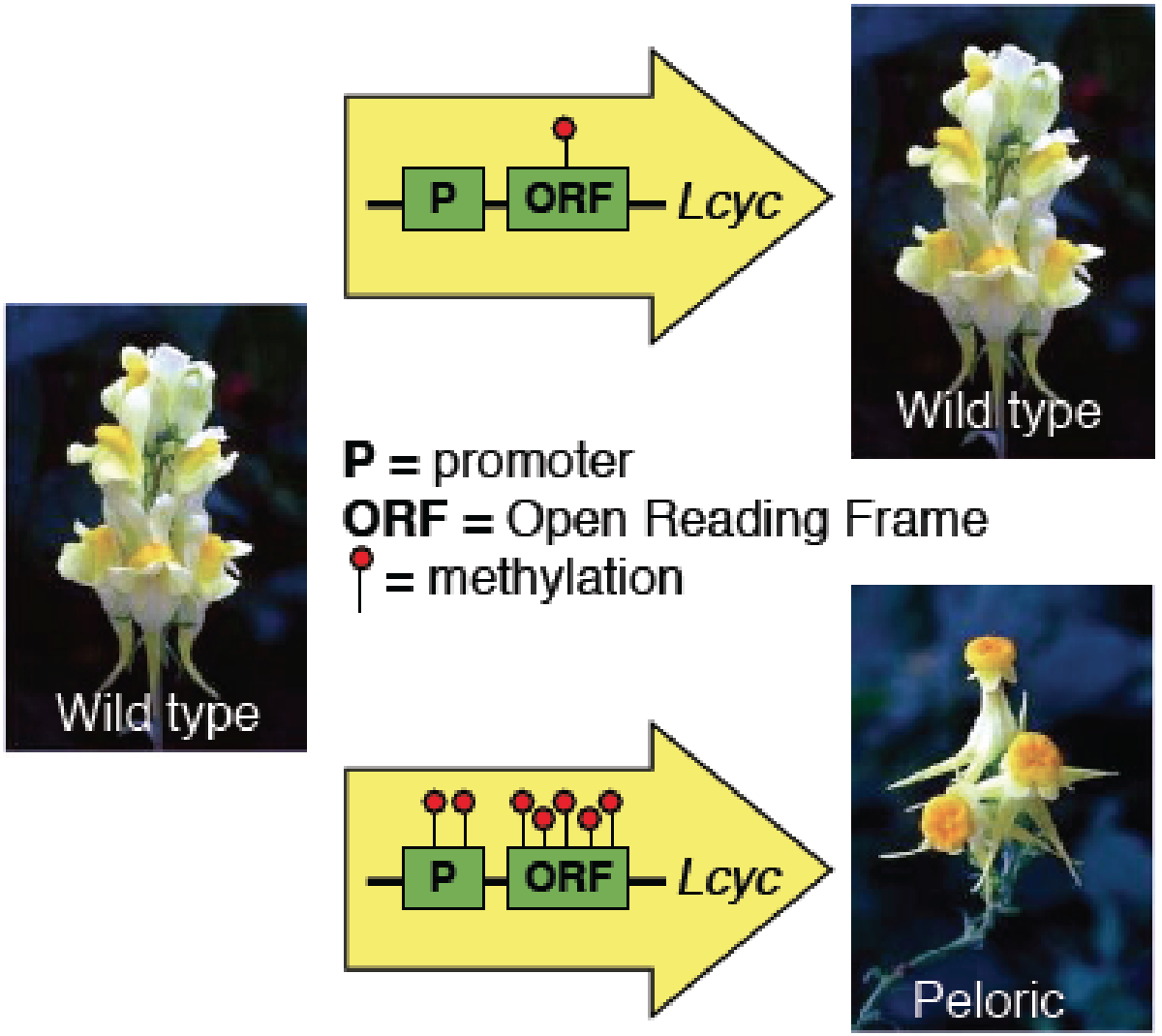
Climate is really important, and it really is changing

Current uses of the term “Epigenetics”

Epigenetics- molecular level mechanisms that can alter gene expression and ultimately phenotype without altering DNA sequence.

