Mutator transposable element behavior across maize genotypes

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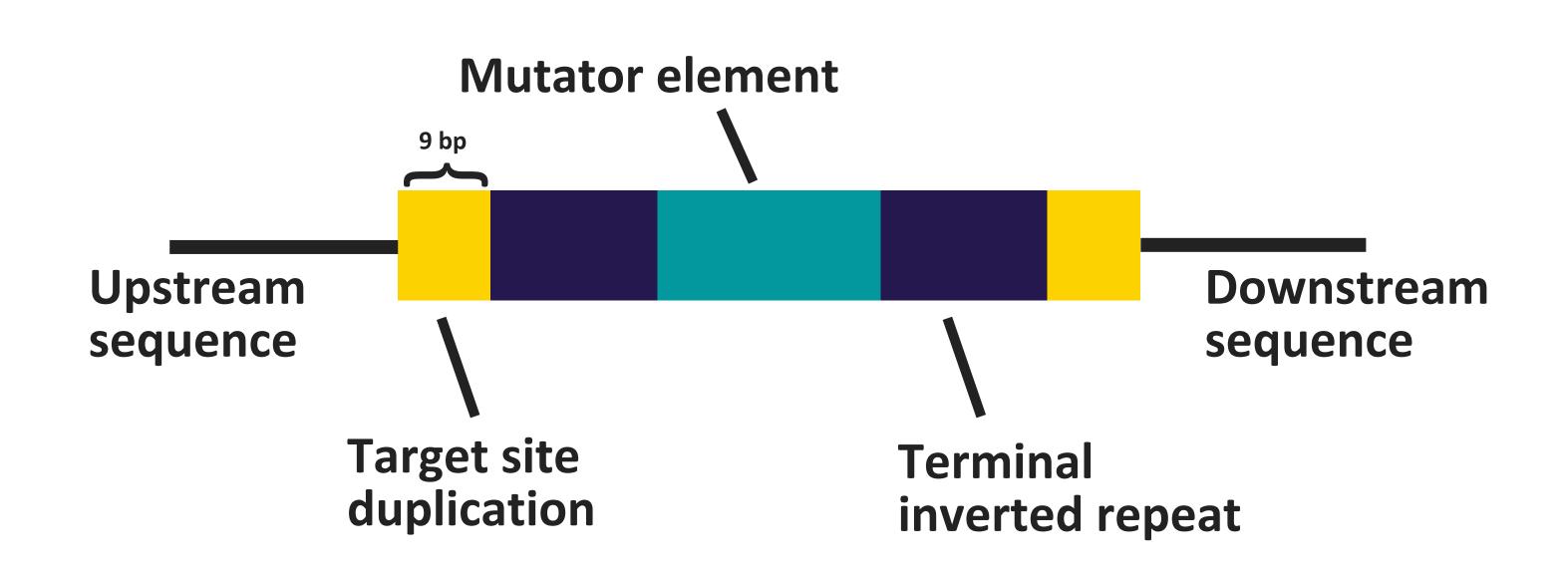
Mutator TEs accumulate in BonnMu and natural populations

Maize population backgrounds

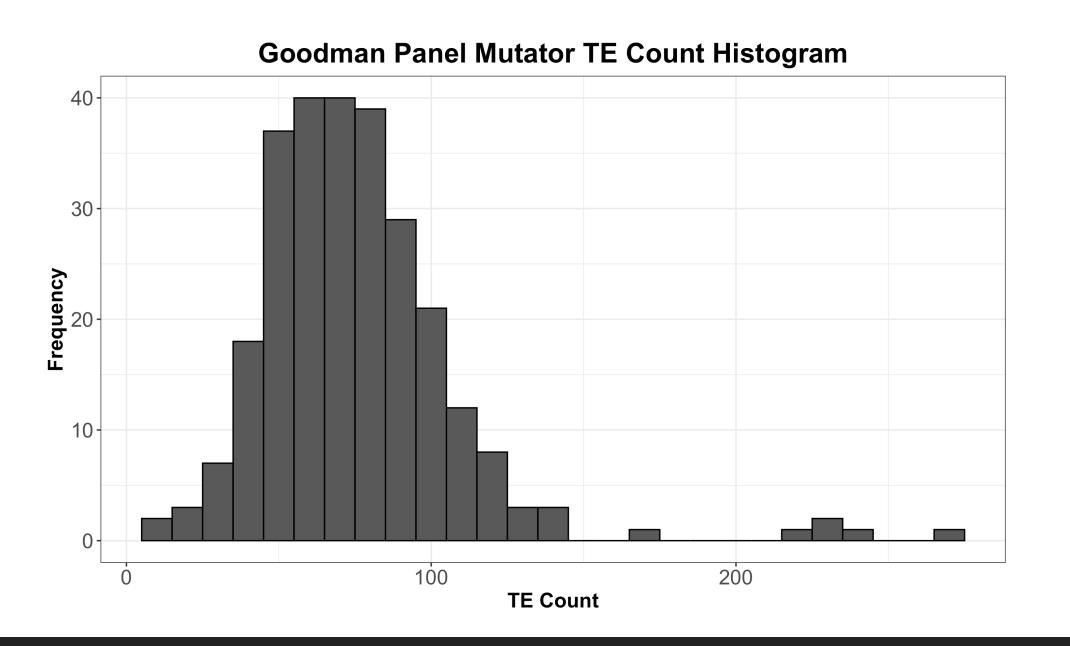
BonnMu: population with active Mutator and corresponding sequence-indexed insertional library

