

Marcadores moleculares, QTLs y Epistasia  
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# EL DILEMA DE LOS FITOMEJORADORES Y LAS CARACTERISTICAS CUANTITATIVAS



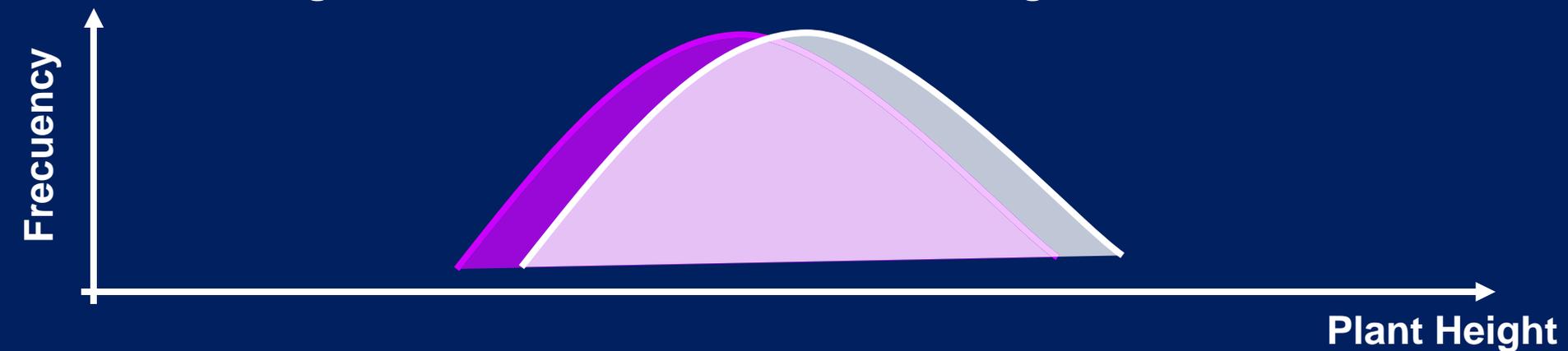
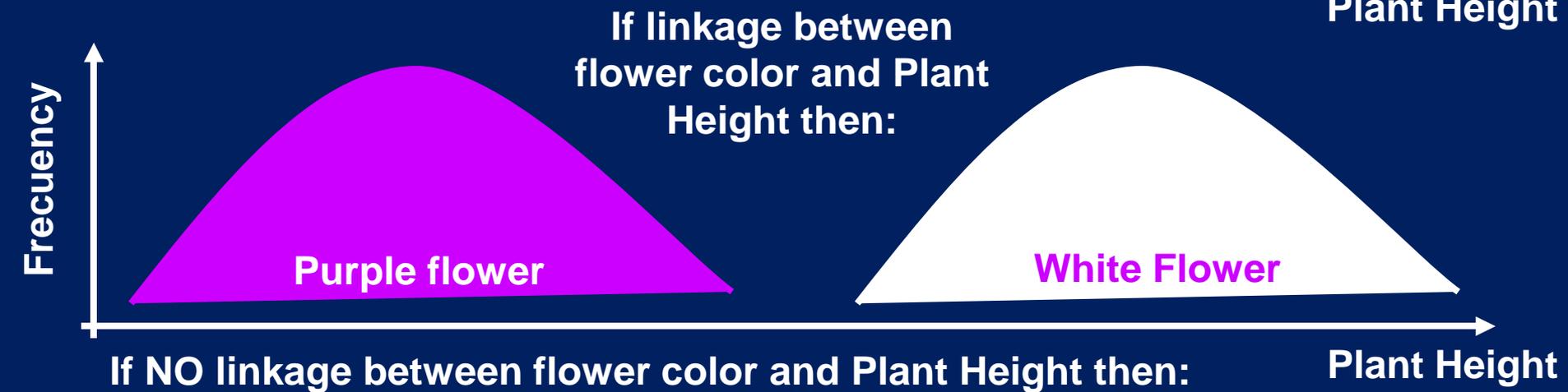
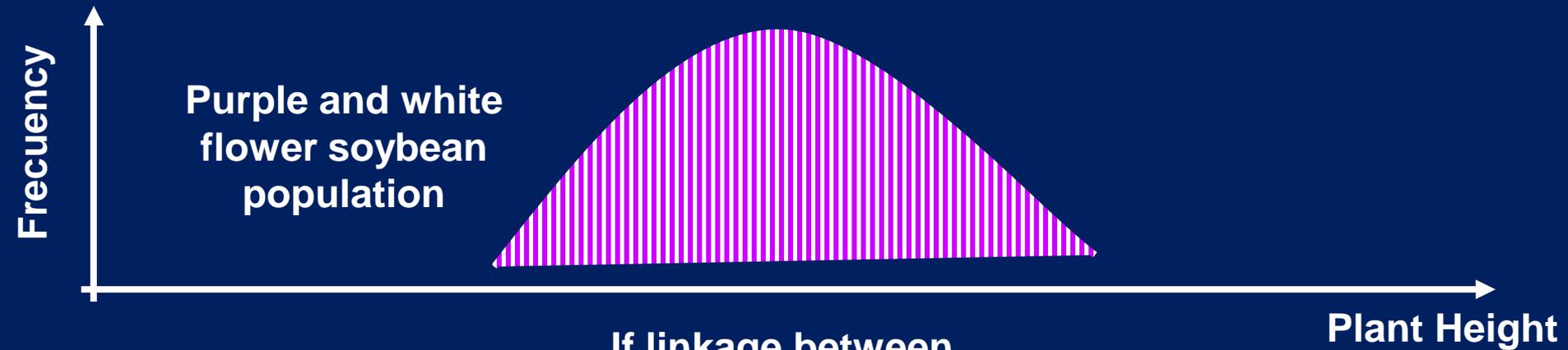
FENOTIPO