- DNA methylation
- histone modification
- micro and siRNA
- cellular location

Heritable epigenetic effects



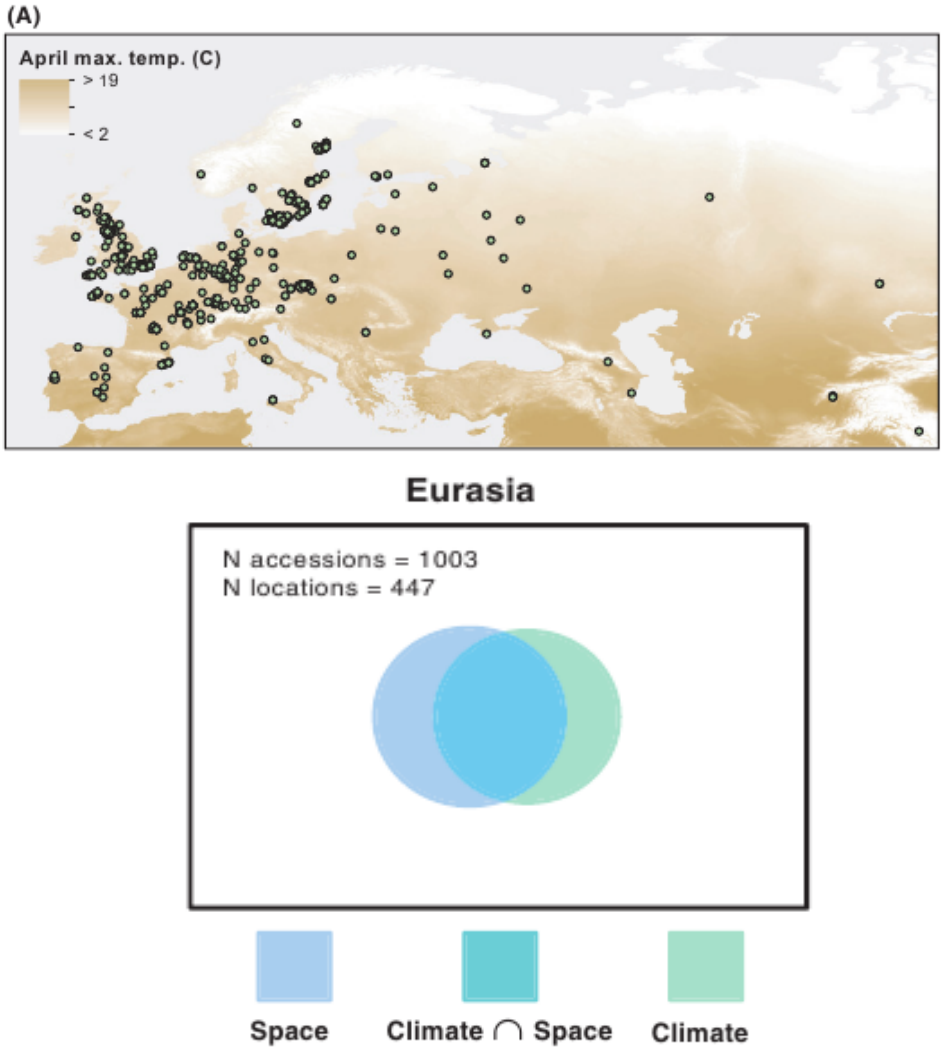
- Lcyc in *Linaria vulgaris*
= bilateral symmetry

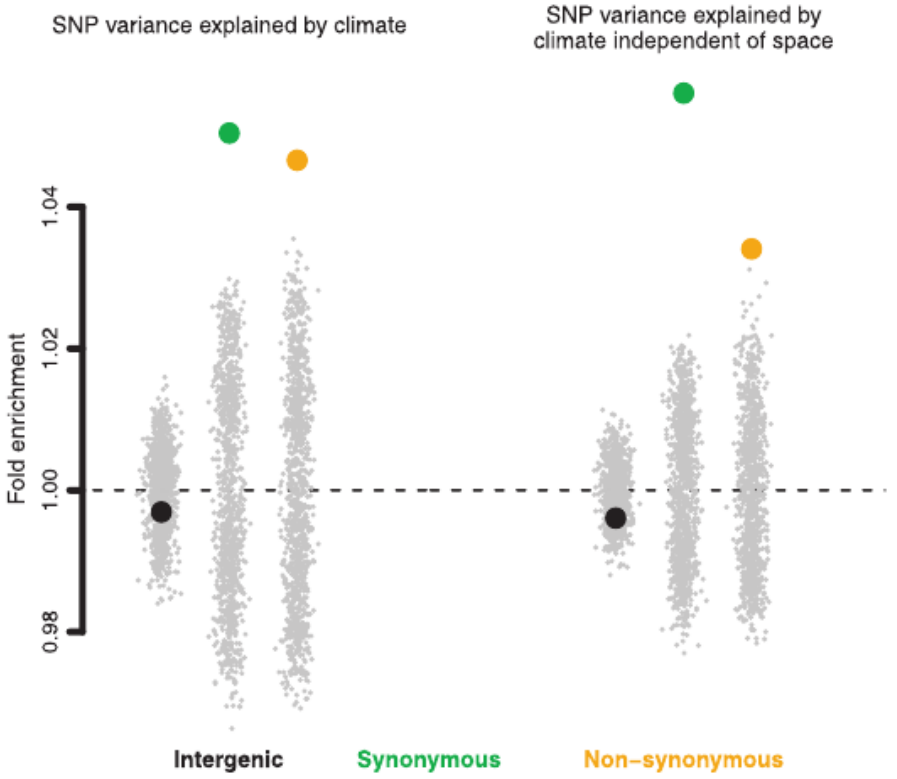
- Lcyc is methylated
= radial symmetry

Cubas, et al. 1999 Nature.

