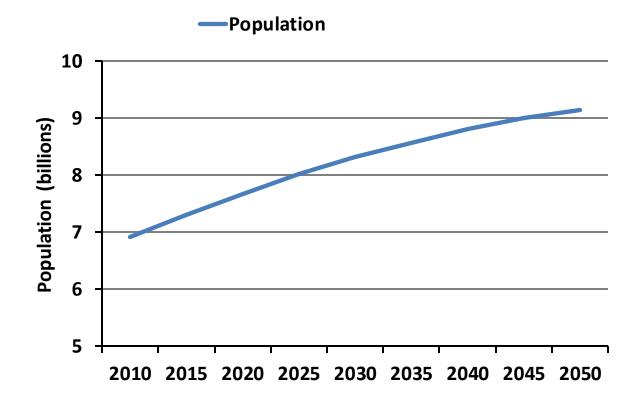
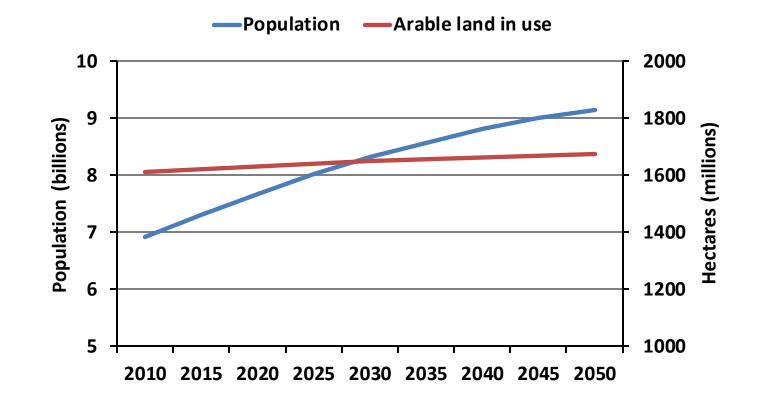
Improving quinoa through the development of genetic and genomic resources

David Jarvis, Jeff Maughan, Rick Jellen

Feeding the world's growing population...



Feeding the world's growing population...



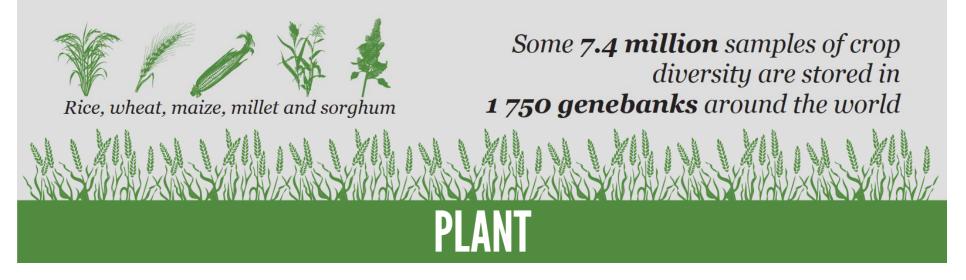
...will require plants that can grow on marginal lands

UN Population Division, FAO

Feeding the world's growing population...

Plants account for over 80% of the human diet

30 000 terrestrial plants are known to be edible
7 000 are cultivated or collected by humans for food
30 crops feed the world
5 cereal crops provide 60% energy intake of the world population



...will require new, highly nutritious crops

Quinoa can help improve global food security



Quinoa can grow on marginal lands



Quinoa is highly nutritious

	Quinoa	Maize	Rice	Wheat
Energy (Kcal/100g)	399	408	372	392
Protein (g/100g)	16.5	10.2	7.6	14.3
Fat (g/100g)	6.3	4.7	2.2	2.3
Total Carbohydrates (g/100g)	69.0	81.1	80.4	78.4

Source: Koziol (1992)

	FAO ^a	Quinoa⁵	Maize ^b	Rice ^b	Wheat ^b
Isoleucine	3.0	4.9	4.0	4.1	4.2
Leucine	6.1	6.6	12.5	8.2	6.8
Lysine	4.8	6.0	2.9	3.8	2.6
Methionine	2.3	5.3	4.0	3.6	3.7
Phenylalanine	4.1	6.9	8.6	10.5	8.2
Threonine	2.5	3.7	3.8	3.8	2.8
Tryptophan	0.66	0.9	0.7	1.1	1.2
Valine	4.0	4.5	5.0	6.1	4.4

^aAmino acid scoring patterns for 3 to 10 year old children, adapted from FAO (2013),

Dietary protein quality evaluation in human nutrition, Report of an FAO Expert Consultation, Rome.

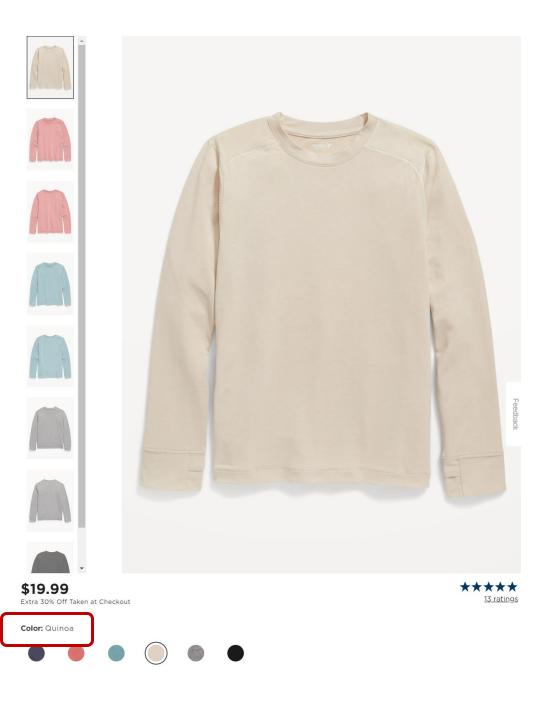
^bKoziol (1992)

