Regulation of inflorescence architecture

Sarah Hake[1], Volker Brendel[2], Dave Jackson[3], Toby Kellogg[4], Rob Martienssen[3], Torbert Rocheford[5] and Bob Schmidt[6]

Plant Gene Expression Center, Albany CA
University of Illinois, Urbana/Champain, IL
Cold Spring Harbor, NY
University of Missouri, St. Louis

Generating new mutants

Working with Dr. Gerry Neuffer, we have produced and screened EMS mutants for the third summer in a row. We have screened B73, Mo17, A619, A632 inbreds and various hybrids. The list of mutants and pictures have gone to MaizeGDB. Below are a few pictures from this summer.

Gerry Neuffer

tasselless

adherent

upright branches

barren inflorescence

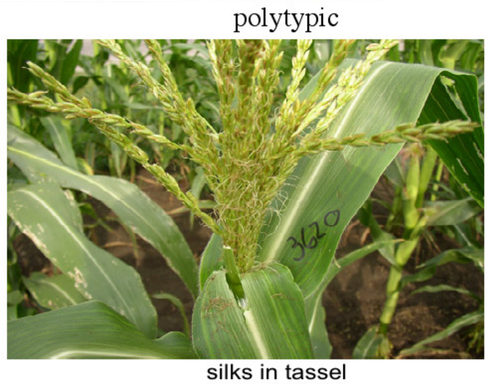
anther ear

ramosa

compact plant

polytypic

unbranched



silks in tassel

leaf mutants others might like

Mapping QTL to known mutants

The Rocheford lab is mapping QTL that regulate inflorescence architecture.