Figure credit S. Deban

Substantial portion of SNP variation in Arabidopsis is due to climate

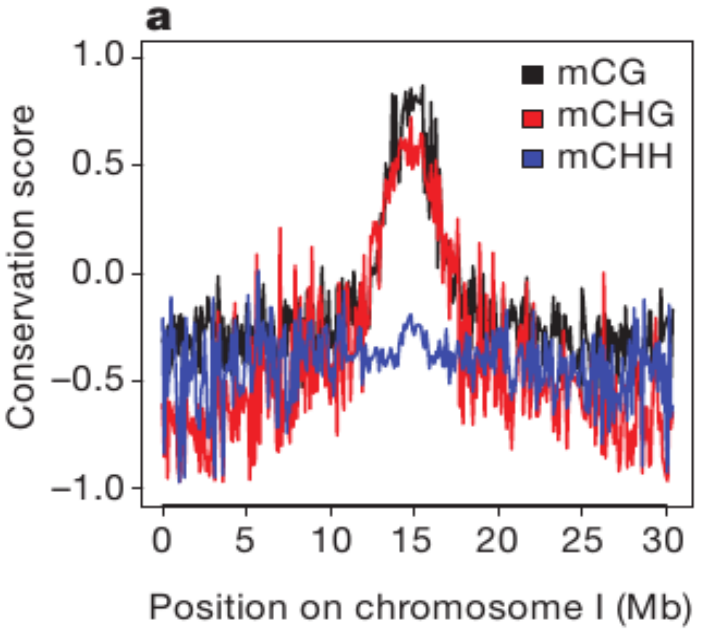




Lasky et al. 2012

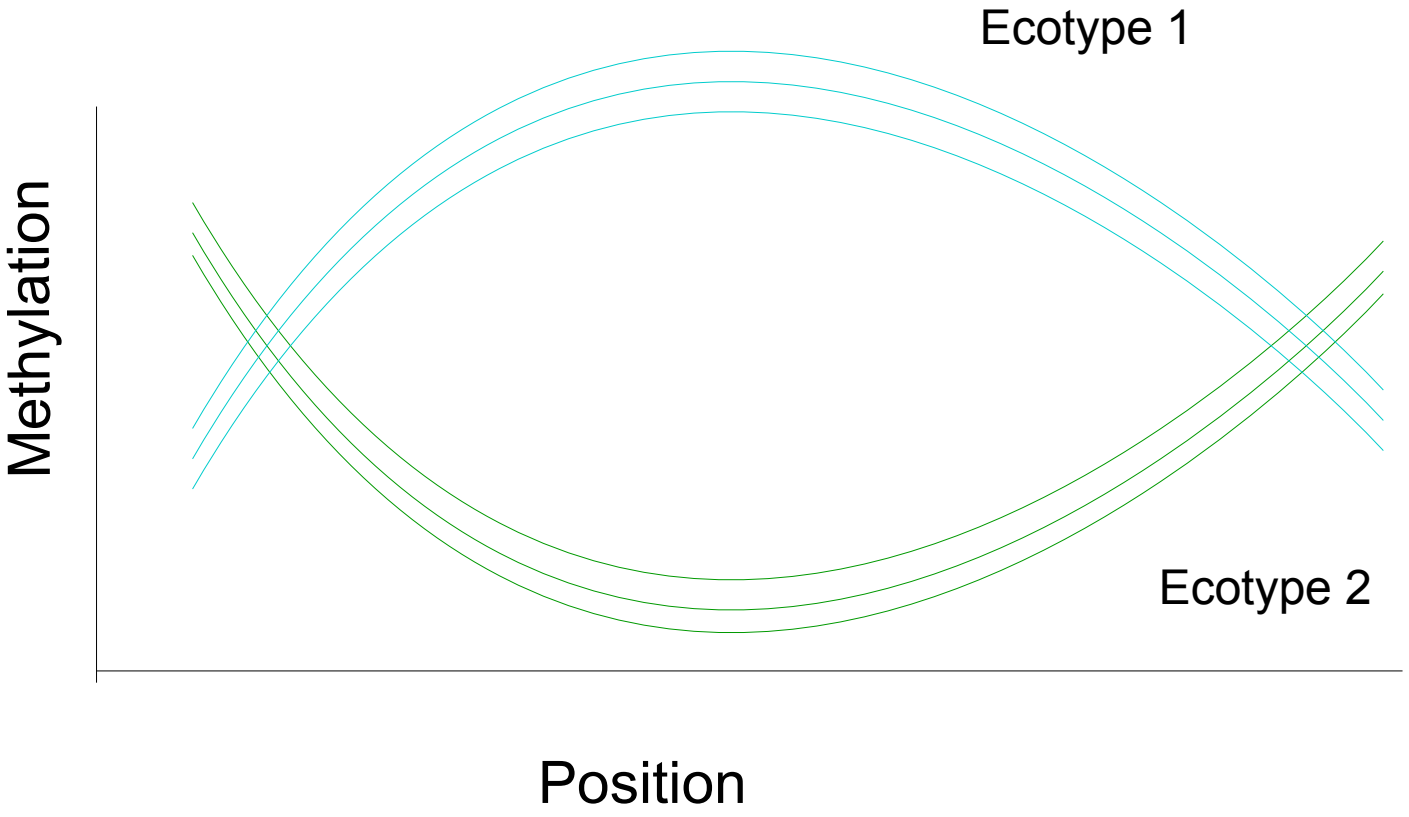
There's also lots of methylation variation in Arabidopsis

- 122 genomes from different parts of the world fully bisulfite sequenced (Schmitz et al 2013)
- 148 genomes from sep. study in Sweden (Dubin et al. 2015)
- Methylation in CG, CHG, CHH context in plants
- H is anything but G

