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23	s of 70 sites
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30	al adaptation
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	agricultural
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55	ean originated
56	rs ago with a
57	vo wild gene
58	e American'
59	tication

60	y because
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63	d common
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69	have
70	3N), the
71	rs 1988;
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86	ries to specific
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89	ividual-based
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96	ble to local
97	process of P.
98	14; Rodriguez
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100	bean races to
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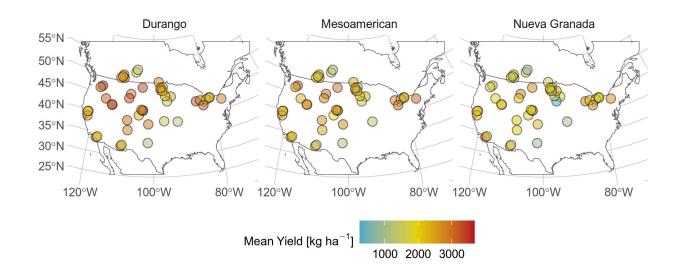
**Table 1**. Implications of home field advantage and heritability for breeding and adaptation. Combining agroecological ecoregion information and heritability of specific traits may help improve selection efficiency while providing insights into processes driving past selection.

Heritability

		Lower	Higher
Home Field	Larger	Processes: High environmental variation among locations, low genetic variation potentially enriched in locally important alleles.  Implications: Inefficient selection on individuals for phenotypic improvement; testing at these sites may reveal conditionally beneficial alleles.	Processes: High environmental variation among locations, high genetic variation potentially enriched in locally important alleles.  Implications: Efficient identification and selection of specialists that may contain large-effect candidate loci for introgression.
Advantage	Smaller	Processes: Low environmental variation among locations, low genetic variation potentially enriched in broadly important alleles.  Implications: Inefficient selection on individual entries for phenotypic improvement, so family based methods are necessary.	Processes: Low environmental variation among locations, high genetic variation potentially enriched in broadly important alleles.  Implications: Efficient selection on individual entries for phenotypic improvement.

103	nate local
104	and across
105	N entry into a
106	ee races within
107	home location,
108	(Ewing et al,
109	ithin each bean
110	s in the CDBN
111	ritability across
112	3). We also
113	ool as genetic
114	time in the

115	ne pools.
116	ential strategies
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121	uded data from
122	nced breeding
123	ars and
124	American
125	Ethree of the
126	from the
127	Franada, which
128	points were
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131 ysis was 132 133 ield variance in 134 on across 135 tries, with only 136 rough the 137 shift is a 138 trial years and 139 field trials. 140 l components 141 erent locations 142 from different 143 ge in the

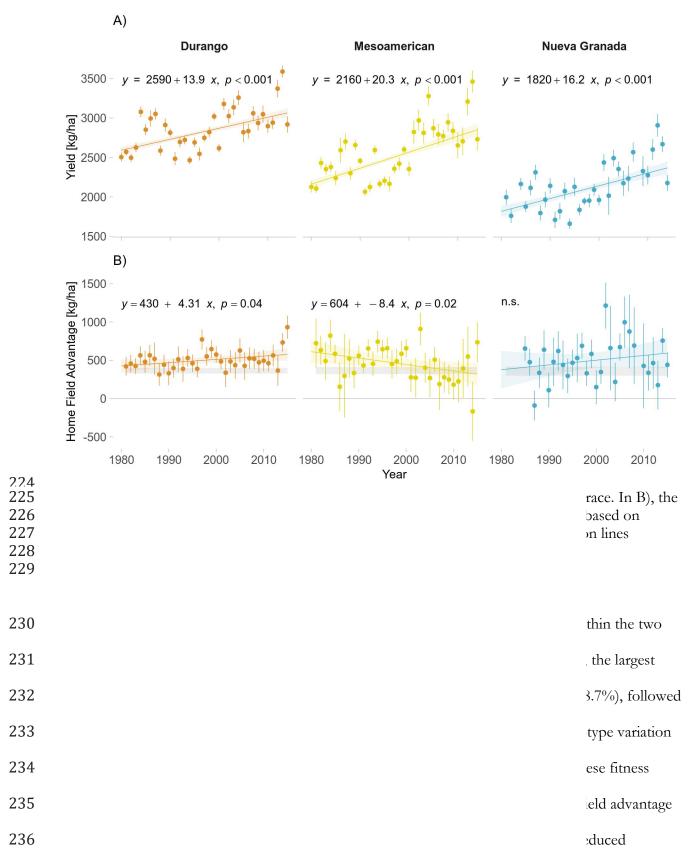
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146	in three groups
147	and entries
148	o and the
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151	ıl, and
152	iquart et al,
153	importantly, we
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158	= 0) and scaling
159	1 predictor
160	ates et al, 2015).
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162	DBN yields
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167	e model, $\mathbf{X}$
168	binary
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172	1e singular
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174	rith an HFA
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177	lodel 2 using
178	ons to test the
179	n site-year, we
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181	observed HFA
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213	ors are standard
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219	t with previous
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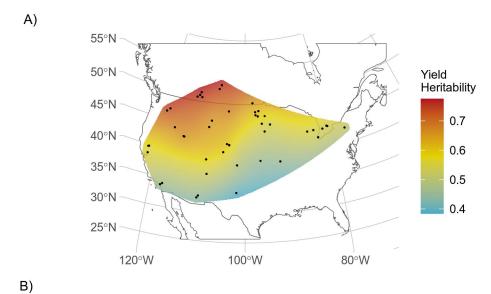
237	or 1.3% of yield
238	of
239	cipal
240	ncluding
241	ueva Granada),
242	9%, 44%, and
243	respectively
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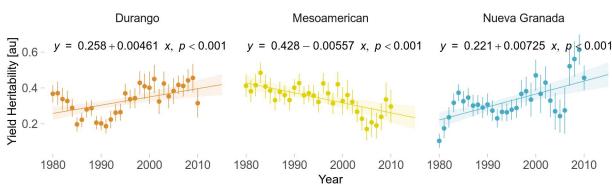
**Table 2** Partitioning of CDBN Yield Variances