^cMethionine + cysteine

^dPhenylalanine + tyrosine

Quinoa is popular

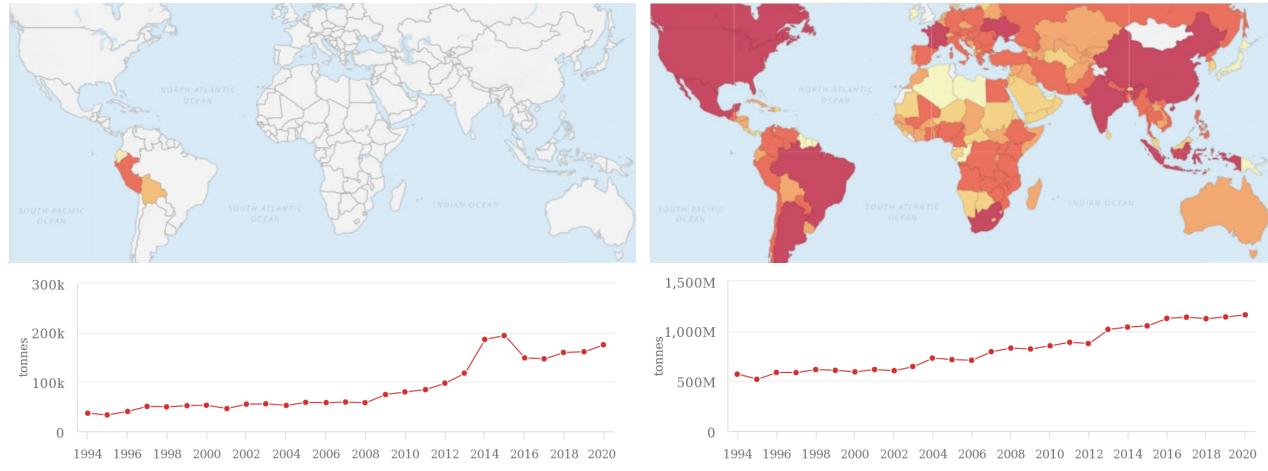
Color: Quinoa



Quinoa production is low

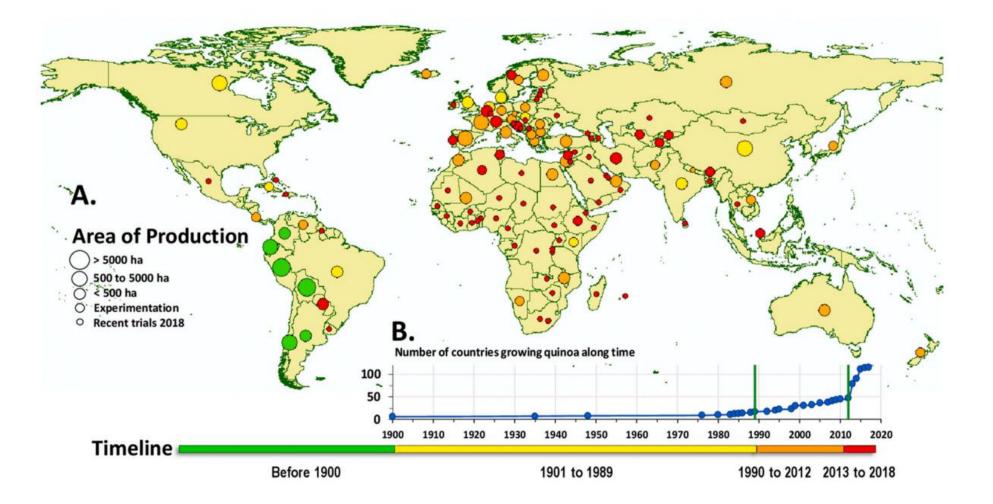
Global quinoa production

Global maize production



http://www.fao.org/faostat/en/

Quinoa production is expanding



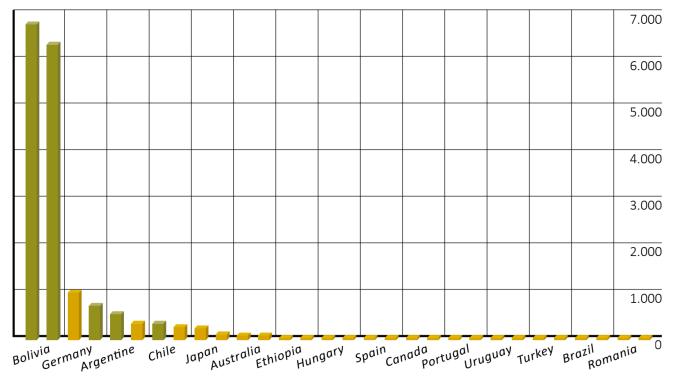
Quinoa isn't well adapted to new environments



Quinoa isn't well adapted to new environments

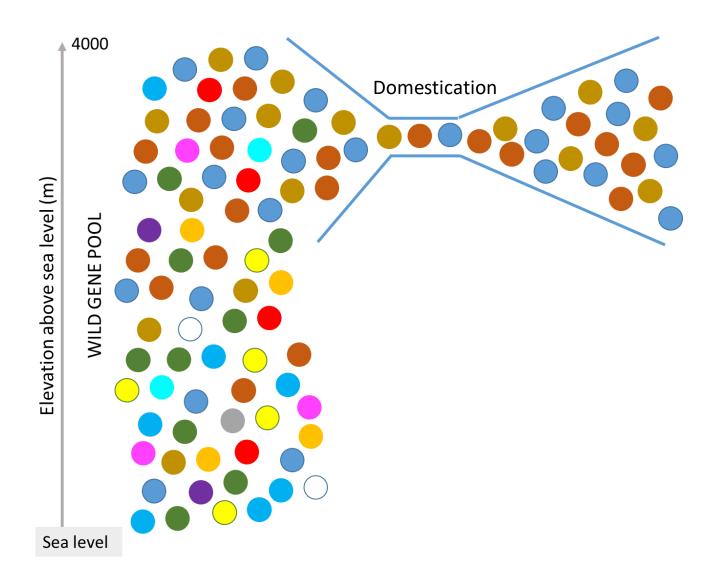


Most quinoa genetic resources are not public



Quinoa accessions in germplasm banks

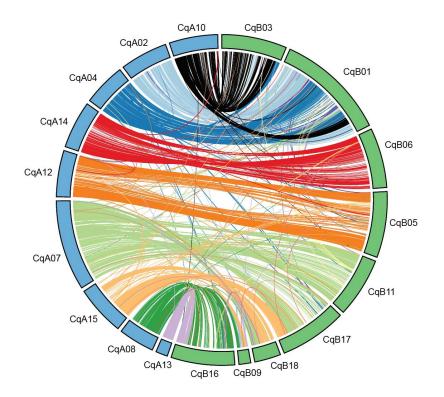
Quinoa has lost genetic diversity



<u>Original domestication of</u> <u>Andean quinoa, ~5000 ybp</u>: Repeated selection for cold tolerance, drought tolerance, saline-soil tolerance at high altitudes

Can we improve quinoa production by increasing genetic diversity?