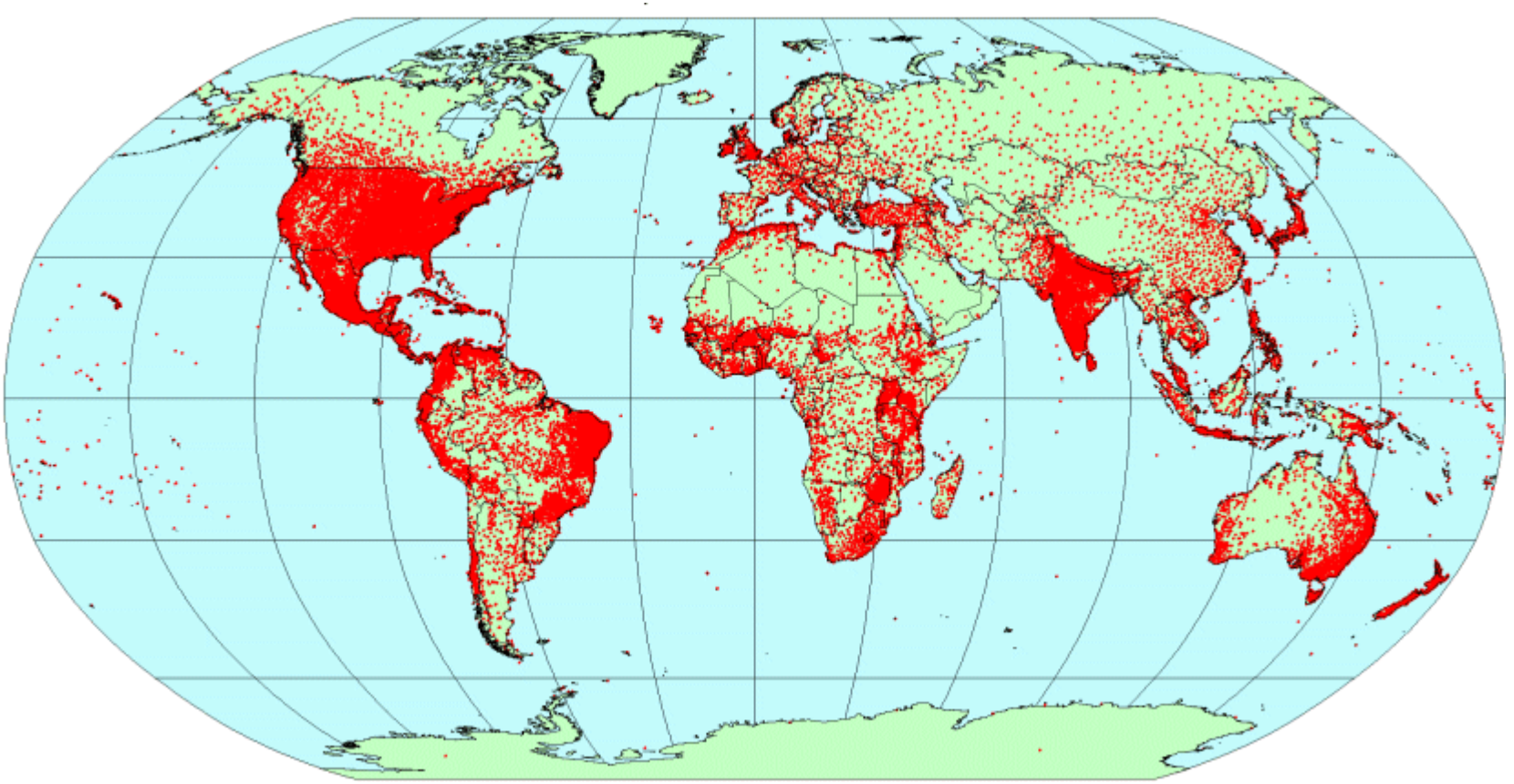


Schmitz et al. 2013

Methylation often correlated along genome; differentially methylated regions (DMRs) between groups



Worldclim in R makes it really easy to do climate stuff



Data collection sites for Worldclim (Hijmans et al. 2005)

Identify correlations with redundancy analysis (RDA)

- We have multivariate explanatory variables (climate,space) and multivariate response variables (biallelic SMPs or DMRs)
- Redundancy analysis is a multivariate analog of linear regression
  - Similar to principle components analysis (PCA)
  - Better at dealing with colinearity
  - Can also deal with the problem of population structure (proxied by space) by factoring that out
  - Vegan package in R

RDA- 42 climate variables ~ 150K methylation sites

	Y1 (Annual Temp)	Y2 (Ann. Precipitation)	.	.	Y42	~	X1 (SMP,SMP, or DMR 1)	X2 (SMP,SMP, or DMR 1)	.	.	X182090
Accession 1	25	53					1	1	0	0	0
Accession 2	23	10					0	0	1	0	1
	.	.					.	.	.	.	.
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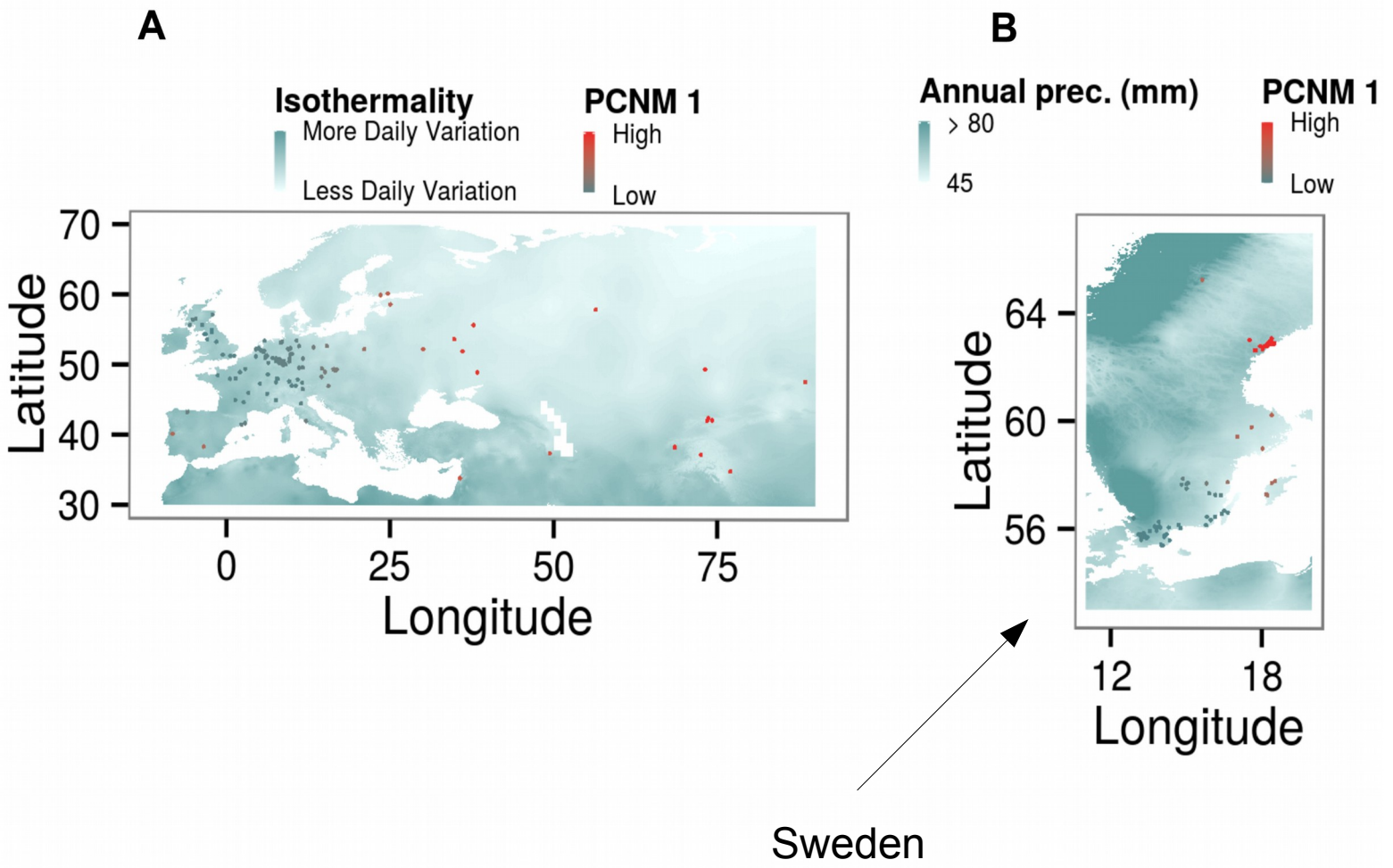
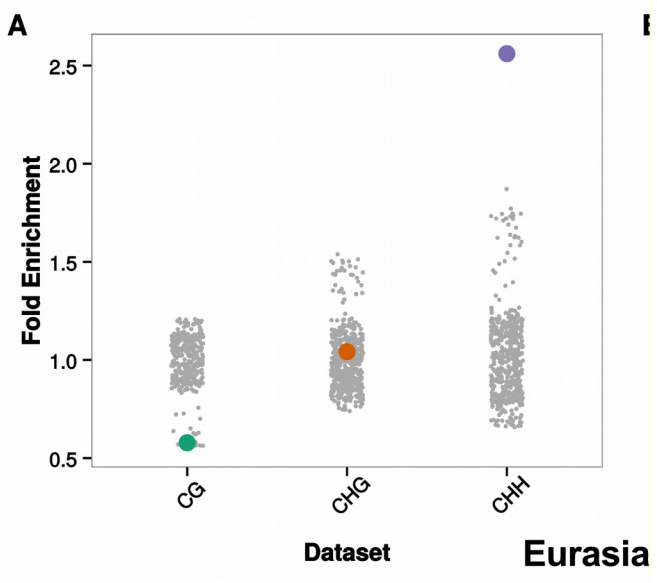
Accession 122	.	.					.	.	.	.	.