	Race		
	Durango	Mesoamerican	Nueva Granada
Home Site	1.3%	1.3%	1.1%
Residuals	14.1%	15.8%	15.6%
Genotype	3.3%	4.1%	3.2%
Site	33.1%	30.9%	29.0%
Year	2.4%	3.0%	2.5%
Site-Year	45.7%	44.9%	48.7%
Residual Reduction <sup>1</sup>	8.3%	7.7%	6.3%
Proportion of residual varian	nce explained	by home site	

246	her these
247	hat were not
248	ariation in
249	verage yield
250	p = 0.002). The
251	for this race.
252	than expected
253	5% of expected
254	mental
255	the
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257	we found
258	: inconsistent,
259	4.82; p = 0.01;
260	± 2.0 kg ha <sup>-1</sup> yr
261	.5 kg ha <sup>-1</sup> yr <sup>-1</sup> (p
262	mutation.
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265	ghest in the
266	stern gradient
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269	e was a
270	deviation in
271	ic heritability
272	was higher in
273	ge yield of
274	s trend was
275	provement on
276	raried by bean
277	< 0.001). In
278	over time,
279	To test for a
280	elated CDBN
281	0.001) and
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283	lity and home
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er 30-years of ites. Symbology

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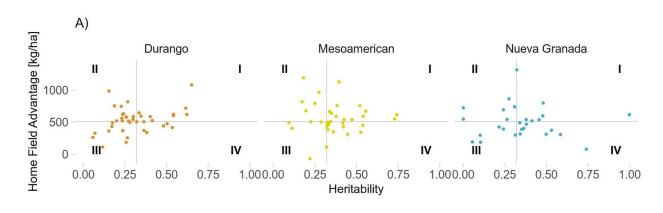
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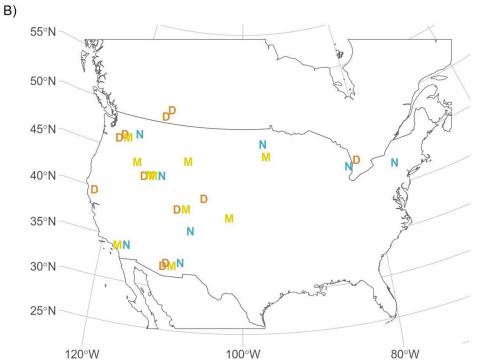
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293 he fitness and
294 ad adaptation
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311	cticed in the
312	HFA are not
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316	ts at that
317	ssed more
318	it heritability is
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321	her trait
322	reeding
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325 326 326 327 328 329 330 100°W 80°W 80°W site, by race. 80°W es. B) Top oamerican; N –

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333	from the
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335	ess, there was
336	ty increased in
337	occurred
338	enetic variation
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341	dean entries
342	many CDBN
343	, which would
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347	ield heritability
348	e course of
349	ty from the
350	ollows the
351	n source, which
352	17; MacQueen
353	urango race in