Inflorescence Mutants and QTL associations

** NOTE ** There are QTLs in bins not listed in this table (to my knowledge,no identified mutant loci in these bins)

Mutant	Name	Bin	QTL associations (traits)
ct2	compact plant2	0.01	
ifa1	indeterminate floral apex1	1.02-1.03	
qcobd5	QTL cob diameter5	1.02	
qcobd11	QTL cob diameter11	1.02	side spike
qcobd27	QTL cob diameter27	1.02	side spike
qcobd32	QTL cob diameter32	1.02	side spike
ts2	tassel seed2	1.03	
qcobd23	QTL cob diameter23	1.03	
clv28	CQRAV28R (clavata1-like gene from pioneer)	1.03	branch #, total spikelets, total meristems, total spikelets/branch #, Branch
qcobd33	QTL cob diameter33	1.06	#/L2, L3/L1, L2/L1
bif2	barren inflorescence2	1.06	L2, branch #, L3/L2, L3/L1,
qcobd6	QTL cob diameter6	1.07	L2/L1
qcobd12	QTL cob diameter12	1.07	L2, branch #, L3/L2, L3/L1, L2/L1
qcobd24	QTL cob diameter24	1.07	L2, branch #, L3/L2, L3/L1, L2/L1
qcobd28	QTL cob diameter28	1.07	L2, branch #, L3/L2, L3/L1, L2/L1
ad1	adherent1	1.08	Branch #, side spike
an1	anther ear1	1.08	Branch #, side spike
id1	indeterminate1	1.08	Branch #, side spike
ts3	tassel seed3	1.09	
tls1	tasselless1	1.09	
kip	bell -like gene interacts with KN1	1.09	
kn1	knotted1	1.10	
knox8	knotted related homeobox8	1.10	
ts6	tassel seed6	1.11	side spike
ids1	indeterminate spikelet1	1.11	side spike
qcobd13	QTL cob diameter13	1.12	branch #, side spike, total
qcobd14	QTL cob diameter14	2.02	spikelets/branch#, branch #/L2
lfyB	leafyB (Doebley)	2.03	seed row number (doebley)
ts1	tassel seed1	2.04	L3, branch #, angle, side spike, L3/L2
ba2	barren stalk2	2.04	L3, branch #, angle, side spike, L3/L2
cen1B	centroradialis-like gene - McSteen	2.04	L3, branch #, angle, side spike, L3/L2
abph1	abphyl1	2.04	L2, total spikelets, total meristems, total spikelets/branch#, branch#/L2,
qcobd15	QTL cob diameter15	2.06	L3/L2, L3/L1, L2/L1
qcobd7	QTL cob diameter7	2.07	angle, total spikelets/branch#
qcobd25	QTL cob diameter25	2.07	angle, total spikelets/branch#
qcobd29	QTL cob diameter29	2.07	angle, total spikelets/branch#
qcobd34	QTL cob diameter34	2.07	angle, total spikelets/branch#
qcobd16	QTL cob diameter16	2.08	meristems
pinA	CBSA021 pinformed-like gene Pioneer	2.09	
knox4	knotted related homeobox4	2.10	L2, total spikelets/branch#
ra2	ramosa2	3.02	branch #, total spikelets/branch#
zag4	Zea AGAMOUS homologue4-transcription factor	3.02	branch #, total spikelets/branch#
tp3	teopod3	3.03	L1, branch #, total spikelets/branch#, branch#/L2
ts4	tassel seed4	3.04	L3, L3/L1, L2/L1
tru1	tassels replace upper ears1	3.04	L3, L3/L1, L2/L1
qcobd1	QTL cob diameter1	3.04	L3, L3/L1, L2/L1
o15	liguleless3	3.04	L3, L3/L1, L2/L1
fea3	fasciated ear3	3.04	L2, L3, branch #, branch#/L2,
te1	terminal ear1	3.05	L3/L2, L3/L1, L2/L1
zag2	Zea AGAMOUS homologue2- expression in female inflorescence	3.05	L2, L3, branch #, branch#/L2, L3/L2, L3/L1, L2/L1
ub1	unbranched1 (may be identical to lg2)	3.06	angle
erf4a	ERF gene in tassels/ears Magnani	3.06	
lg2	liguleless2	3.06	angle
ba1	barren stalk1	3.06	angle main spike, total
pinB	CBSA021 pinformed-like gene Pioneer	3.09	spikelets/branch#
ra3	ramosa3	4.01	
sos1	supressor of sessile spikelets1	4.02	
pd1	paired rows1	4.02	
ts5	tassel seed5	4.03	
qcobd8	QTL cob diameter8	4.05	
fea2	fasciated ear2	4.05	
qcobd17	QTL cob diameter17	4.06	side spike
tu1	tunicate1	4.07	
qcobd2	QTL cob diameter2	4.07	branch#, main spike, total spikelets, total meristems, total
mpA	CFRME53monopterous-like gene Pioneer	4.08	spikelets/branch#, branch#/L2,
qcobd18	QTL cob diameter18	5.00	
fea1	fasciated ear 1	5.00-5.01	
clv40	CCRBA40R clavata1-like gene Pioneer	5.01	
qcobd19	QTL cob diameter19	5.03	angle, side spike
mpB	CFRME53monopterous-like gene Pioneer	5.03	angle, side spike
td1	thick tassel dwarf1	5.04	L2, side spike
qcobd9	QTL cob diameter9	5.04	L2, side spike main spike, total spikelets, total
qcobd3	QTL cob diameter3	5.05	meristems
pt*	polytypic-McClintock (bearded ear)	5.06	
si1	silky1	6.02	L3/L2, L3/L1, L2/L1 total spikelets/branch#,
zag1	Zea AGAMOUS homologue1- strong expression in female	6.05	branch#/L2
pt1	polytypic ear1	6.06	
rs1	rough sheath1	7.00	side spike, branch#/L2
clv64	CRWAX64R clavata1-like gene Pioneer	7.01	
ra1	ramosa1	7.02	branch #, branch#/L2
tp1	teopod1	7.03	L1, L2, Branch#/L2
qcobd10	QTL cob diameter10	7.03	L1, L2, Branch#/L2
qcobd20	QTL cob diameter20	7.03	L1, L2, Branch#/L2
qcobd26	QTL cob diameter26	7.03	L1, L2, Branch#/L2
qcobd30	QTL cob diameter30	7.03	L1, L2, Branch#/L2
qcobd35	QTL cob diameter35	7.03	L1, L2, Branch#/L2
ra3	ramosa3	7.04	
o15	opaque endosperm15 (ear in tassel)(may be identical to gzr1)	7.05	branch#
bd1	branched silkless1	7.06	
bif1	barren inflorescence1	8.00	
zmm2	Zea mays MADS2	8.02	
ap21	??	8.03	
clt1	clumped tassel1	8.04	
pd2	paired rows2	8.04	
knox5	knotted related homeobox5	8.05	branch#, branch#/L2
qcobd31	QTL cob diameter31	8.07	
qcobd36	QTL cob diameter36	8.07	
qcobd21	QTL cob diameter21	8.08	L2, branch#
baf1	barren stalk fastigiate1	9.00	side spike
qcobd4	QTL cob diameter4	9.01	side spike
fas1	fascicled ear1	9.05	L2
pinC	CBSA021 pinformed-like gene Pioneer	9.05	
cr4	crinkly4	10.02	
cen2	CERAJ94 centroradialis gene - Pioneer	10.02	
tp2	teopod2	10.04	branch #, side spike
qcobd22	QTL cob diameter22	10.04	branch #, side spike
cen1A	centroradialis-like gene McSteen	10.04	side spike L1, L2, L3, branch#, angle, main spike, side spike, total spikelets, total meristems, total spikelets/branch#, branch#/L2, L3/L2, L3/L1, L2/L1
ra2-like1	ra2 like gene	10.10	