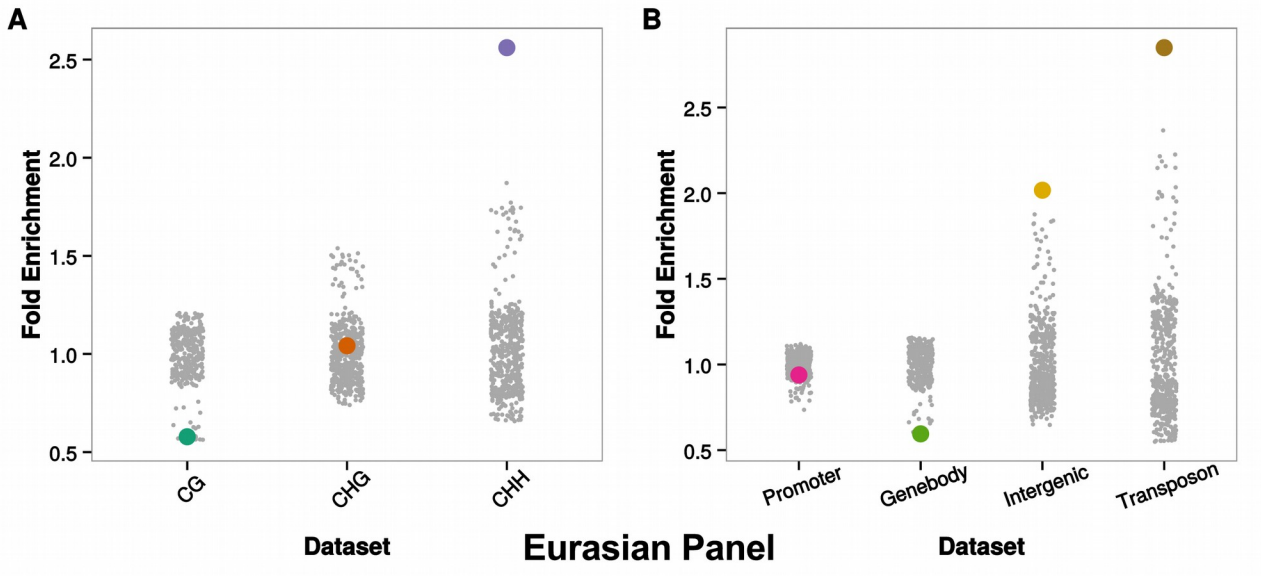
Single climate gradients with highest association to SMPs