Goodman Panel: a set of ~300 inbreds selected to exemplify both temperate and tropical maize diversity, sequenced to 6-20x coverage

Target site duplication sequences act as an ID for each Mutator insertion

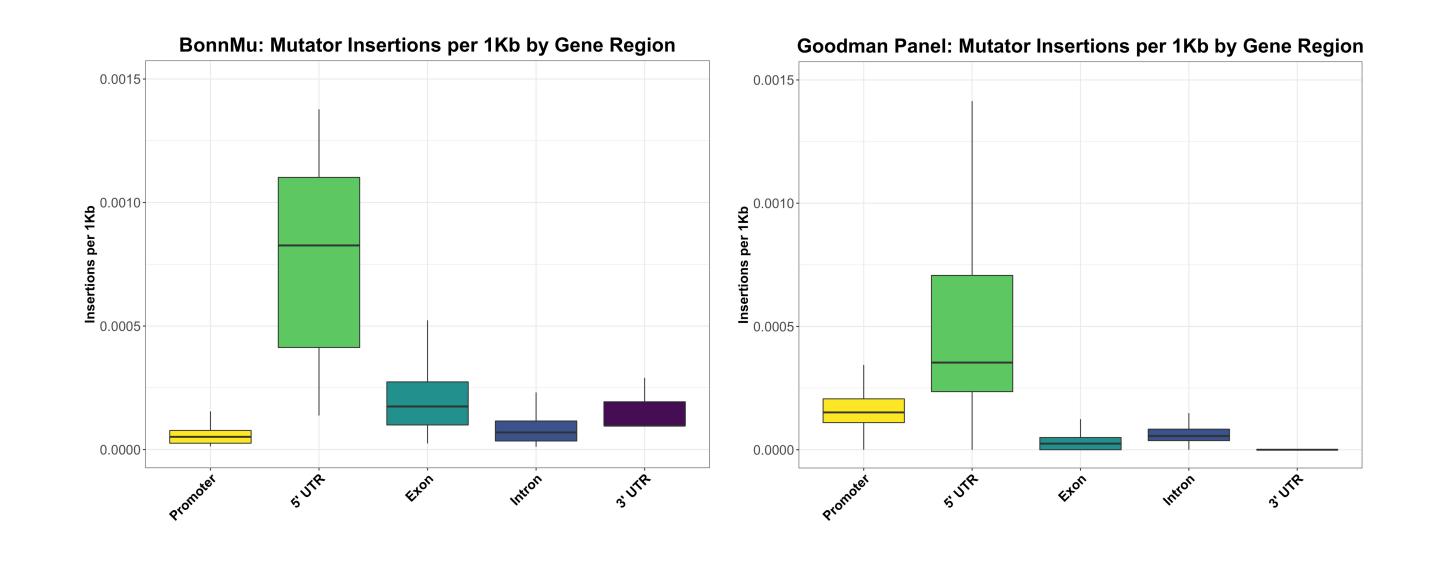


8 to 266 Mutator insertions were identified in Goodman Panel inbreds

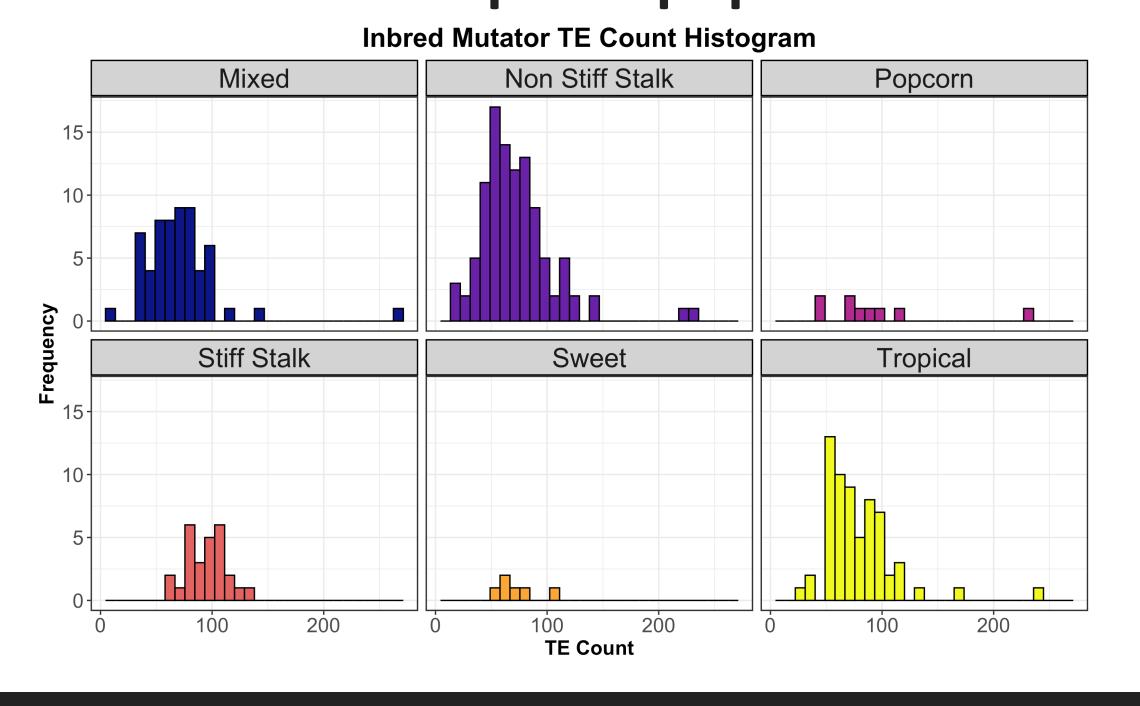


Mutator preferentially inserts in 5' UTR, exhibits population differentiation