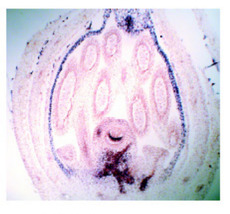
Evolutionary studies

The Kellogg lab has carried out in situs in different grasses that span the major diversification of the family using the MADS box gene, leafy hull sterile. In sorghum, maize, millet and rice, which have florets that mature from top to bottom (basipetally) in the spikelet, LHS1 is expressed only in the upper floret. In contrast, LHS1 is expressed in several florets of the spikelets of Chasmanthium which have florets that develop from bottom to top (acropetally).

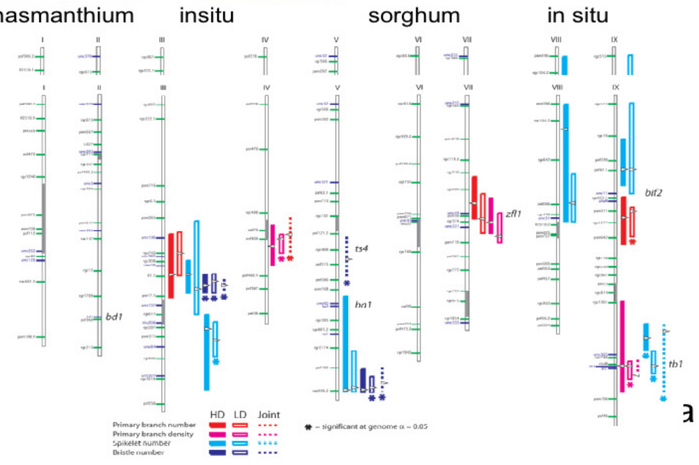
Chasmanthium

insitu

sorghum



in situ



QTL mapping in Setaria

Positional cloning

We have successfully walked to the *ramosa2*, *ramosa3*, and *tasselseed4*. We are close to *polytypic2*.