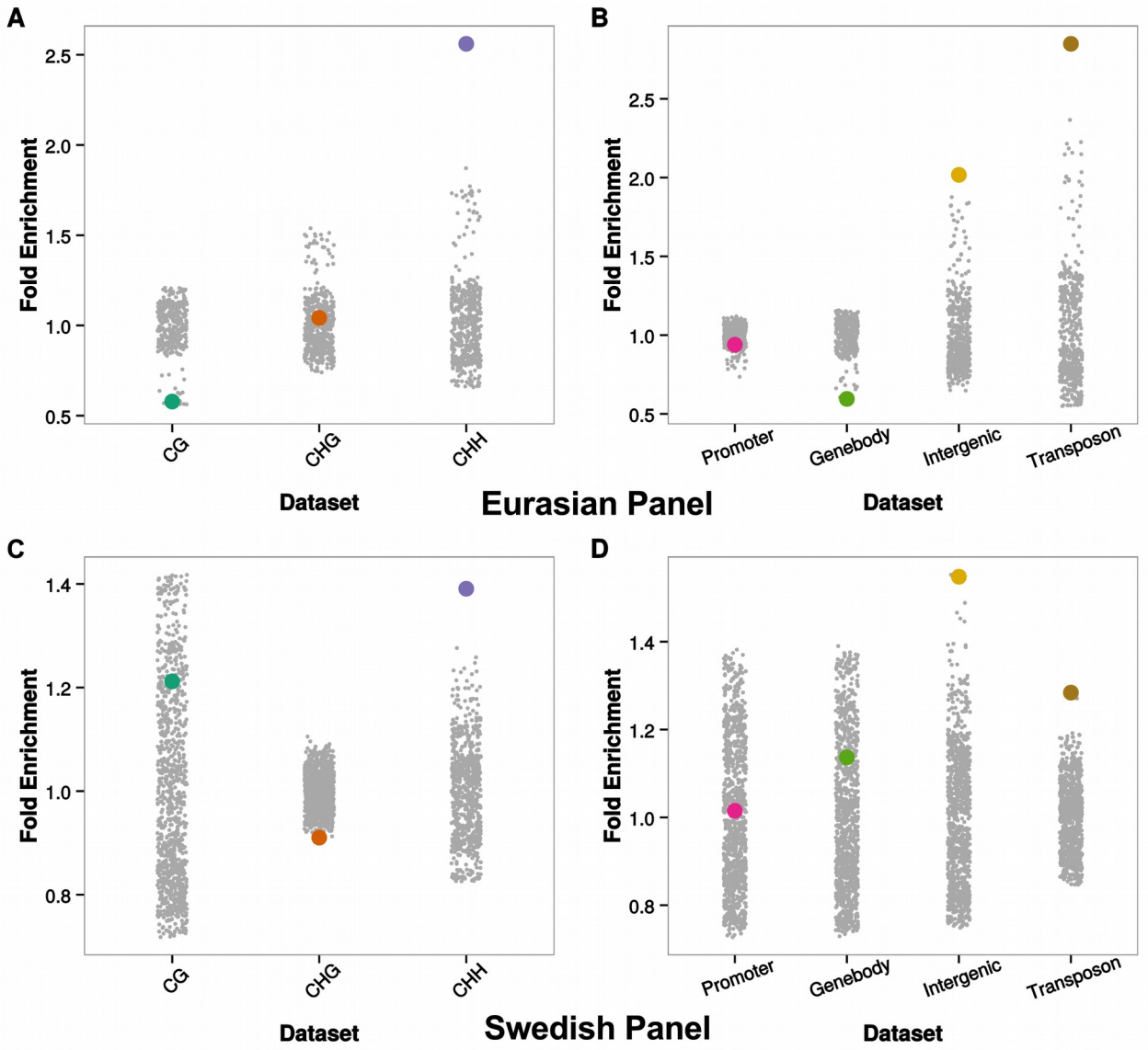
First axis of variation enriched for CHH compared to shuffled nulls



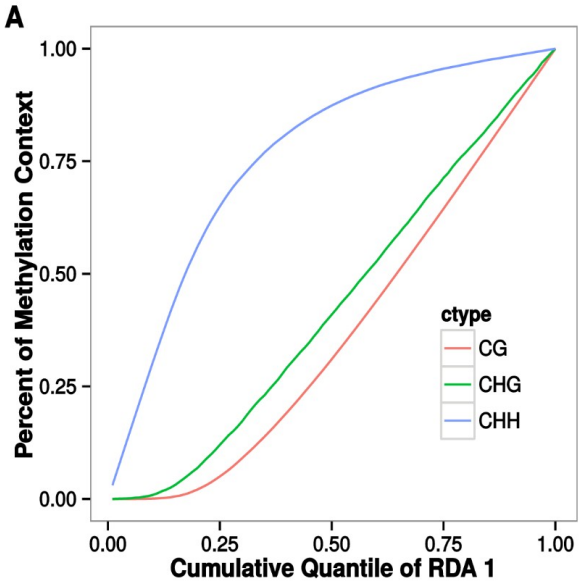
...and these are usually found in intergenic and transposon regions



Swedish panel shows similar CHH and non-genic enrichment patterns



Top RDA axes discriminate methylation context



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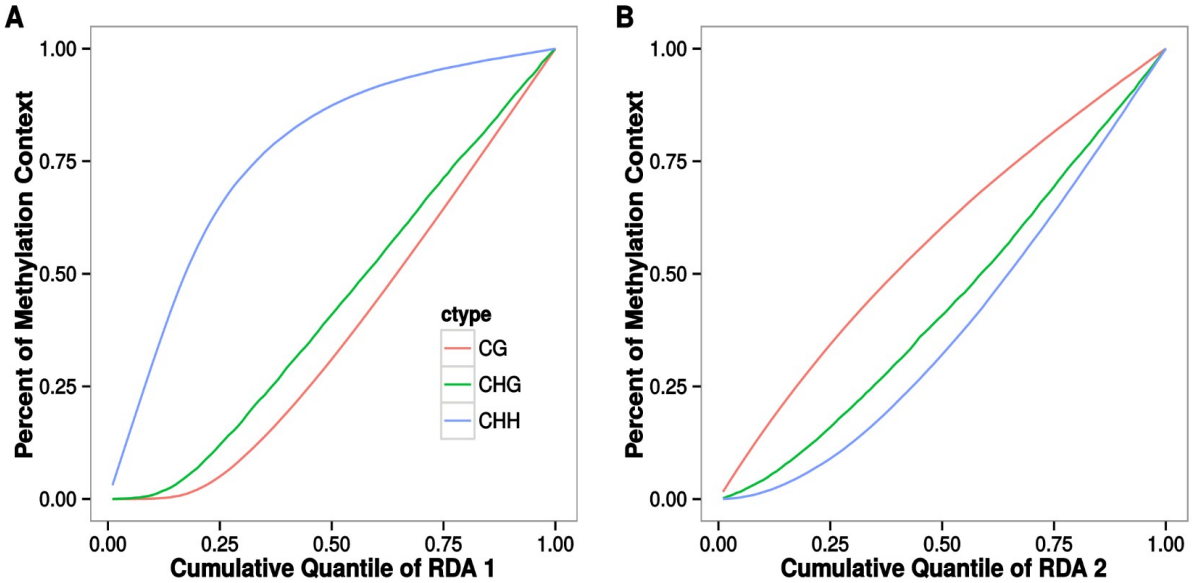