5' UTR has largest amount of insertions/Kb out of all gene regions

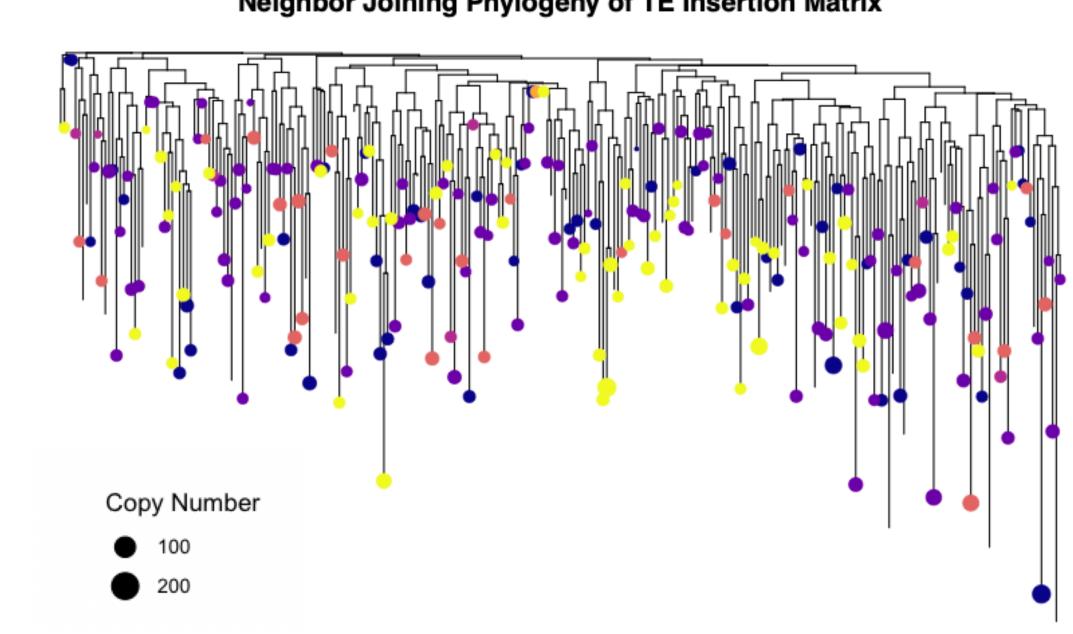


Median TE insertion count varies across Goodman panel populations



Mutator TEs lack strong population structure

Neighbor Joining Phylogeny of TE Insertion Matrix



Mutator is associated with days to anthesis (DTA) in the Goodman Panel

Set-up

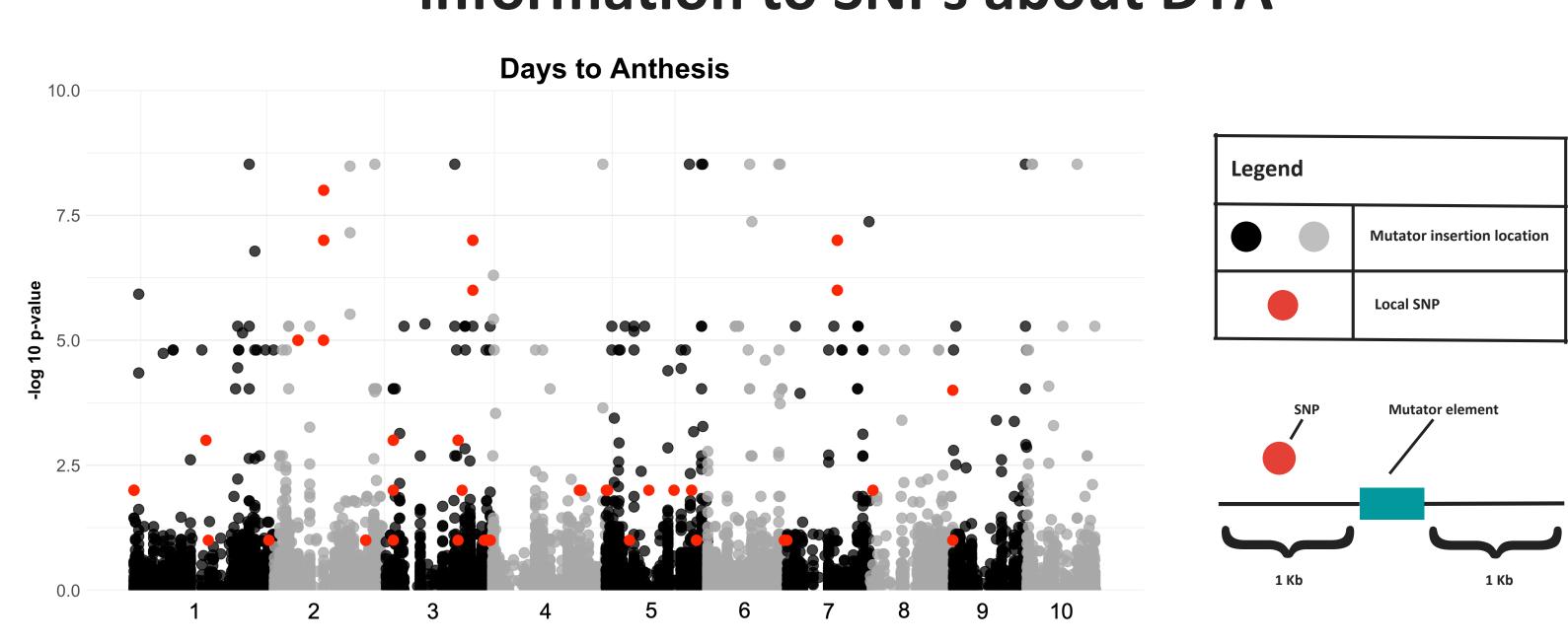
DTA_BUCKLER2009

TE Insertion Matrix

		1					-	
	DTA_BUCKLER2009			TE 1	TE 2	TE 3		Т
INBRED 1	79.53		INBRED 1	0	0	1		
INBRED 2	81.44		INBRED 2	1	0	1		
:	:		:	:	:	:	-	
INBRED 270	74.84		INBRED 270	1	1	0		
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Mutator TEs provide complementary information to SNPs about DTA

Tropical



Next steps

- Investigate genes associated with significant loci for DTA
- Extend association analyses to additional phenotype
- Explore linkage disequilibrium of Mutator insertions with SNPs