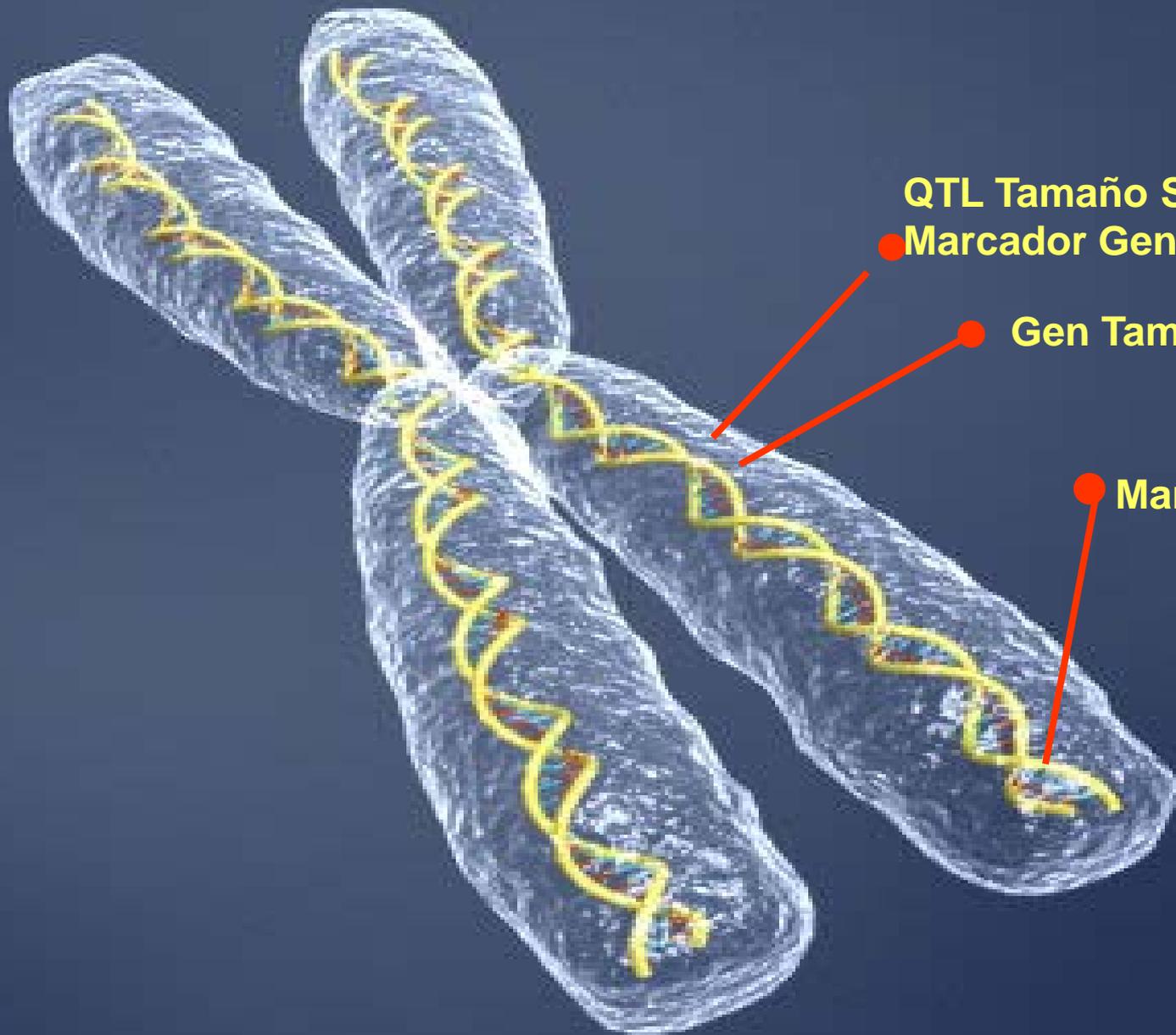
GENOTIPO

## EN 1923 KARL SAX INDICATED:

“The relative effect of various factors and the cumulative effect of factor combinations have been difficult to analyze because the size factors could not readily be isolated and studied independently. **If, however, certain size factors can be found linked with factors for qualitative characters it should be possible to study independently the size factor or factors within each linkage group.** This is now possible in a limited way with the size differences in beans.”

EN 1923 KARL SAX AFIRMÓ: "El efecto relativo de diversos factores y el efecto acumulativo de las combinaciones de factores han sido difíciles de analizar debido a que los factores de tamaño no podían ser aislados fácilmente ni estudiados de forma independiente. **Si ciertos factores de tamaño pudiesen ESTAR LIGADOS a otros factores de caracteres cualitativos, DEBERIA ser posible estudiar el factor o los factores de tamaño dentro de cada grupo de LIGAMIENTO de forma independiente.** Ahora esto es posible, de manera limitada, respecto de las diferencias de tamaño en el frejol".





**QTL Tamaño Semilla**

**● Marcador Gen Color de flor**

**● Gen Tamaño de Semilla**

**● Marcador No ligado**

# Method Single Seed Descent

Minsoy X Noir1

Inbreeding (%)

$F_1$

										0,00
$F_{2,1}$	$F_{2,2}$	$F_{2,3}$	$F_{2,4}$	$F_{2,5}$	$F_{2,6}$	$F_{2,7}$	$F_{2,8}$	$F_{2,9}$	$F_{2,10}$	50,00
$F_{3,1}$	$F_{3,2}$	$F_{3,3}$	$F_{3,4}$	$F_{3,5}$	$F_{3,6}$	$F_{3,7}$	$F_{3,8}$	$F_{3,9}$	$F_{3,10}$	75,00
$F_{4,1}$	$F_{4,2}$	$F_{4,3}$	$F_{4,4}$	$F_{4,5}$	$F_{4,6}$	$F_{4,7}$	$F_{4,8}$	$F_{4,9}$	$F_{4,10}$	87,50
$F_{5,1}$	$F_{5,2}$	$F_{5,3}$	$F_{5,4}$	$F_{5,5}$	$F_{5,6}$	$F_{5,7}$	$F_{5,8}$	$F_{5,9}$	$F_{5,10}$	93,75
$F_{6,1}$	$F_{6,2}$	$F_{6,3}$	$F_{6,4}$	$F_{6,5}$	$F_{6,6}$	$F_{6,7}$	$F_{6,8}$	$F_{6,9}$	$F_{6,10}$	96,88

# Poblaciones de mapeo para soya (*Glycine max*)

	<b>SIZE</b>	<b>STATUS</b>
<b>Minsoy x Noir 1</b>	<b>240 RILs</b>	<b>Pública USDA</b>
<b>Minsoy x Archer</b>	<b>233 RILs</b>	<b>Pública USDA</b>
<b>Noir 1 x Archer</b>	<b>240 RILs</b>	<b>Pública USDA</b>
<b>PI 437654 x BSR 101</b>	<b>300 RILs</b>	<b>Comprada por Pioneer a Iowa State University</b>