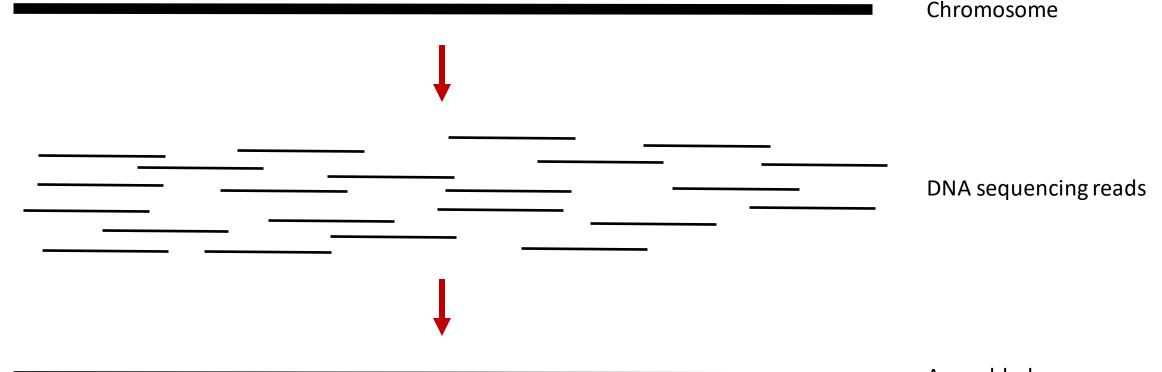
Genomic resources



Genetic resources



Sequence reads are shorter than chromosomes Assembly is the process of putting reads back together





of people staged "die-ins" across

Seek Early Call On '16 Nominee

By NICHOLAS CONFESSORE the country last week to protest the deaths of unarmed black men Dozens of the Republican Par-at the hands of police officers, ty's leading presidential donors young African-American activand fund-raisers have begun pri-ists were in the Oval Office lodgment candidate to carry the par- He of all people - the first prolonged primary would constent States - was in a position to the Hillary Rodham Clinton, the like tify to the sense of injustice that tide of the bring charges and tread very carefully," said ly Democratic candidate. The conversations, described with the police every day, the ac-

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G.O.P. Donors Unrest Over Race Is Testing Obama's Legacy Louis who attended the meeting, had killed unarmed black men, it was not enough. "It hurt that he president has not stood bedidn't seem to want to go out hind the protesters or linked WASHINGTON - As crowds

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Clash Over Torture Report

\$2.50

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Guard Is Said to Falsify Inmate Check Record

By MICHAEL SCHWIRTZ A correction officer who was on duty when a homeless veteran died in an overheated cell at Rikers Island was charged on Monday with lying on jail records, falsely claiming she had checked on the inmate that night, according to prosecutors.

The charges against the



"All the News That's Fit to Print"

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White House and G.O.P. Clash Over Torture Report

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Security Risks Seen as Senate Prepares to Release Details of Bush-Era Tactics

Late Edition







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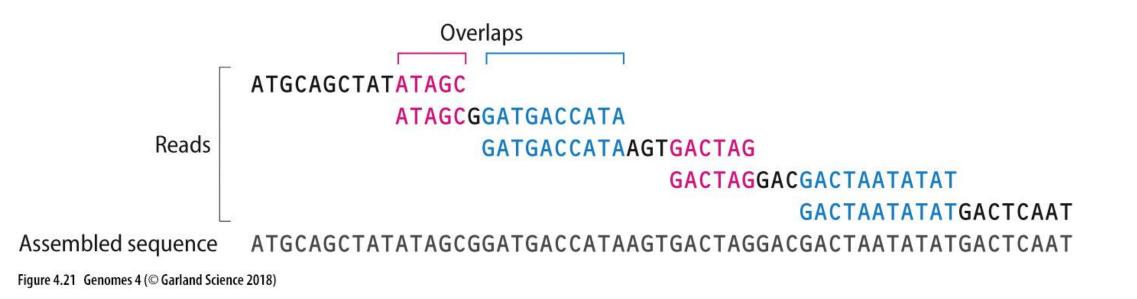
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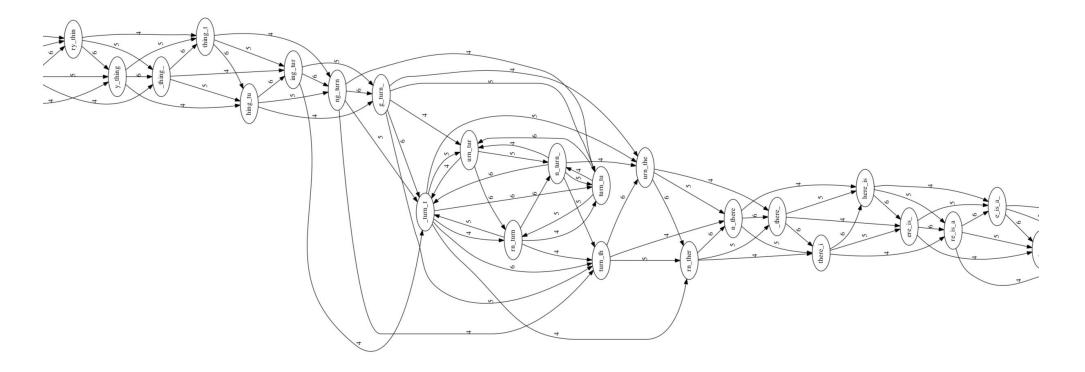
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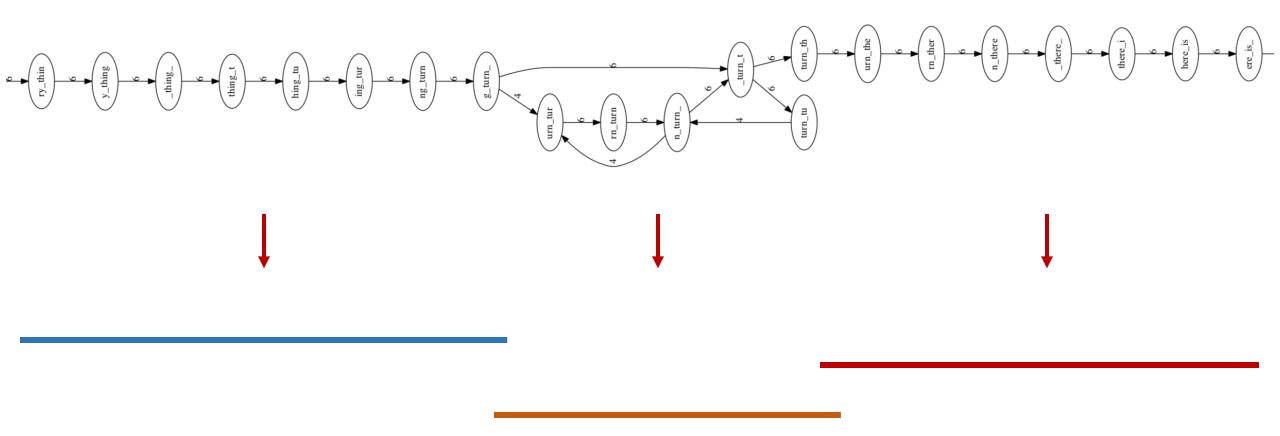
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to_every_thing_turn_turn_turn_there_is_a_season
l = 4, k = 7