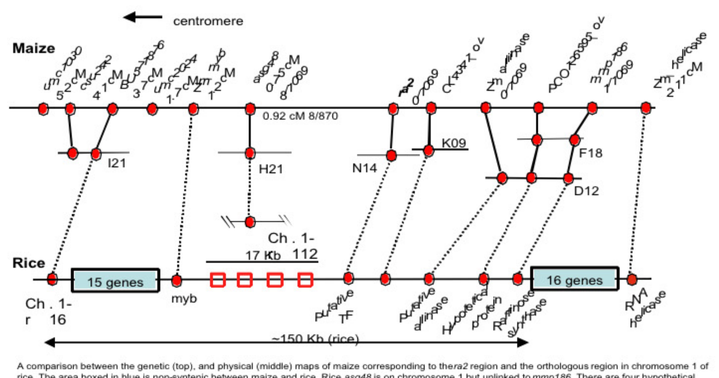
tassel seed4

ra3

ra2

polytypic2 makes extra silks

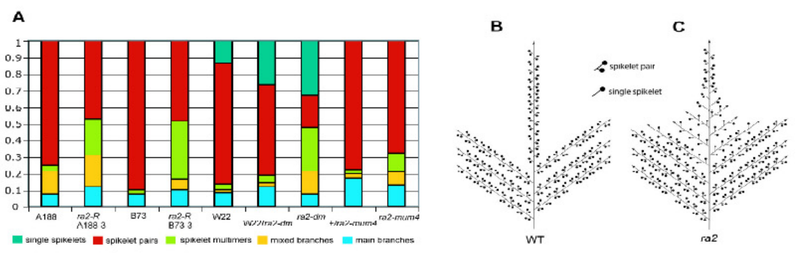
wild-type kernels have single silks



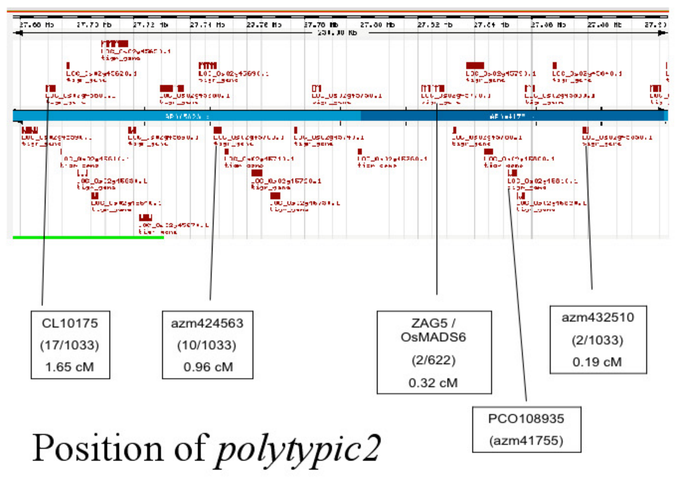
A comparison between the genetic (top), and physical (middle) maps of maize corresponding to the*ra2* region and the orthologous region in chromosome 1 of rice. The area boxed in blue is non-syntenic between maize and rice. Rice *asg48* is on chromosome 1 but unlinked to *mmp186*. There are four hypothetical protein ORFs (empty boxes) between the rice *myb* and *LOB* genes for which there are no significantly similarmai ze sequences. Solid lines represent BAC-marker correspondence by PCR and/or Southerns. Broken lines represent matches obtained by BLAST in various databases. MaizeBACs are epresented by their last three address numbers. Not drawn to proportion but the number and order of rice genes follow their annotation in GenBank.

Walk to *ramosa2*

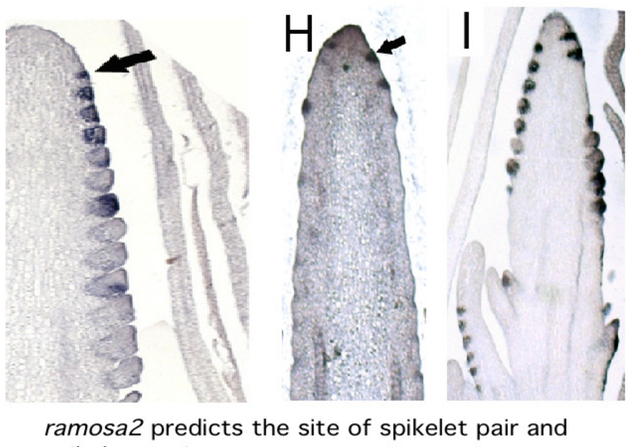
Screening and crossing in the Illinois field



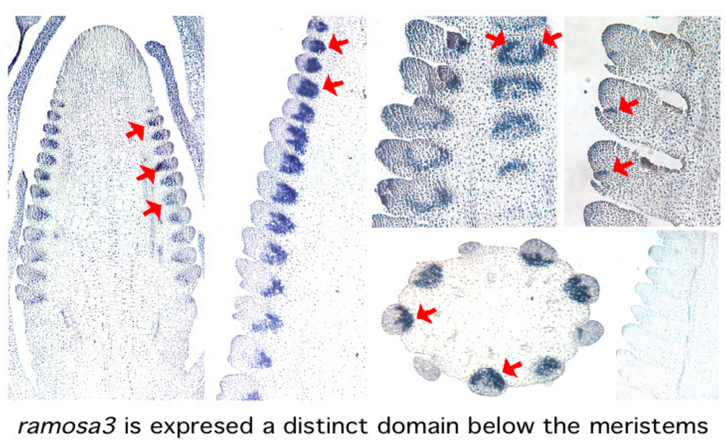
analysis of the *ramosa2* phenotype



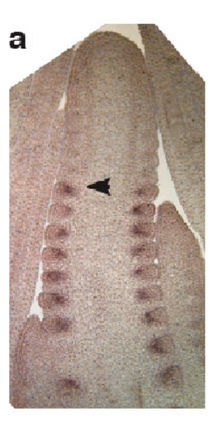
Position of *polytypic2*



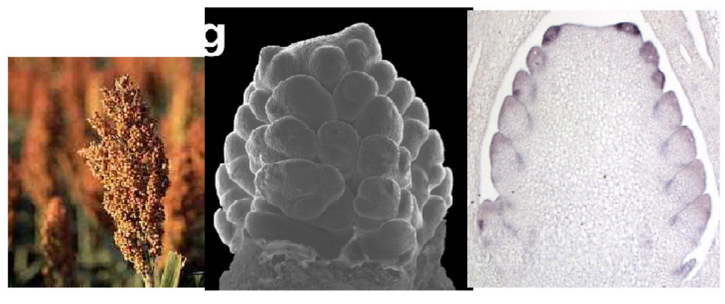
ramosa2 predicts the site of spikelet pair and spikelet meristem



ramosa3 is expresed a distinct domain below the meristems



ramosa1 is expressed at the base of the SPM



ra2 is expressed in sorghum in all branch meristems