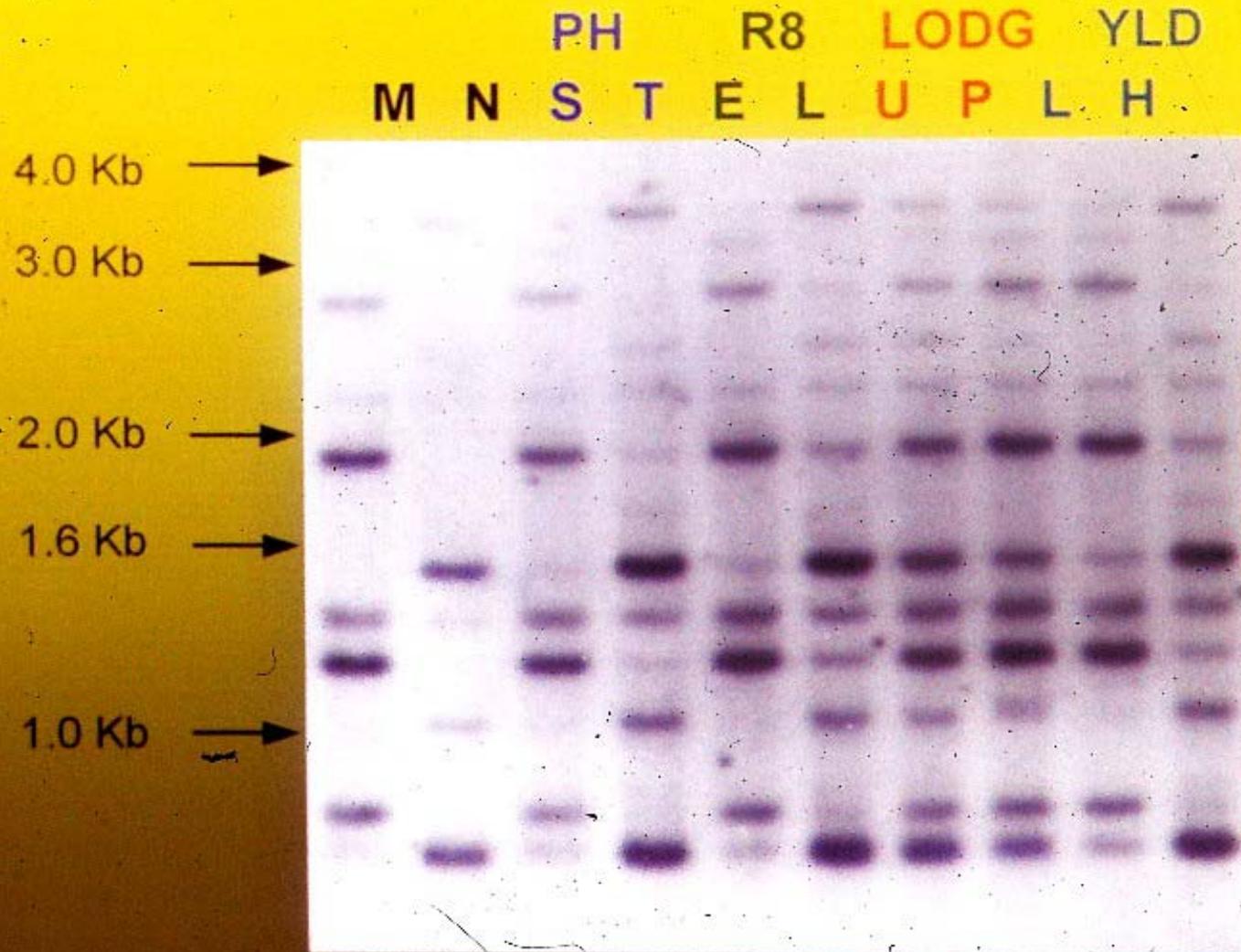


# MEANS STD. DEV. AND RANGES FOR TRAITS IN THE THREE RI POPULATIONS

TRAIT	Minsoy-Archer			Noir 1-Archer			Minsoy-Noir 1			Archer	Minsoy	Noir 1
	MEAN	STD	RANGE	MEAN	STD	RANGE	MEAN	STD	RANGE	MEAN		
YIELD (qq/Há)	24	2.6	15-31	27	2.5	21-33	20	4	5.5-27	31	18	26
R8 (days)	108	8.2	91-124	101	5.8	87-115	105	6.2	91-119	118	100	102
R1 (days)	40	5.7	31-55	38	2.6	33-44	41	3.8	35-51	46	42	40
Height (cm)	85	20	43-140	99	9.8	71-124	74	19	25-132	103	57	96
Lodging (1-5)	3.0	0.6	1.3-4.2	2.6	0.5	1.6-3.8	2.6	0.7	1.0-4.5	2.0	3.3	2.7
Leaf Area (cm <sup>2</sup> )	81	13	51-134	101	15	67-152	78	11	46-119	109	67	107
Seed Weight (mg/seed)	135	14	101-172	147	15	108-189	141	14	105-183	661	123	138

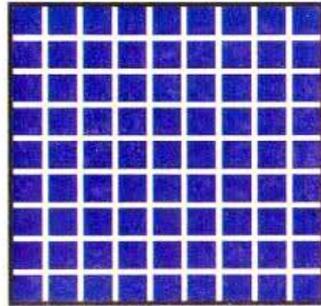


Mansur L.M., J. Orf, and K.G. Lark. 1993. Determining the linkage of quantitative trait loci to RFLP markers using extreme phenotypes of recombinant inbreds of soybean (*Glycine max* L. Merr.). *Theor. Appl. Genet.* 86:914-918.

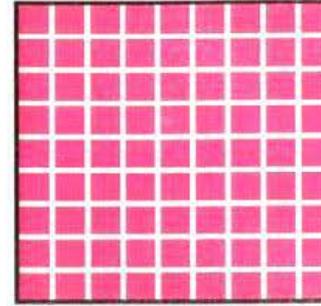


**RIL: RECOMBINANT INBRED LINES O LINEAS  
HOMOZIGOTAS RECOMBINANTES**

**MINSOY**

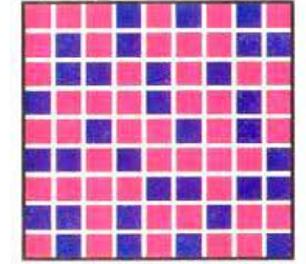
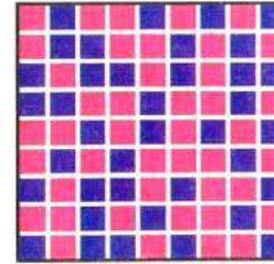
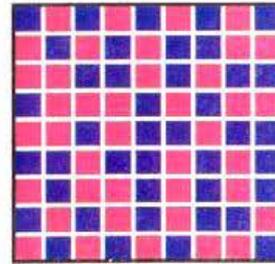
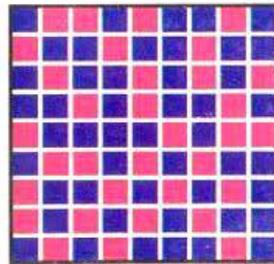
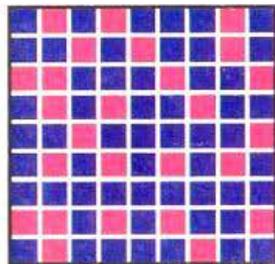