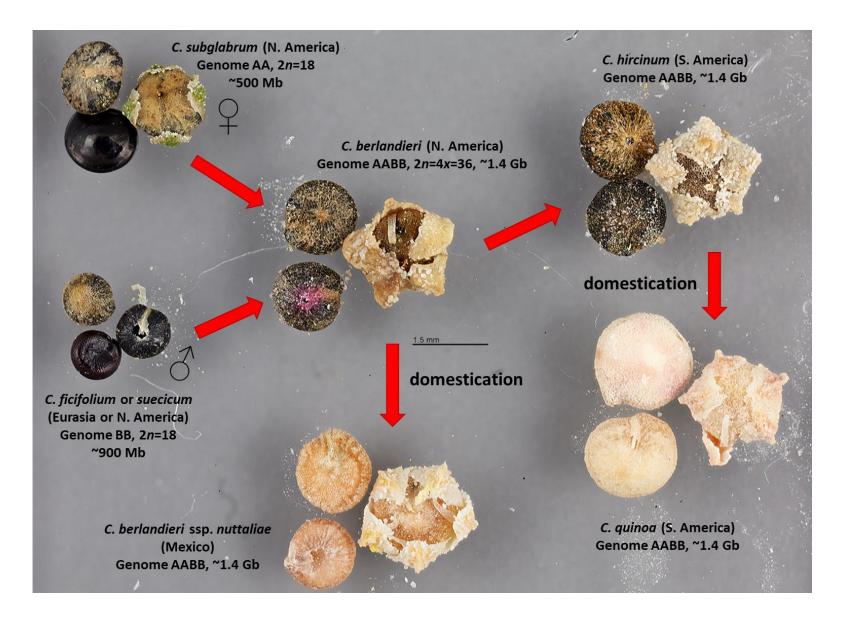
http://www.langmead-lab.org/teaching-materials/

TAGATTACACAGATTACTGA TTGATGGCGTAA CTA TAGATTACACAGATTACTGACTTGATGGCGTAAACTA TAG TTACACAGATTATTGACTTCATGGCGTAA CTA TAGATTACACAGATTACTGACTTGATGGCGTAA CTA TAGATTACACAGATTACTGACTTGATGGCGTAA CTA

Take reads that make up a contig and line them up

Take *consensus*, i.e. majority vote

Quinoa and wild relatives genomic resources



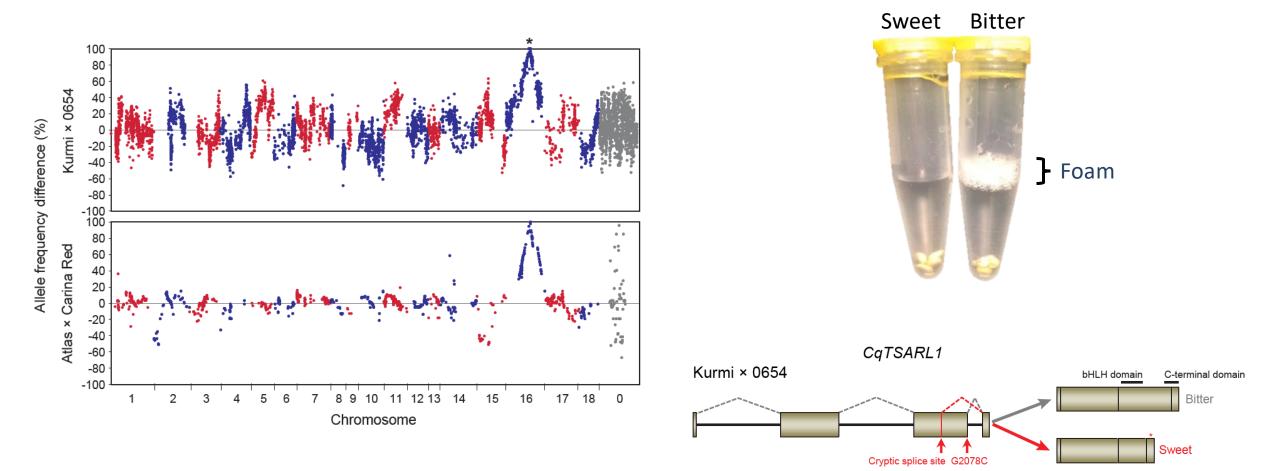
Application of quinoa genomic resources



Application of quinoa genomic resources

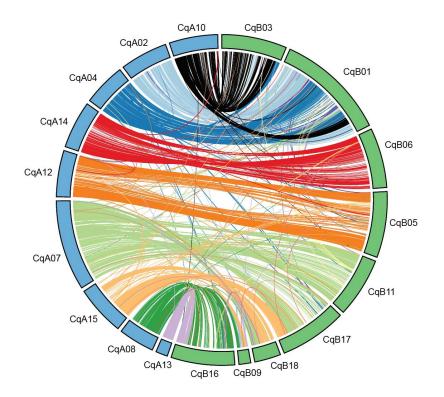


Application of quinoa genomic resources



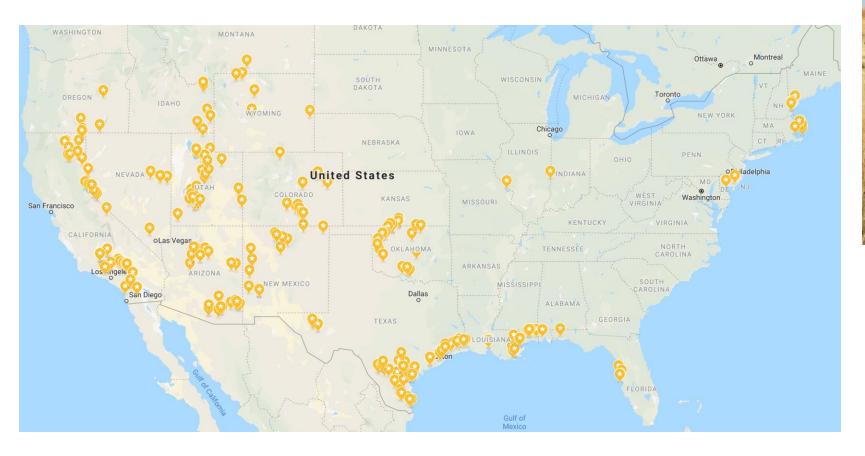
Can we improve quinoa production by increasing genetic diversity?