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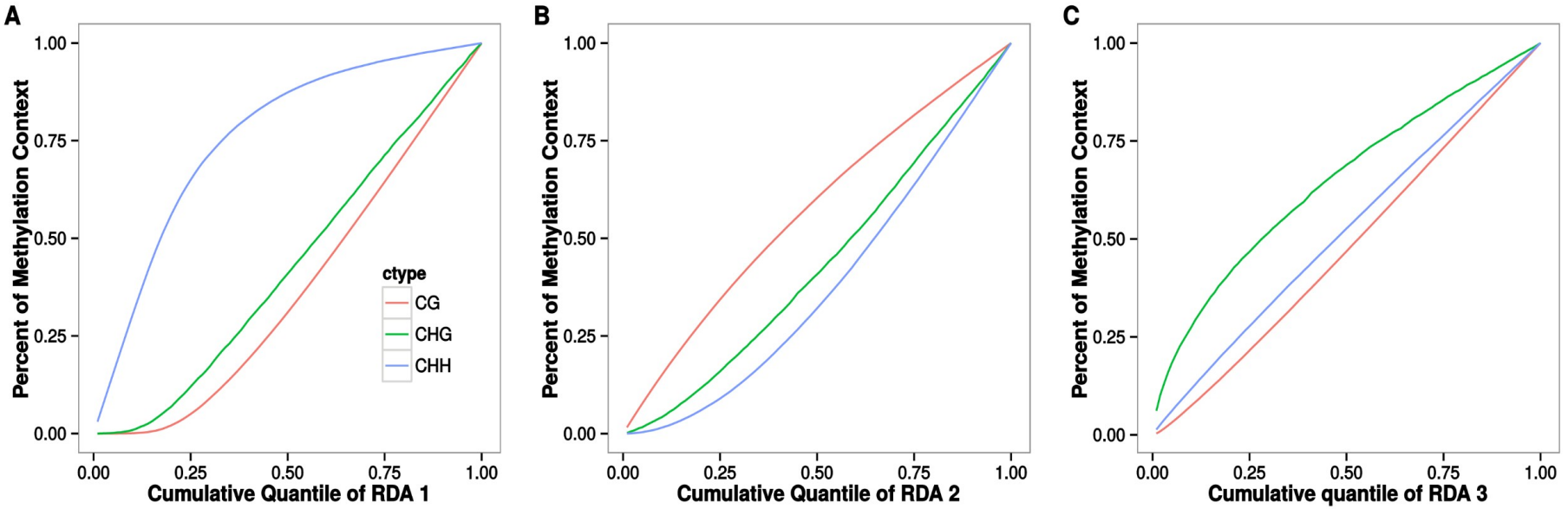

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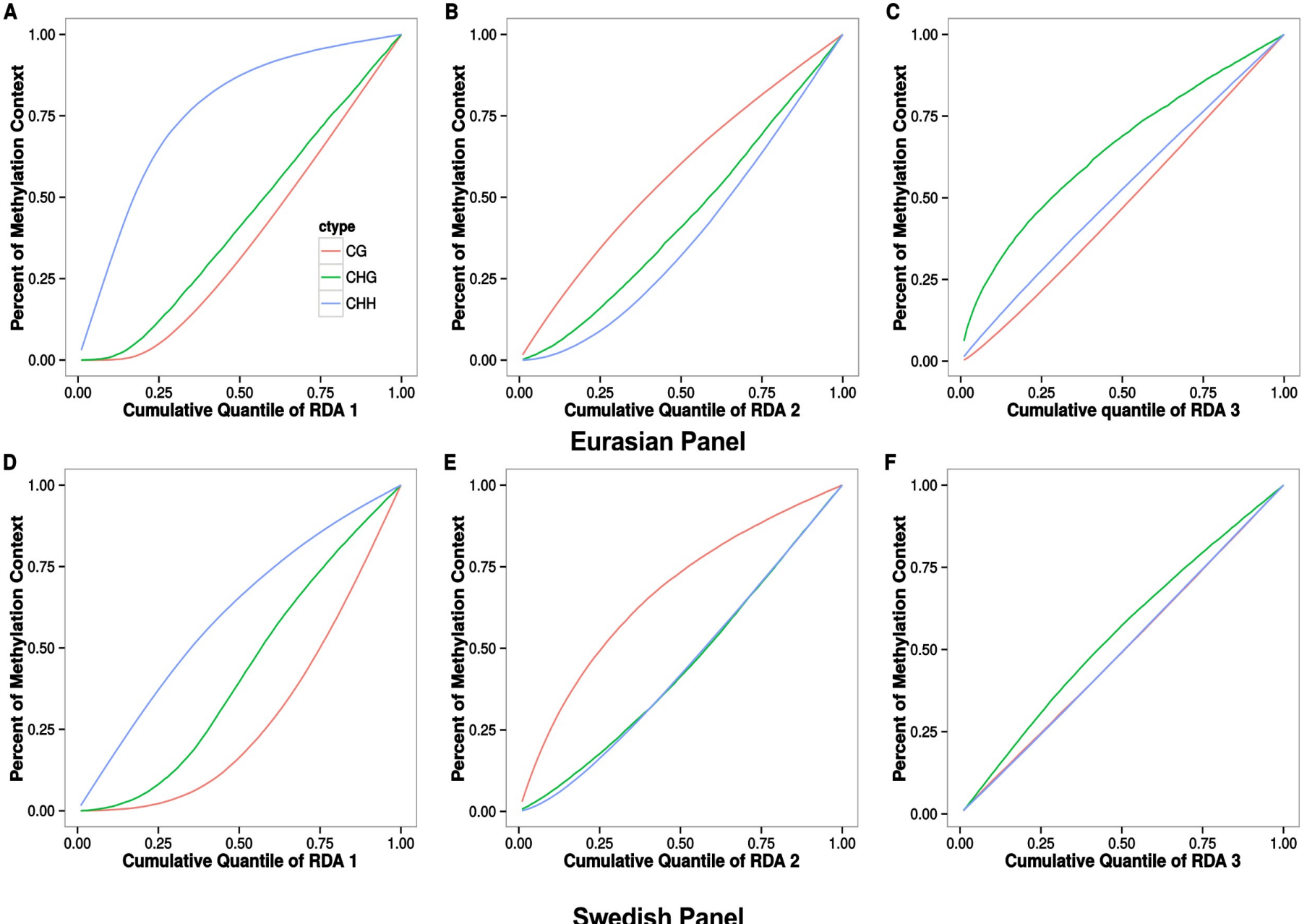