**NOIR1**

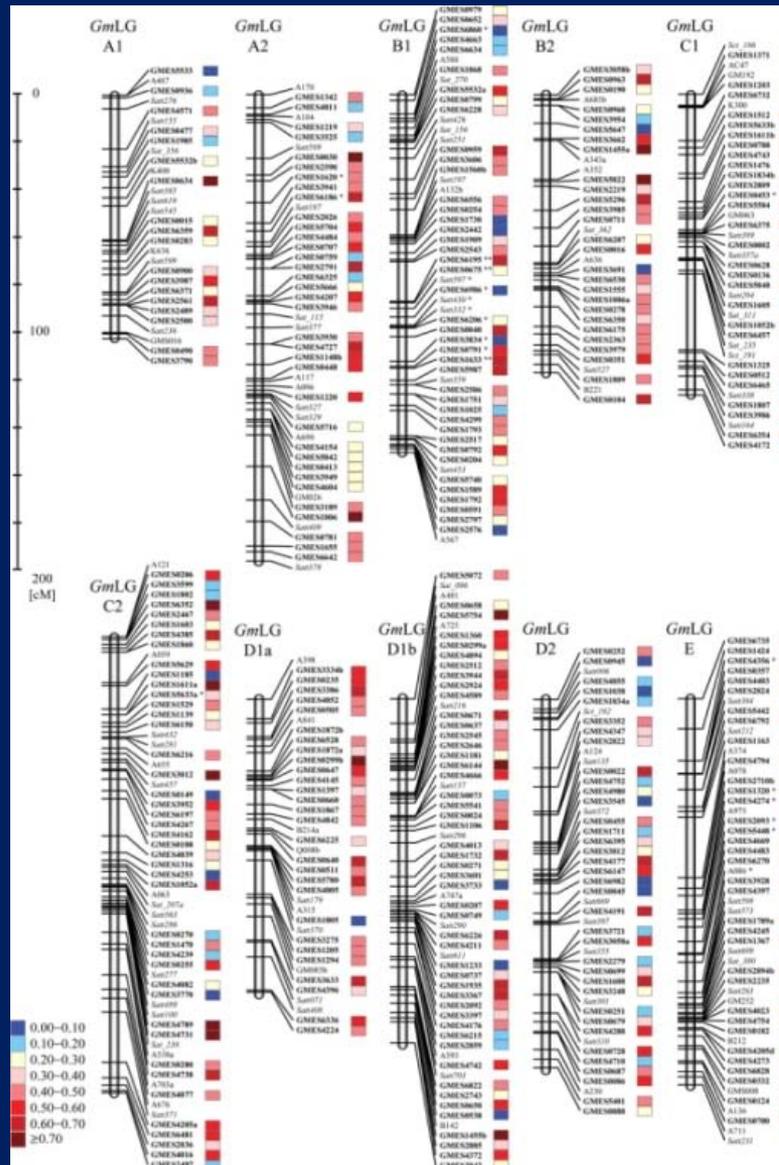


**X**

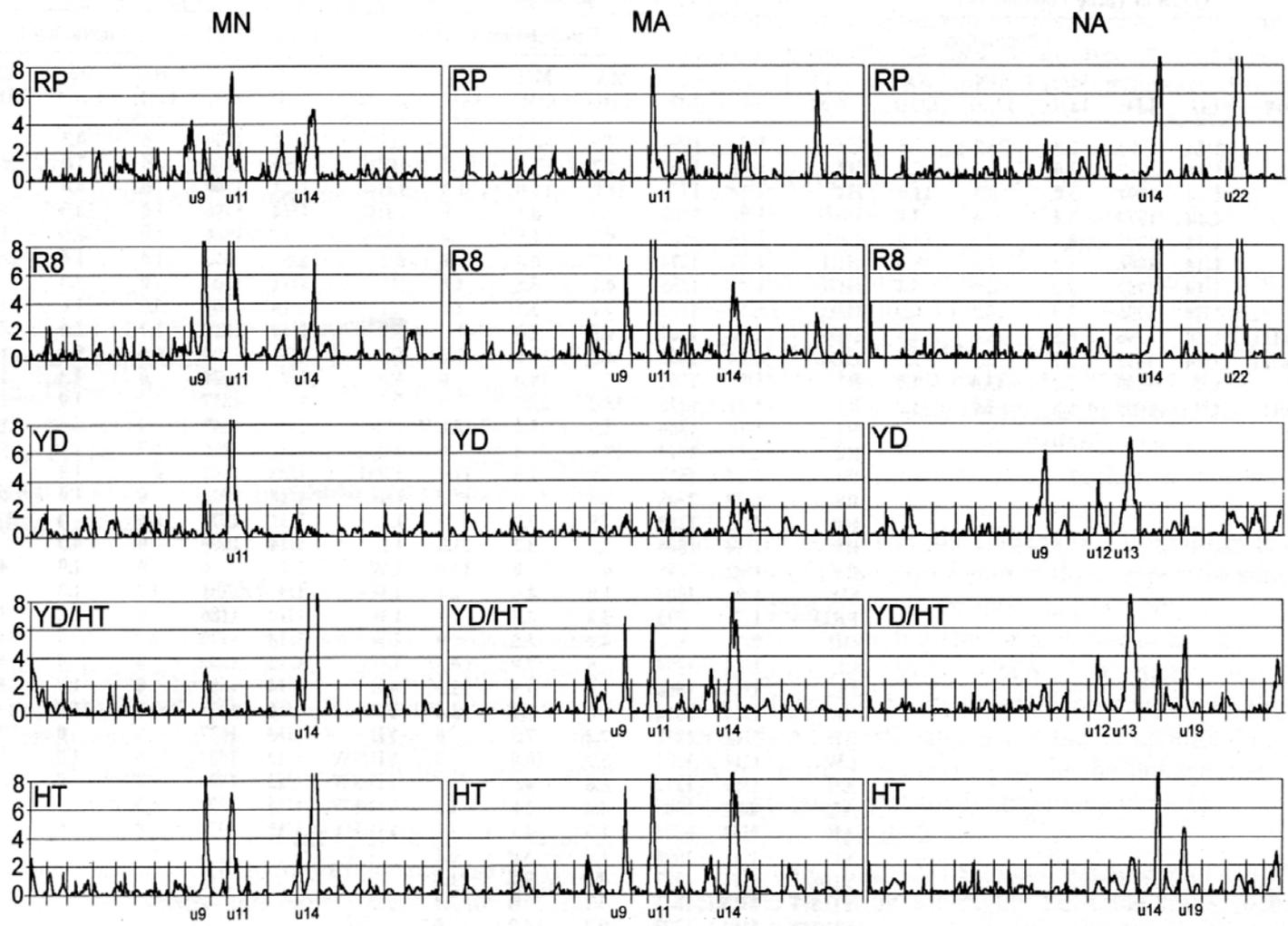
**=RIL**



# Mapa de Ligamiento Soya



Zhenqiu et al  
DNA Res (2007) 14 (6): 257-269



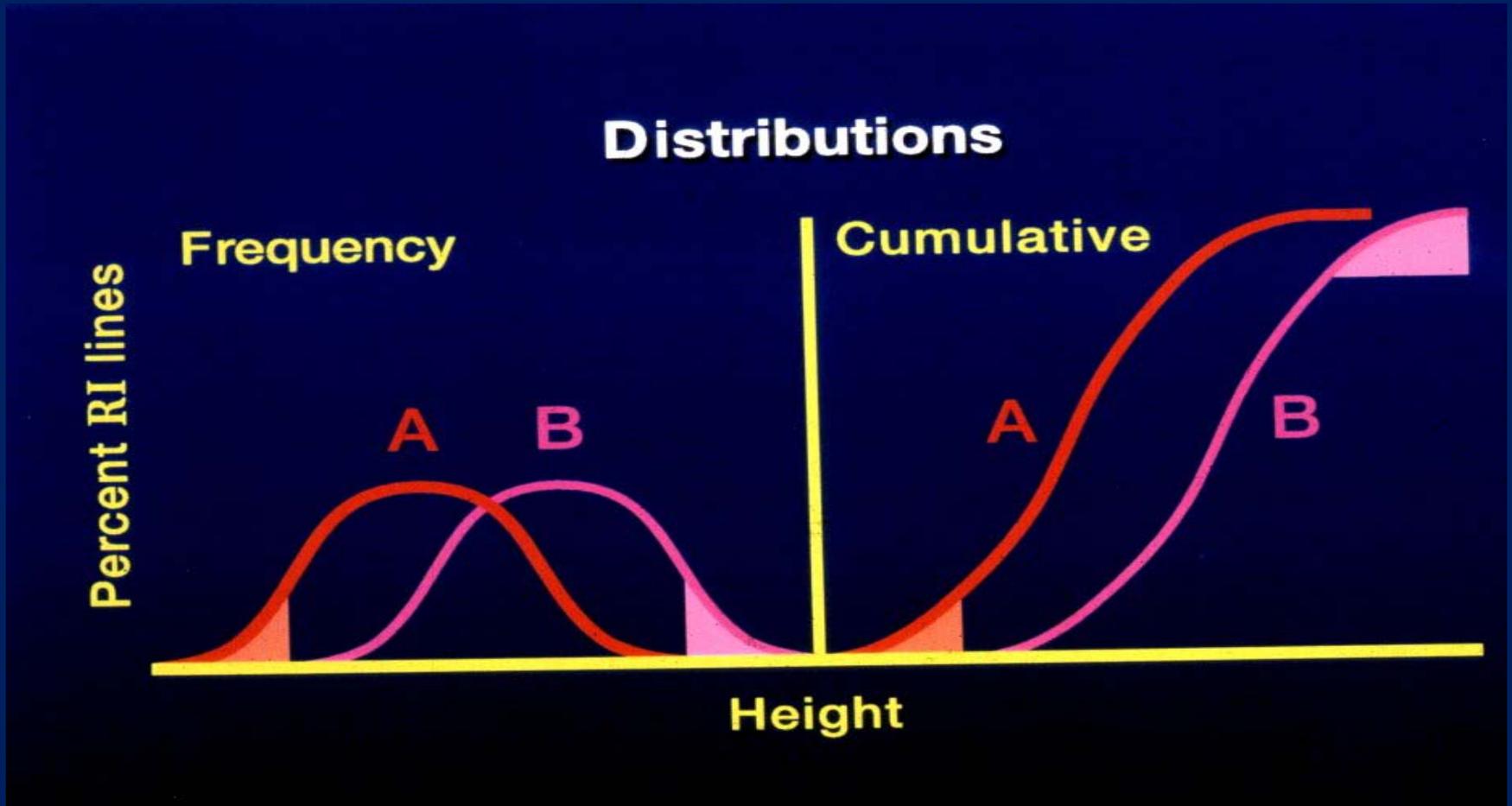
**Fig. 3.** QTL genome scans for five different traits in each of the three RI populations. Each graph displays the complete simple interval-mapping scan for a particular population and trait (see materials and methods). The genome position (x-axis) is graphed against the LOD score (y-axis). Vertical lines on the x-axis indicate the boundaries of linkage groups. For these populations a LOD score of 3.7 is significant at a threshold of 0.05 for the experiment (the probability of finding a QTL with a LOD of 3.7 by chance, after scanning all of the markers in the genome). The populations are MN = Minsoy-Noir 1, MA = Minsoy-Archer, and NA = Noir 1-Archer. The traits are (RP) reproductive period, (R8) maturity, (YD) seed yield, (YD/HT) yield per unit height, and (HT) height.