Genomic resources



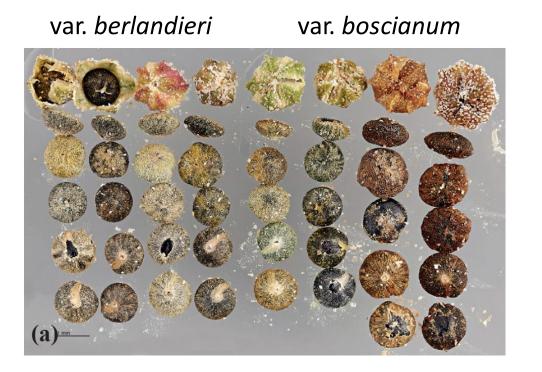
Genetic resources







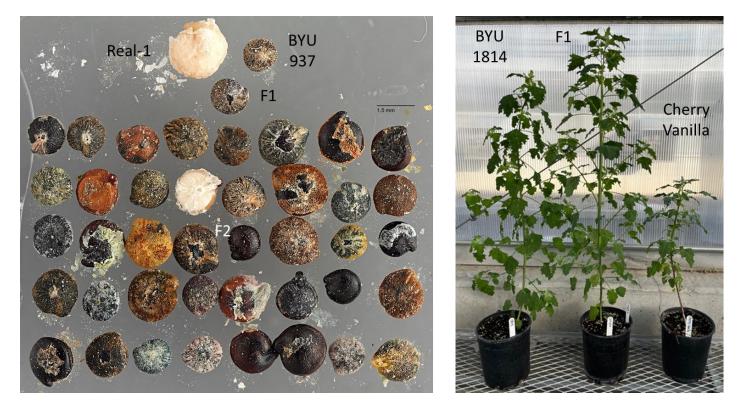




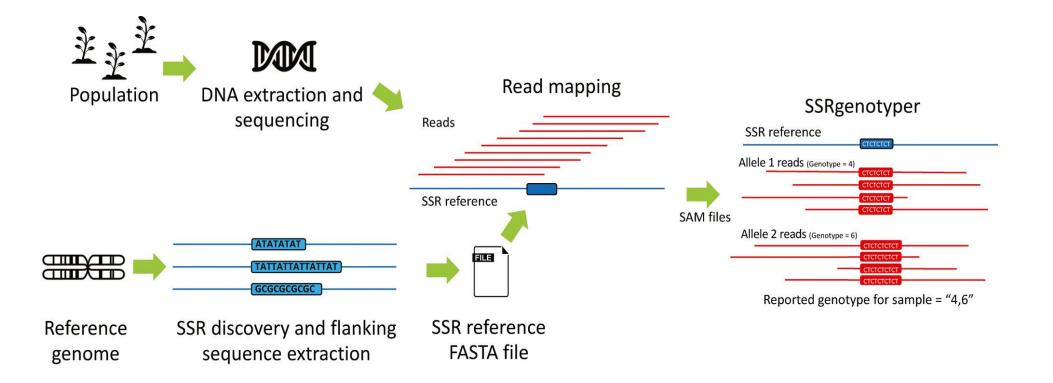
var. *macrocalycium*



Generate interspecific quinoa × *C. berlandieri* crosses

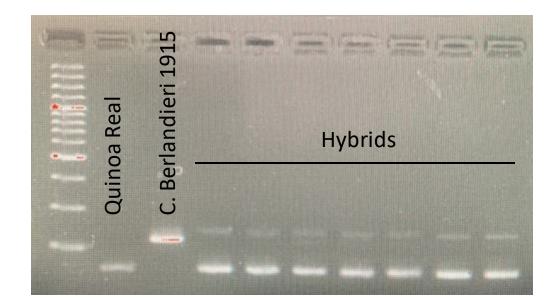


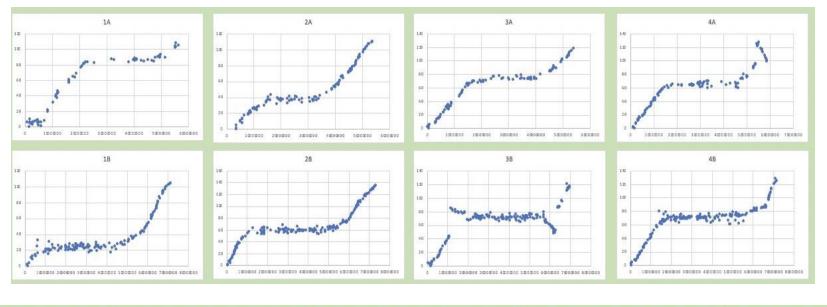
Identification of true hybrids using molecular markers

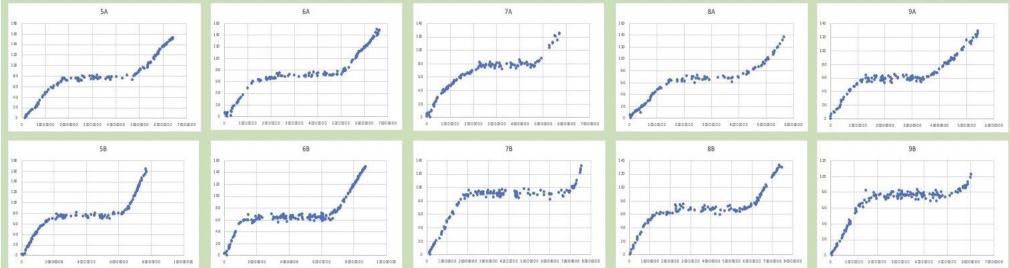


>Scaffold10:55985856-55986082

RefName	Ref	10175_Real	10177_Chir	10188_Cherr	BYU1312	BYU1856	BYU1904	BYU937
Scaffold10:55985856-55986082	5	5,5	0,-4	5,5	4,4	5,5	5,5	3,3



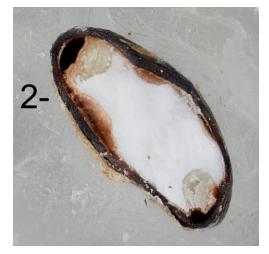


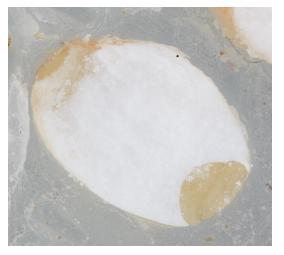


Perform crosses and advance populations

Quinoa	C. berlandieri	<i>C. berlandieri</i> ecotype	<i>C. berlandieri</i> origin
Real-1	BYU 937	var. boscianum	Galveston, TX (Gulf of Mexico Coast)
Surimi	BYU 937	var. boscianum	Galveston, TX
Co407D	BYU 937	var. boscianum	Galveston, TX
654	BYU 937	var. boscianum	Galveston, TX
Real-1	BYU 1814	var. berlandieri	Falfurrias, TX (Interior South Texas)
Cherry Vanilla	BYU 1814	var. berlandieri	Falfurrias, TX
Real-1	BYU 1856	var. macrocalycium	Sandwich Beach, MA (Cape Cod)
Cherry Vanilla	BYU 18102	var. zschackei	Beckham Co., OK (Great Plains)
Real-1	BYU 1915	var. zschackei	Sanpete Co., UT (Great Basin)
Cherry Vanilla	BYU 14118	var. zschackei	Victorville, CA (Mojave Desert)