CG-DMRs correlate with both climate and expression

- Some GO terms suggestive for local adaptation enriched, such as abiotic stimulus, reproduction, development, metabolism
- Gene-body CG-DMRs have average weak positive correlation (0.044-0.05) with expression
- GxE genes relating to cold and drought tolerance have more climate-associated CG-SMPs

Summary

- Two plant panels show evidence of local epigenetic adaptation to climate, not just space/structure
- Strongest signal was in CHH context, intergenic and transposon regions
- DMRs show stronger signal with climate than individual sites
- Analyzing climate holistically rather than individual components is important

Thanks!

- Keller, Lasky, Yi 2016 Molecular Ecology doi 10.1111/mec.13573
- Part of a whole issue on epigenetics in ecology!
- Thanks to Yi lab (Ixa and Dan especially)
- Georgia Tech

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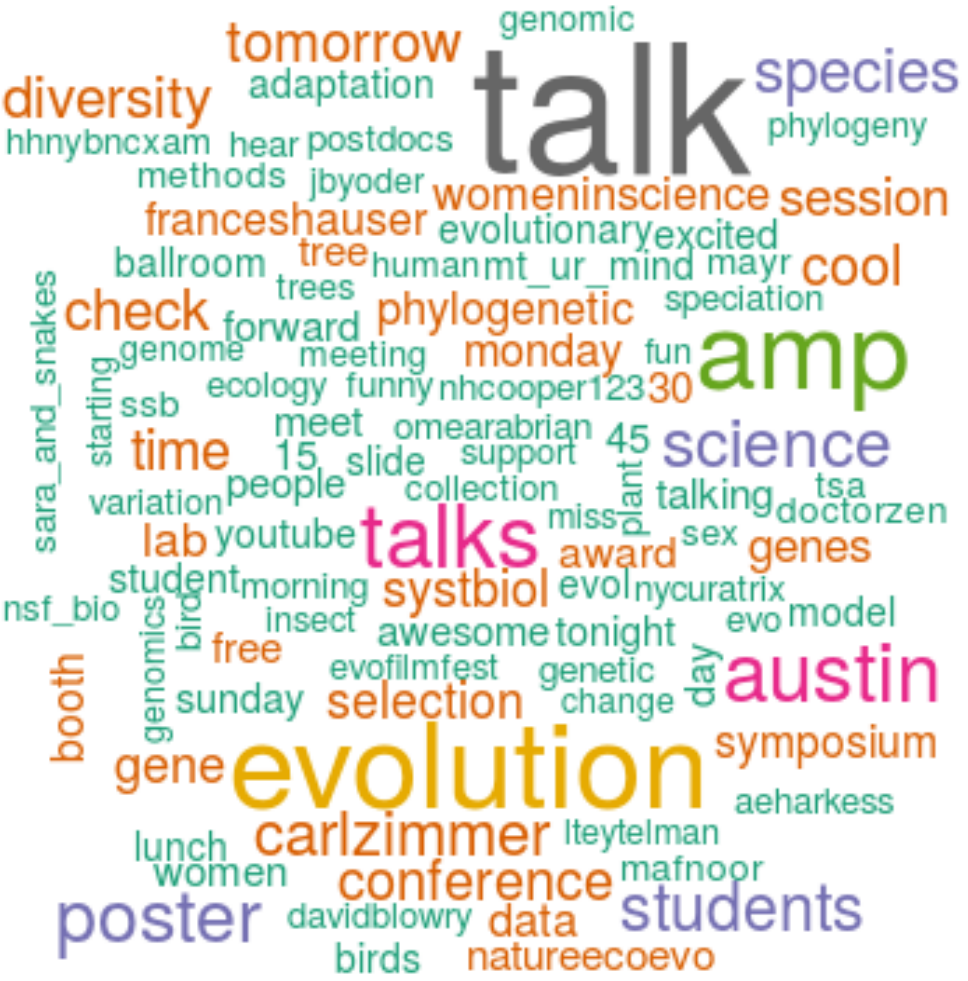
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