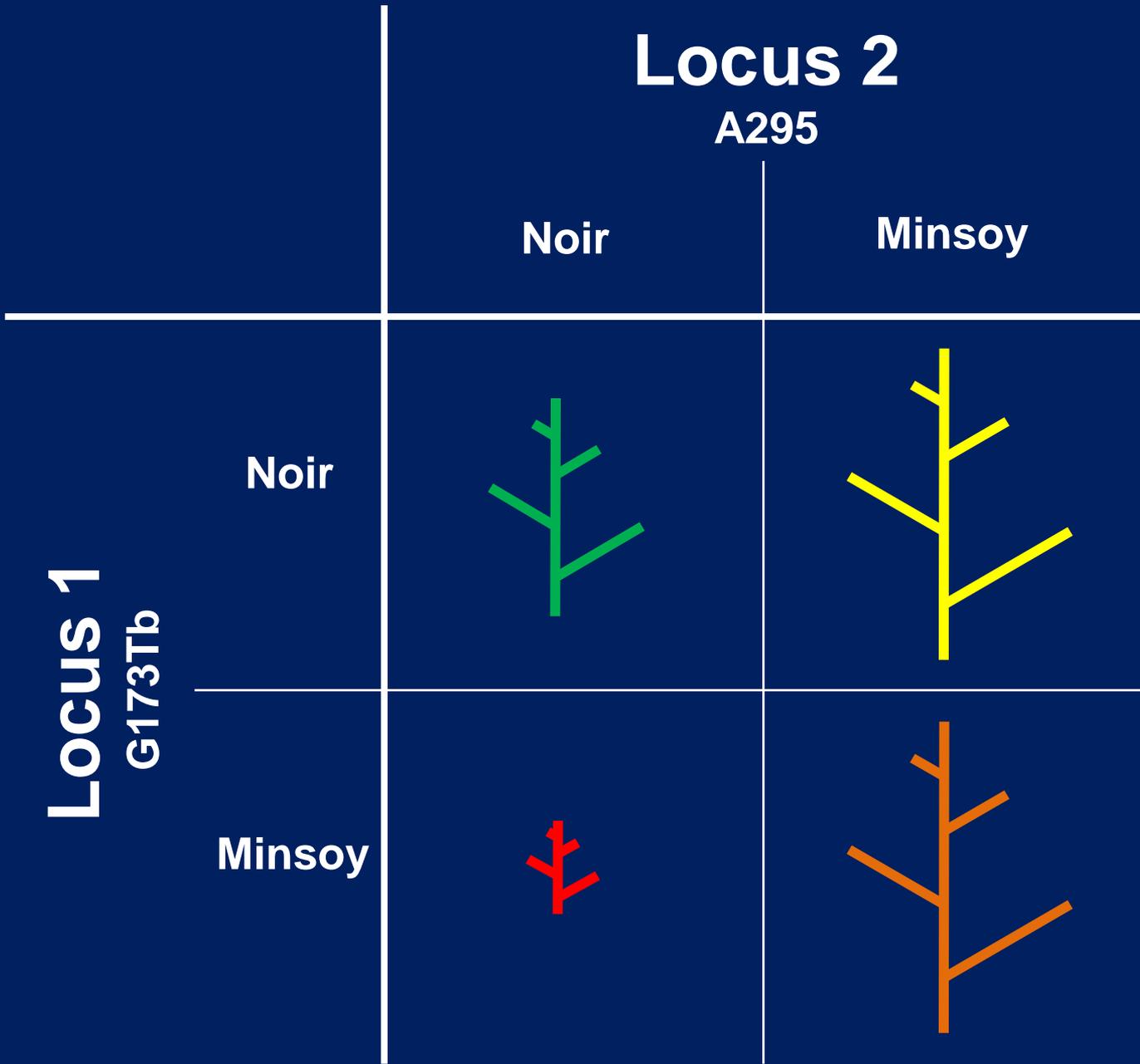
# EPISTASIS

Lark, K.G., J. Orf, and L.M. Mansur. 1994. Epistatic expression of quantitative trait loci (QTL) in soybean [*Glycine max* (L.) Merr.] determined by QTL association with RFLP alleles. *Theor. Appl. Genet.* 88:485-489.

Lark K.G., K. Chase, F. Adler, L.M. Mansur, and J. Orf. 1995. Interactions between quantitative traits loci in soybean in which trait variation at one locus is conditional upon a specific allele at another. *Proc. Nat. Acad. of Sci.* 92:4656-4660.

# FREQUENCY VS CUMULATIVE DISTRIBUTION





Locus 2

A295

Noir

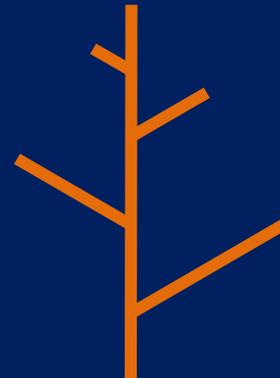
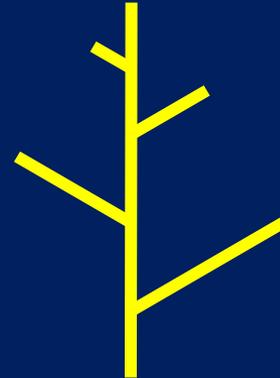
Minsoy