Phenotype segregating traits to map the underlying genes





Other target traits: seed size, height, abiotic stress tolerance, biotic stress tolerance











Cougar Quinoa: BYU, Washington State University release new quinoa varieties to address global food security, nutrition

June 01, 2023

Cougar, Shisha and Gikungu quinoa thrive in harsh African climates



Acknowledgments

Alejandro Bonifacio, PROINPA (Bolivia) Bozena Kolano, Univ Silesia (Poland) Daniel Bertero, Univ Buenos Aires (Argentina) David Brenner, USDA-ARS, Iowa State Univ (USA) Eulogio de la Cruz Torres, ININ (Mexico) Eve Emshwiller Lab, Univ Wisconsin (USA) Francisco Fuentes, Pontifical Univ Chile (Chile) Helena Storchova Lab, Inst Exp Botany (Czech Rep) Bohumil Mandak Lab, Czech Univ Life Sciences • Karol Krak, Gabrielle Philippi, Tereza Pospisilikova

Jorge Rojas-Beltran, Univ Mayor San Simon (Bolivia)

Kevin Murphy Lab, Washington State Univ (USA) Luz Gomez, Univ Nac Agraria - La Molina (Peru) Mark Tester Lab, KAUST (Saudi Arabia)

• Elodie Rey

Nuri Benet-Pierce, San Diego State Univ (USA) **Patricia Mollinedo, Univ Mayor San Andrés (Bolivia) Ramiro Curti, Univ Nac Salta (Argentina)** Robert van Loo and Theo Borm Labs, Wageningen Univ (Holland) Sergei Mosyakin, M.G. Kholodny Inst Botany (Ukraine) Tom Davis Lab, Univ New Hampshire (USA)

BYU Students/Postdocs: Lauren Young, Kate Jaggi, Heather Warner, Doug Brown, Veronica Cepeda-Cornejo, Ryan Brady, Kristin Durrant, Steven Jellen



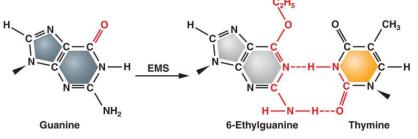
Funding Sources: USDA-NIFA, Holmes Family Foundation, KAUST, Czech Government, McKnight Foundation CCRP, CONACYT, IAEA, USDA-NPGS

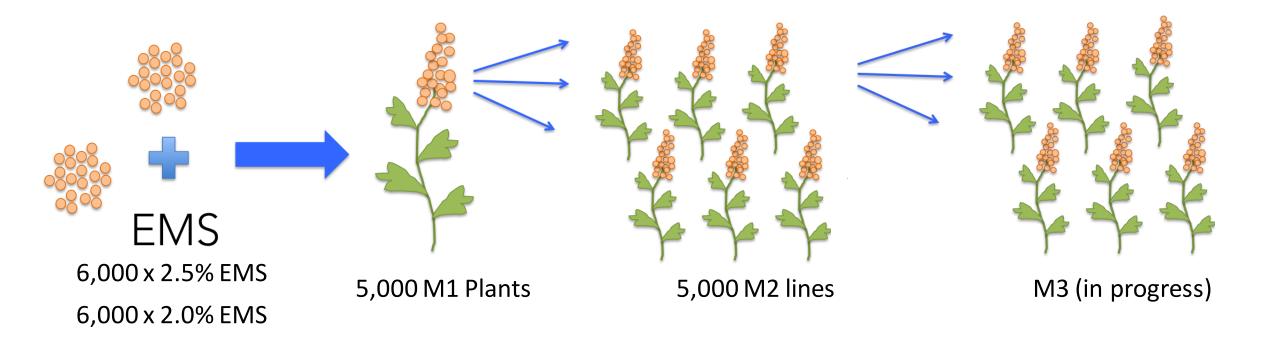


Thank you!

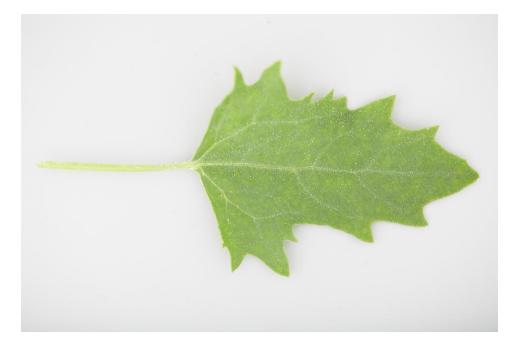


EMS is a chemical mutagen G/C \rightarrow A/T changes





Wild type quinoa (QQ74)





Branching mutants



Meristem mutants



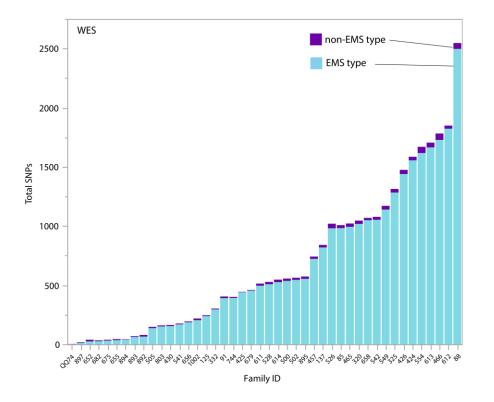
Other mutants

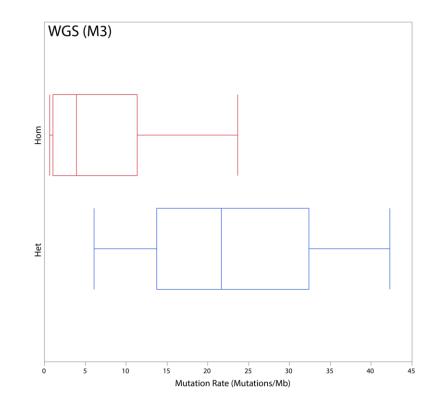




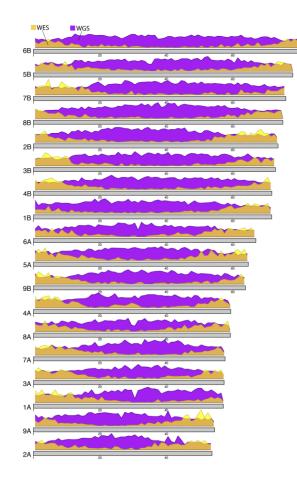


Genome sequencing of ~500 mutants





Genome sequencing of ~500 mutants



VEP mutation type	Number	Modifier	Low	Moderate	High
intergenic_variant	315559	*			
downstream_gene_variant	98535	*			
upstream_gene_variant	94010	*			
intron_variant	48121	*			
missense_variant	31105			*	
synonymous_variant	12781		*		
3_prime_UTR_variant	8657	*			
5_prime_UTR_variant	5175	*			
stop_gained	1946				*
splice_region_variant	1355		*		
missense_variant,splice_region_variant	502			*	
splice_acceptor_variant	319				*
splice_donor_variant	288				*
coding_sequence_variant	80	*			
start_lost	52				*
stop_gained,splice_region_variant	45				*
stop_retained_variant	42		*		
frameshift_variant	21				*
stop_lost	4				*
start_retained_variant	3		*		
start_lost,splice_region_variant	1				*