354	or yield within
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365	ights the
366	ed yield, and
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377	ere required to
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384	ual breeding
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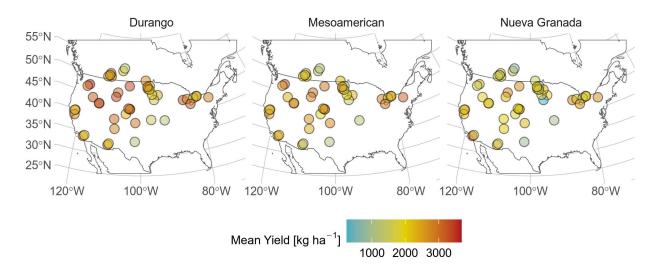
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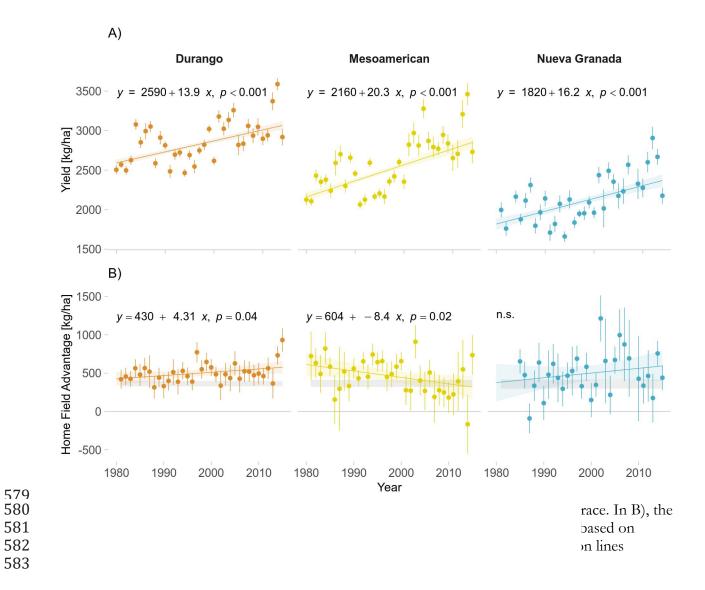
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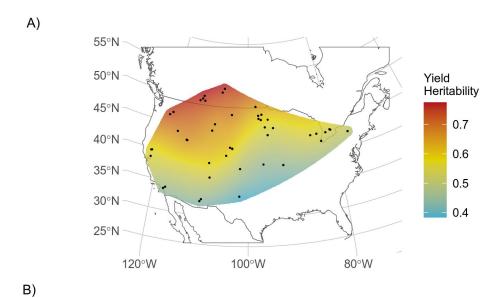
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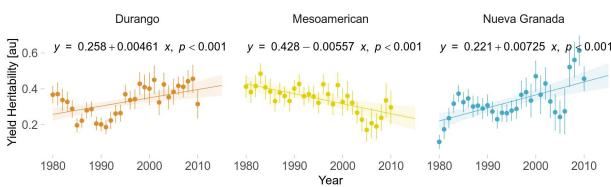
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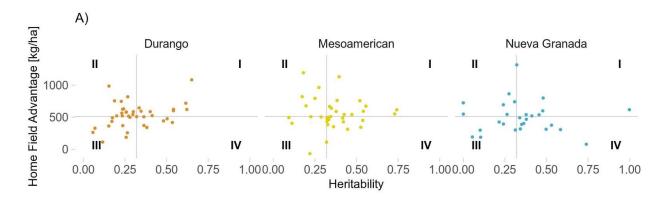


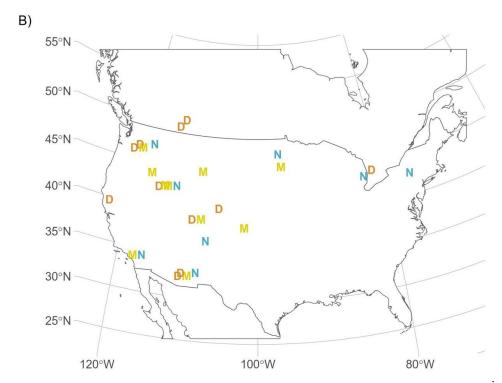






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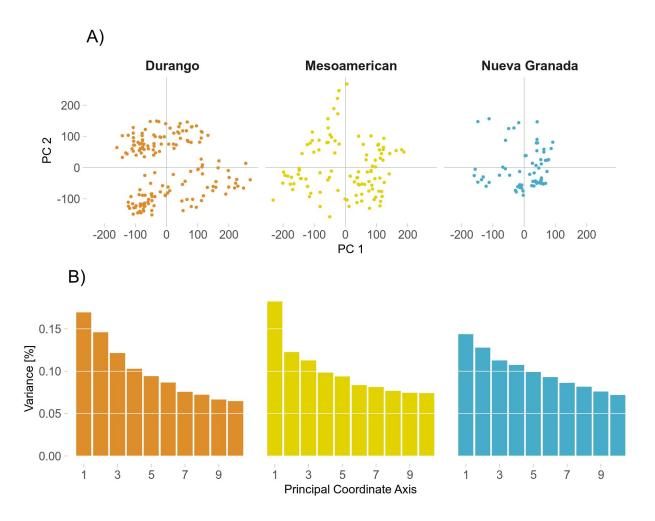
es. B) Top oamerican; N –

**Table 1.** Implications of home field advantage and heritability for breeding and adaptation. Combining agroecological ecoregion information and heritability of specific traits may help improve selection efficiency while providing insights into processes driving past selection.