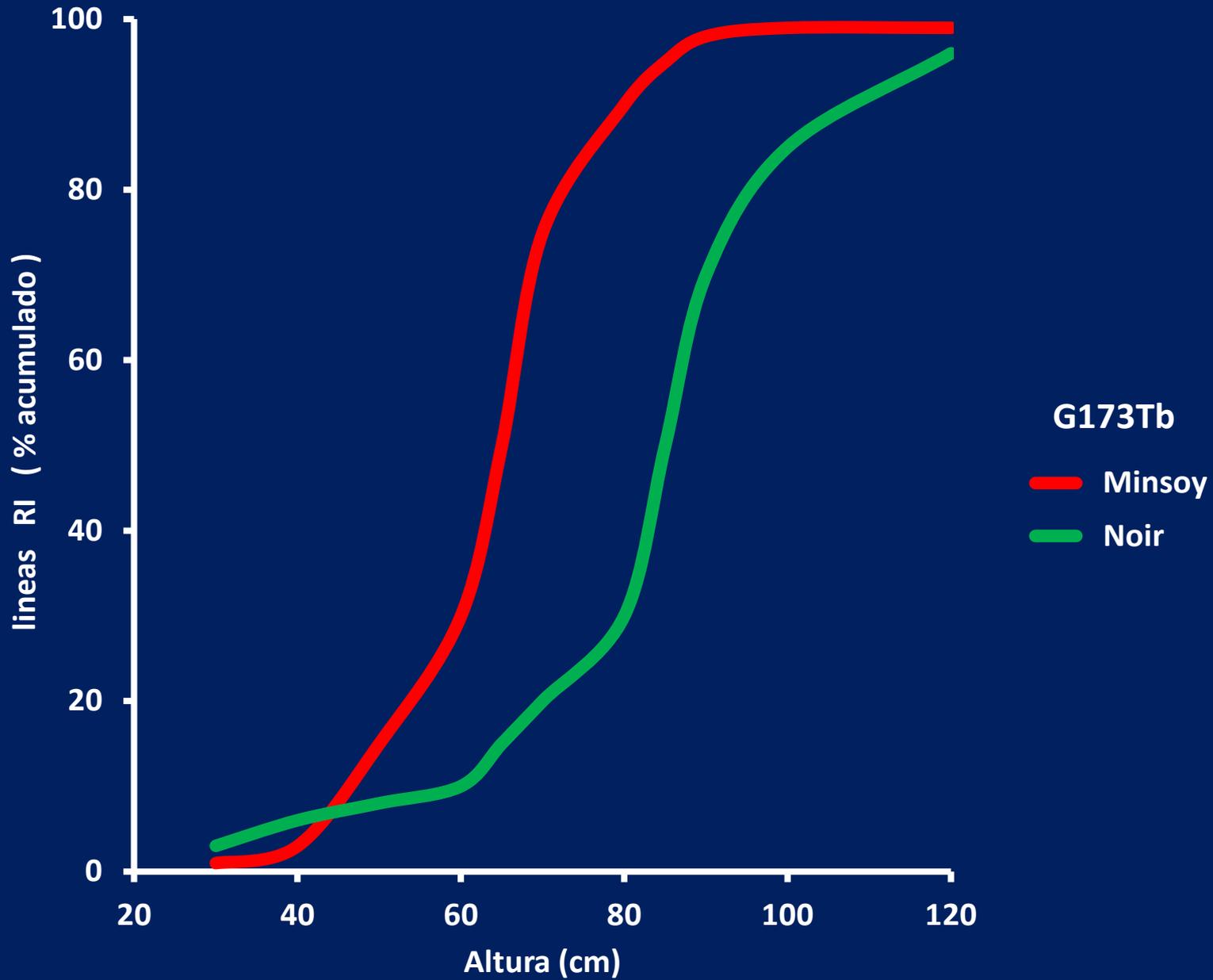
Noir

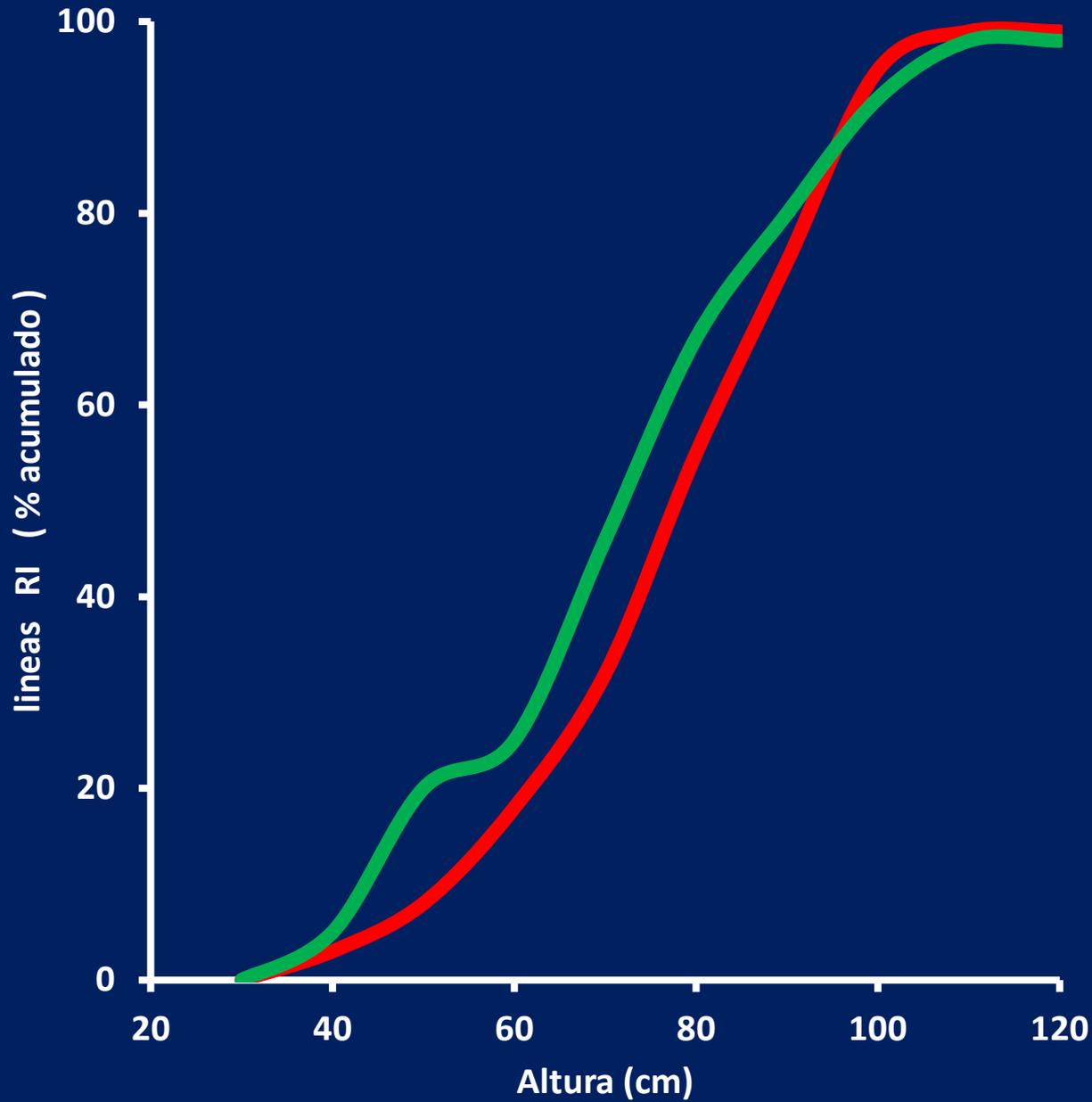
Locus 1

G173Tb

Minsoy



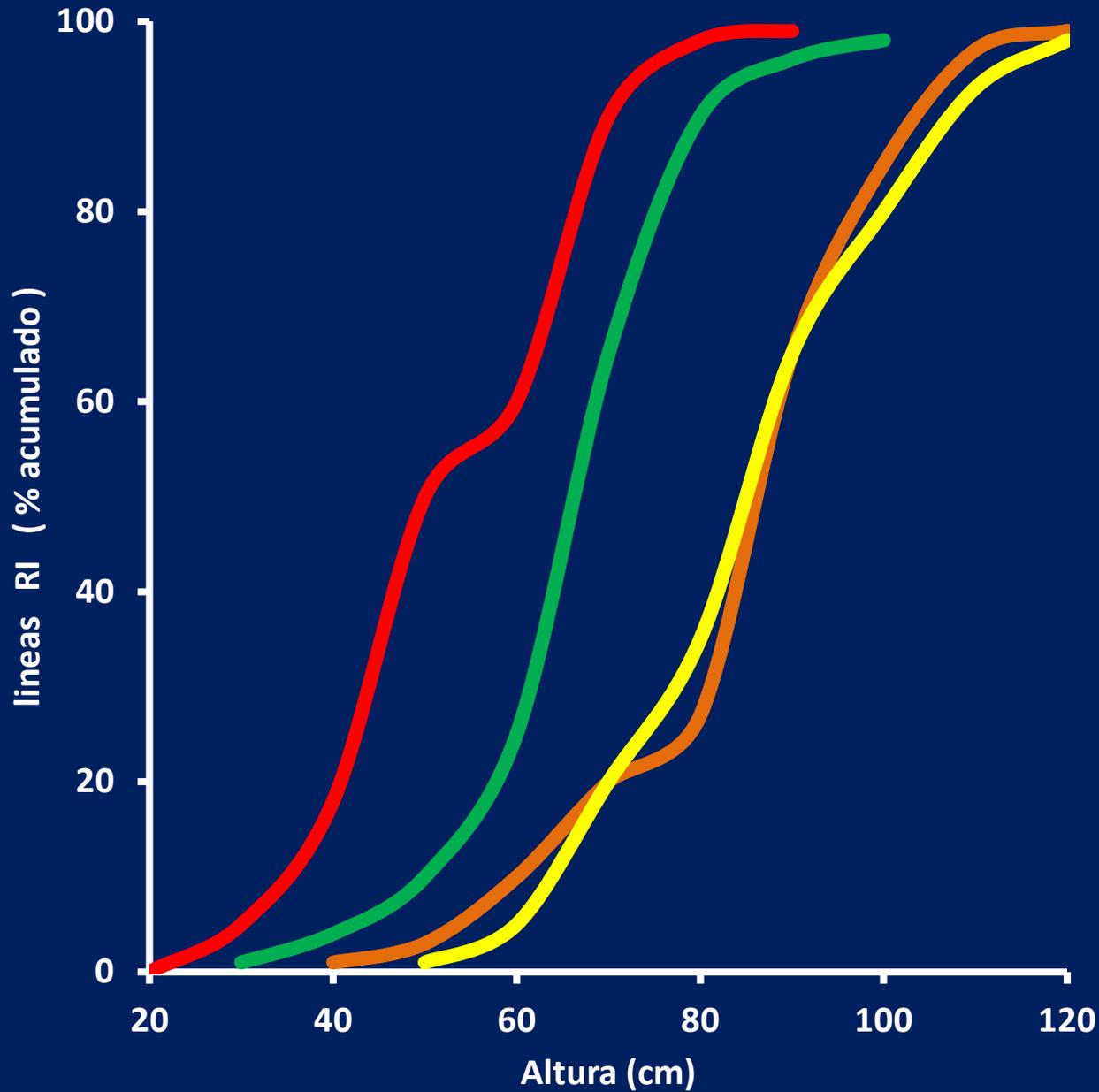




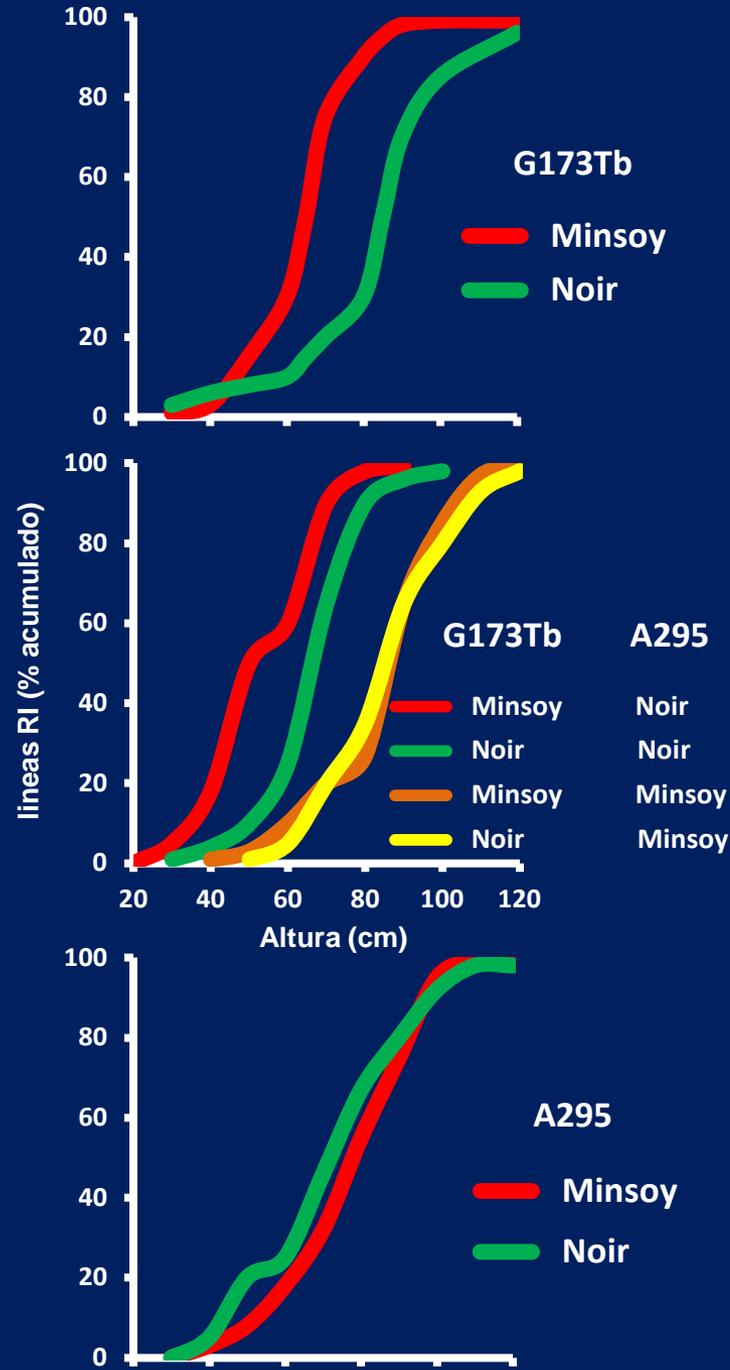
**A295**

**Minsoy**

**Noir**



	G173Tb	A295
Minsoy	Minsoy	Noir
Noir	Noir	Noir
Minsoy	Minsoy	Minsoy
Noir	Noir	Minsoy



# Locus 2

214H10

Noir

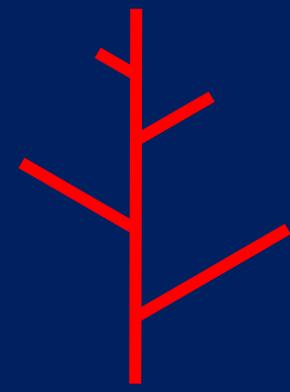
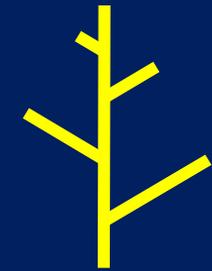
Minsoy