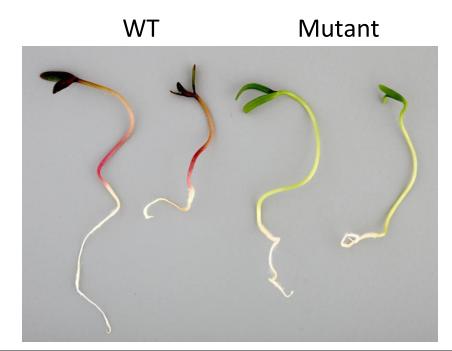


Genome sequencing of ~500 mutants

#GeneID U	ploaded_variation	Location	Allele	Feature_type c	DNA_position	CDS_pos	ition	Protein_position Amino_acids Existing_variation Gene_description
CQ000002	EMS2427 Contig	92_pilon:29015	Т	missense_variant	394	132	V/I	Gta/Ata Note=Similar to KCS11: 3-ketoacyl-CoA synthase 11 (Arabidopsis thaliana OX%3D3702);
CQ000004	EMS3288 Contig	92_pilon:43678	С	missense_variant	695	232	N/S	aAc/aGc Note=Protein of unknown function;
CQ000004	EMS3288 Contig	92_pilon:43648	А	missense_variant	725	242	P/L	cCg/cTg Note=Protein of unknown function;
CQ000008	EMS2427 Contig	92_pilon:123790	Т	5_prime_UTR_variar	nt -			- Note=Similar to BRK1: Protein BRICK 1 (Arabidopsis thaliana OX%3D3702);
CQ000173	EMS3118 Contig	92_pilon:2077208	Т	missense_variant	391	131	G/R	Ggg/Agg Note=Similar to At1g65750: Putative ribonuclease H protein At1g65750 (Arabidopsis thaliana 0X%3D3702);
CQ000175	EMS2427 Contig	92_pilon:2148447	Т	synonymous_variant	t 534	178	E	gaG/gaA Note=Similar to RE2: Retrovirus-related Pol polyprotein from transposon RE2 (Arabidopsis thaliana OX%3D3702);
CQ000178	EMS2427 Contig	92_pilon:2208493	Т	missense_variant	649	217	L/F	Ctt/Ttt Note=Similar to SUC3: Sucrose transport protein SUC3 (Arabidopsis thaliana OX%3D3702);
CQ000197	EMS1849 Contig	92_pilon:2420986	Т	missense_variant	226	76	D/N	Gat/Aat Note=Similar to WRKY72: Probable WRKY transcription factor 72 (Arabidopsis thaliana 0X%3D3702);
CQ000197	EMS1445 Contig	92_pilon:2420897	G	synonymous_variant	t 315	105	N	aaT/aaC Note=Similar to WRKY72: Probable WRKY transcription factor 72 (Arabidopsis thaliana 0X%3D3702);
CQ000212	EMS3287 Contig	92_pilon:2616807	Т	3_prime_UTR_variar	nt -			- Note=Similar to RAD52-2: DNA repair RAD52-like protein 2%2C chloroplastic (Arabidopsis thaliana 0X%3D3702);
CQ000219	EMS2427 Contig	92_pilon:2652959	А	3_prime_UTR_variar	nt -			- Note=Similar to At1g28120: Ubiquitin thioesterase otubain-like (Arabidopsis thaliana OX%3D3702);
CQ000227	EMS3118 Contig	92_pilon:2736384	Т	missense_variant	99	33	M/I	atG/atA Note=Similar to CRN: Inactive leucine-rich repeat receptor-like protein kinase CORYNE (Arabidopsis thaliana 0X%3D3702);
CQ000232	EMS3299 Contig	92_pilon:2765081	Т	missense_variant	257	86	S/F	tCt/tTt Note=Similar to NXD1: Protein NEOXANTHIN-DEFICIENT 1 (Solanum lycopersicum 0X%3D4081);
CQ000233	EMS2427 Contig	92_pilon:2766773	Т	3_prime_UTR_variar	nt -			- Note=Similar to SCPL45: Serine carboxypeptidase-like 45 (Arabidopsis thaliana 0X%3D3702);
CQ000234	EMS2077 Contig	92_pilon:2781532	3TTT	5_prime_UTR_variar	nt -			- Note=Similar to SCD2: Coiled-coil domain-containing protein SCD2 (Arabidopsis thaliana 0X%3D3702);
CQ000236	EMS3118 Contig	92_pilon:2793407	Т	missense_variant	88	30	G/R	Gga/Aga Note=Protein of unknown function;
CQ000240	EMS2077 Contig	92_pilon:2830582	Т	missense_variant	610	204	G/R	Gga/Aga Note=Similar to LAX2: Protein LAX PANICLE 2 (Oryza sativa subsp. japonica OX%3D39947);
CQ000240	EMS409 Contig	92_pilon:2830721	Т	stop_gained 47	71 157	W/*	tgG/tg	A Note=Similar to LAX2: Protein LAX PANICLE 2 (Oryza sativa subsp. japonica OX%3D39947);

Genome sequencing of ~500 mutants

1. Find a mutant phenotype, work back to causative gene



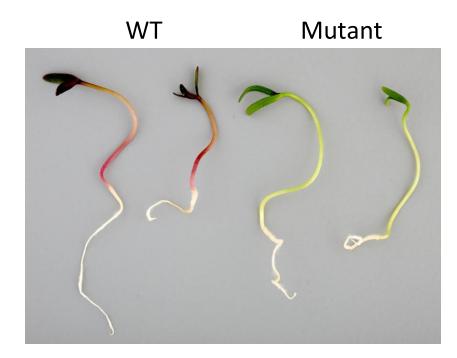
31,564 mutations in this mutant family 9,331 within genes