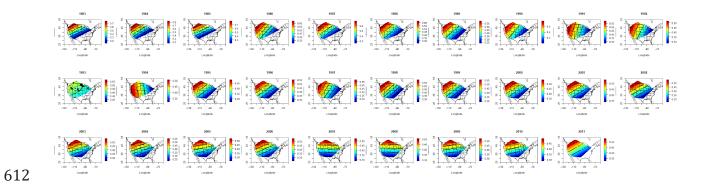
		Heritability	
		Lower	Higher
Home Field	Larger	Processes: High environmental variation among locations, low genetic variation potentially enriched in locally important alleles.  Implications: Inefficient selection on individuals for phenotypic improvement; testing at these sites may reveal conditionally beneficial alleles.	Processes: High environmental variation among locations, high genetic variation potentially enriched in locally important alleles.  Implications: Efficient identification and selection of specialists that may contain large-effect candidate loci for introgression.
Home Field Advantage	Smaller	Processes: Low environmental variation among locations, low genetic variation potentially enriched in broadly important alleles.  Implications: Inefficient selection on individual entries for phenotypic improvement, so family based methods are necessary.	Processes: Low environmental variation among locations, high genetic variation potentially enriched in broadly important alleles.  Implications: Efficient selection on individual entries for phenotypic improvement.

**Table 2**Partitioning of CDBN Yield Variances

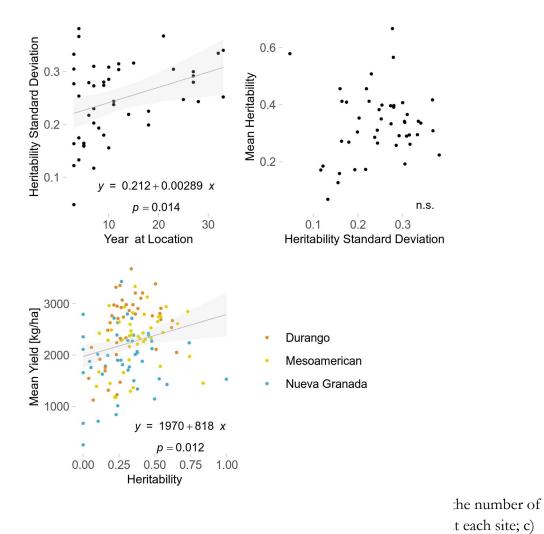
		Race	
	Durango	Mesoamerican	Nueva Granada
Home Site	1.3%	1.3%	1.1%
Residuals	14.1%	15.8%	15.6%
Genotype	3.3%	4.1%	3.2%
Site	33.1%	30.9%	29.0%
Year	2.4%	3.0%	2.5%
Site-Year	45.7%	44.9%	48.7%
Residual Reduction	8.3%	7.7%	6.3%
<sup>1</sup> Proportion of residual variance explained by home site			



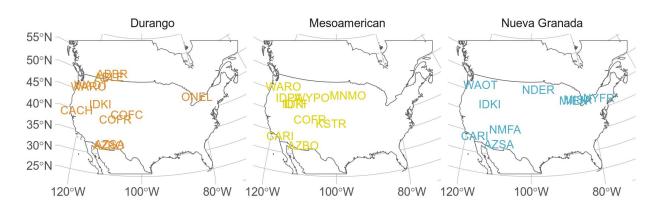
608 s along principal axes.



613 -2013) centered 614



at at p < 0.10



625 :eviations

## ANOVA of Yield Across Time

	Sum Sq	Df	F value	Pr(>F)
Year	252,500,000	1	292.70	0.000
Race	1,050,000,000	2	608.26	0.000
Year*Race	6,895,000	2	4.00	0.018
Residuals	11,370,000,000	13174	-	-

 $\operatorname{AIC}^1 \text{ of Competing Home Field Advantage Models}$ 

	Durango	Mesoamerican	Nueva Granada
With Home Field	6772	5095	3434
Variety, Site, Year	7323	5421	3599
With Home Field, Kinship	7662	5703	3773
With Kinship	8143	5997	3926

<sup>&</sup>lt;sup>1</sup>Akaike Information Criterion

Table S3
ANOVA of Home Field Advantage Across Time

	Sum Sq	Df	F value	<b>Pr(&gt;F)</b>
Year	4.755	1	0.00	0.992
Race	36,290	2	0.43	0.654
Year * Race	410,000	2	4.82	0.010
Residuals	3,994,000	94	-	-