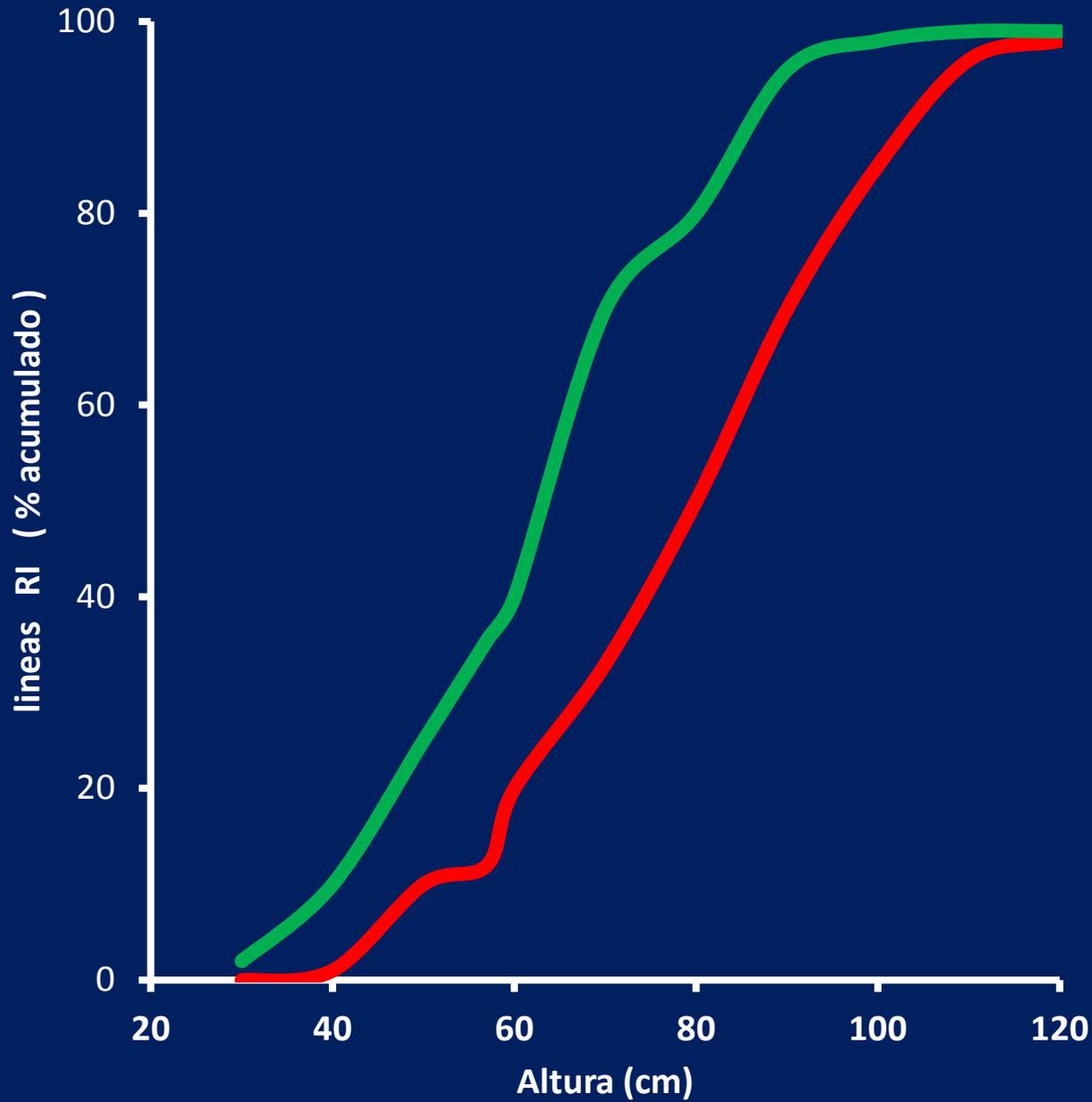
# Locus 1

A397

Noir

Minsoy

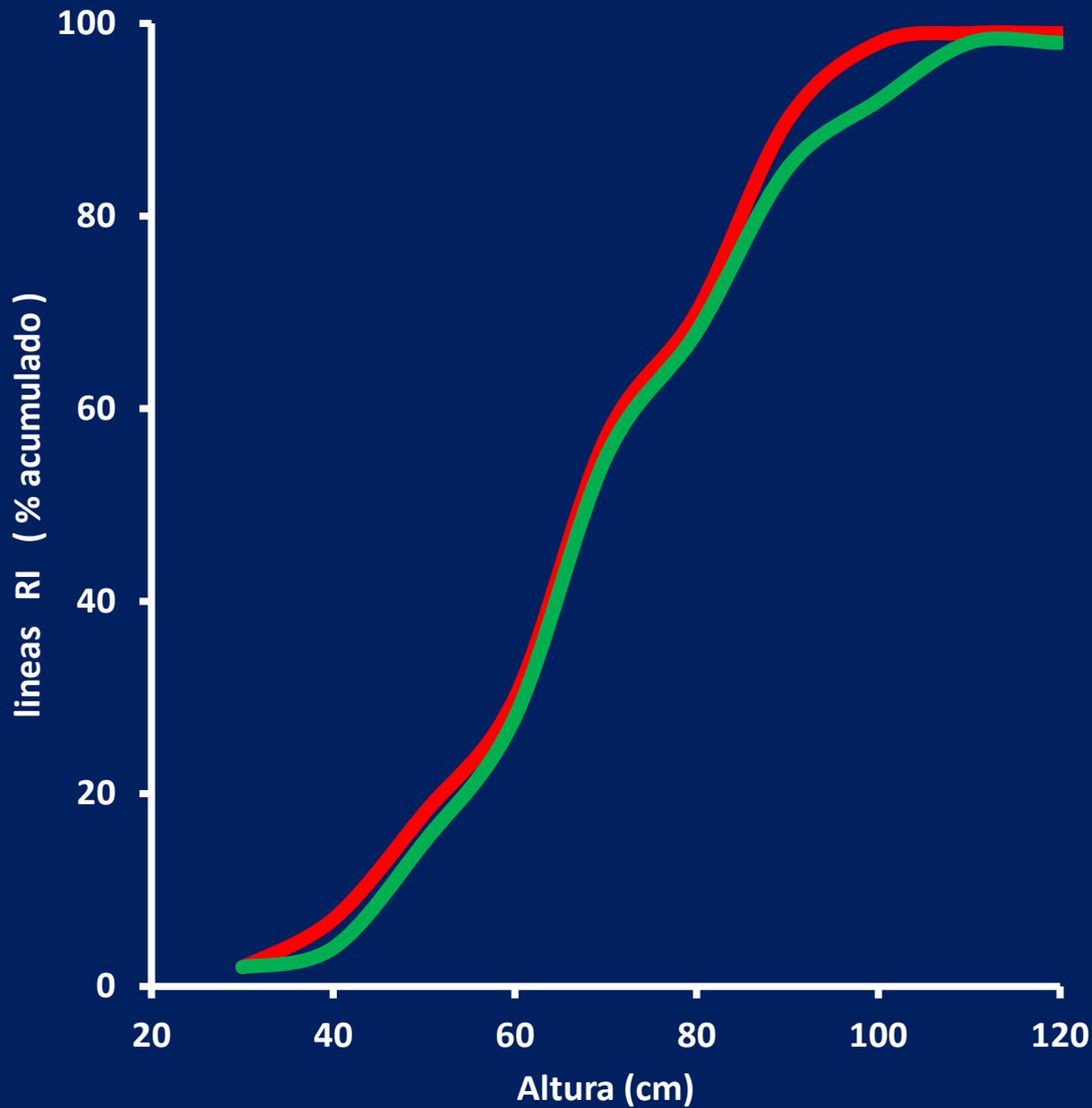




**A397**

**Minsoy**

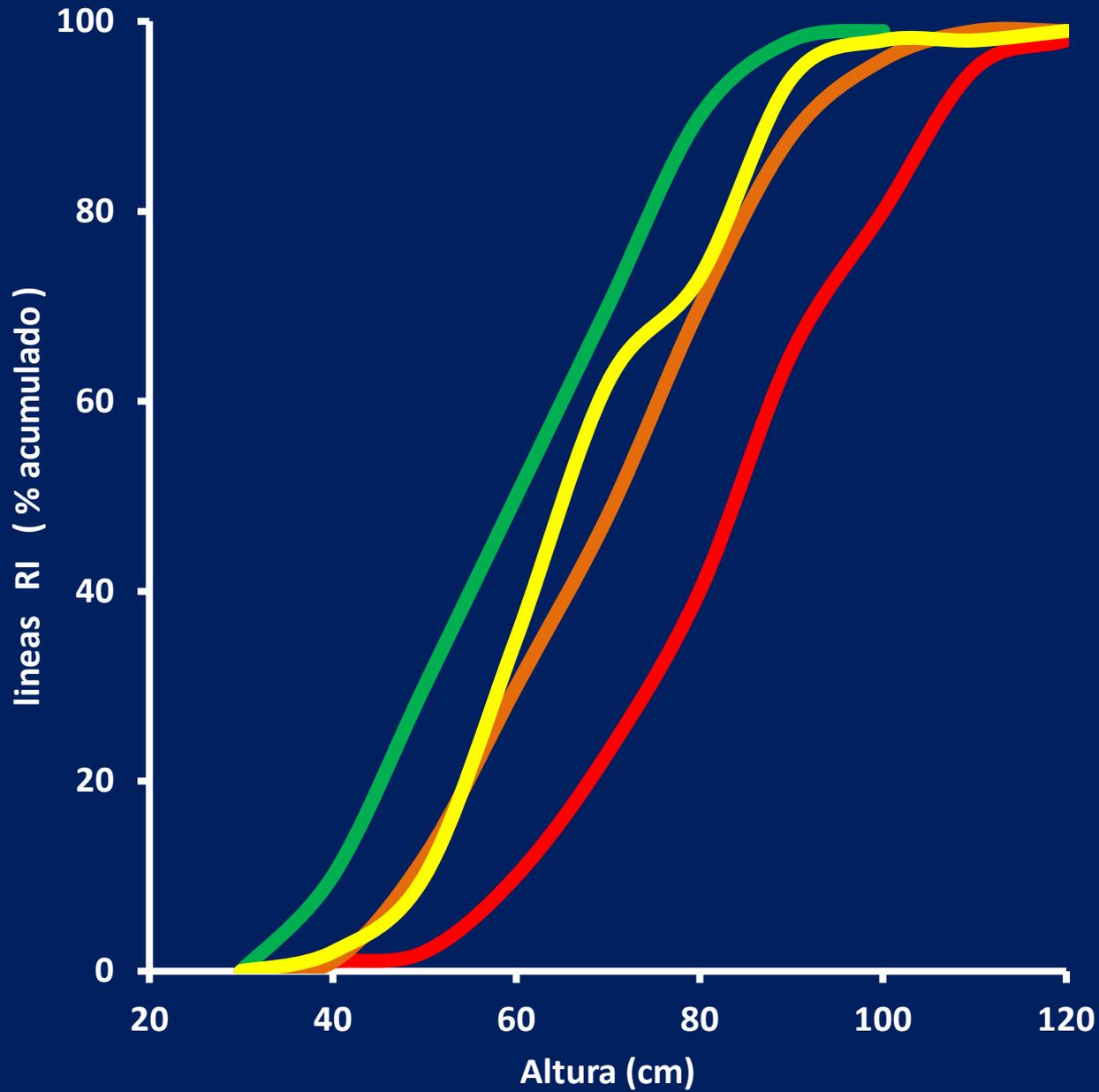
**Noir**



**214H10**

**Minsoy**

**Noir**



	<b>A397</b>	<b>214H10</b>
	<b>Minsoy</b>	<b>Noir</b>
	<b>Noir</b>	<b>Noir</b>
	<b>Minsoy</b>	<b>Minsoy</b>
	<b>Noir</b>	<b>Minsoy</b>