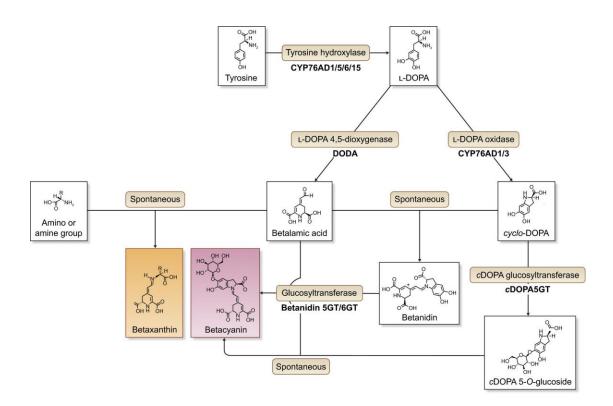
CQ000002	EMS2427 Contig92_pilon:29015 T	missense_variant	394	132	V/I	Gta/Ata Note=Similar to KCS11: 3-ketoacyl-CoA synthase 11 (Arabidopsis thaliana OX%3D3702);
CQ000008	EMS2427 Contig92_pilon:123790 T	5_prime_UTR_variant				- Note=Similar to BRK1: Protein BRICK 1 (Arabidopsis thaliana 0X%3D3702);
CQ000014	EMS2427 Contig92_pilon:183134 T	missense_variant	175	59	L/F	Ctt/Ttt Note=Similar to GRDP1: Glycine-rich domain-containing protein 1 (Arabidopsis thaliana 0X%3D3702);
CQ000071	EMS2427 Contig92_pilon:828561 T	missense_variant	197	66	G/E	gGg/gAg Note=Protein of unknown function;
CQ000076	EMS2427 Contig92_pilon:864128 T	missense_variant	838	280	A/T	Gcg/Acg Note=Similar to PUMP3: Mitochondrial uncoupling protein 3 (Arabidopsis thaliana 0X%3D3702);
CQ000082	EMS2427 Contig92_pilon:941695 T	5_prime_UTR_variant				- Note=Similar to NAP2: NAC domain-containing protein 2 (Solanum lycopersicum 0X%3D4081);
CQ000123	EMS2427 Contig92_pilon:1337673 T	splice_donor_variant				- Note=Similar to APY6: Probable apyrase 6 (Arabidopsis thaliana 0X%3D3702);
CQ000175	EMS2427 Contig92_pilon:2148447 T	synonymous_variant	534	178	E	gaG/gaA Note=Similar to RE2: Retrovirus-related Pol polyprotein from transposon RE2 (Arabidopsis thaliana 0X%3D3702);
CQ000178	EMS2427 Contig92_pilon:2208493 T	missense_variant	649	217	L/F	Ctt/Ttt Note=Similar to SUC3: Sucrose transport protein SUC3 (Arabidopsis thaliana OX%3D3702);
CQ000219	EMS2427 Contig92_pilon:2652959 A	3_prime_UTR_variant				- Note=Similar to At1g28120: Ubiquitin thioesterase otubain-like (Arabidopsis thaliana 0X%3D3702);
CQ000233	EMS2427 Contig92_pilon:2766773 T	3_prime_UTR_variant	-	-	-	 Note=Similar to SCPL45: Serine carboxypeptidase-like 45 (Arabidopsis thaliana 0X%3D3702);



Genome sequencing of ~500 mutants

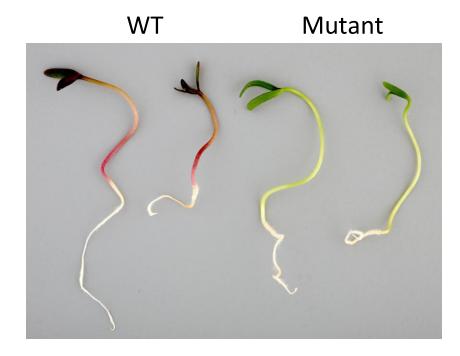
1. Find a mutant phenotype, work back to causative gene

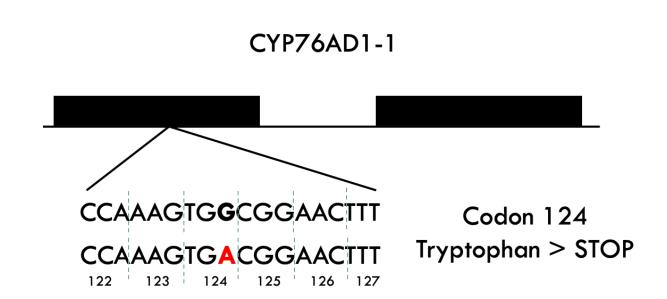




Genome sequencing of ~500 mutants

1. Find a mutant phenotype, work back to causative gene





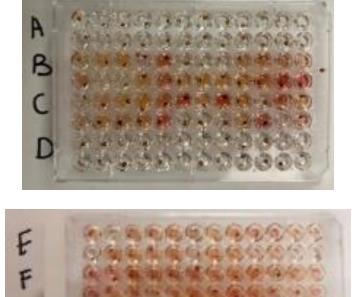
Genome sequencing of ~500 mutants

1. Find a mutant phenotype, work back to causative gene

Saponins: develop single-seed detection assay

Screen 24 seeds of each pooled M3 family to identify saponin-free mutants





6

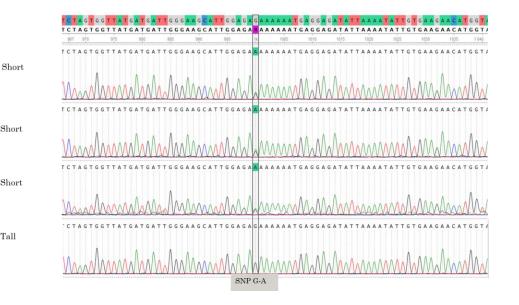
Genome sequencing of ~500 mutants

- 1. Find a mutant phenotype, work back to causative gene
- 2. Find a mutant gene, work forward to mutant phenotype

Plant height: find mutations in GA signaling and biosynthesis

Gene	EMS Family	Variant
	3067	Missense
	549	Missense
GAI1		Missense &
	88	Upstream
	541	Stop Gained
GID1-C		Missense &
GID1-C	1679	Downstream
		Missense &
LE	500	Downstream
(GA3OX)		Missense &
	2427	Downstream
CARRON R		Missense &
GA20OX-2	170	Upstream







Genome sequencing of ~500 mutants

- 1. Find a mutant phenotype, work back to causative gene
- 2. Find a mutant gene, work forward to mutant phenotype

Projects for new students in my lab (PWS 494R)

#GeneID	Uploaded_variation	Location	Allele	Feature_type	cDNA_position	CDS_pos	ition	Protein_position Amino_acids Existing_variation Gene_description
CQ000002	EMS2427 Contig	2_pilon:29015	Т	missense_variant	394	132	V/I	Gta/Ata Note=Similar to KCS11: 3-ketoacyl-CoA synthase 11 (Arabidopsis thaliana 0X%3D3702);
CQ000004	EMS3288 Contig	2_pilon:43678	с	missense_variant	695	232	N/S	aAc/aGc Note=Protein of unknown function;
CQ000004	EMS3288 Contig	2_pilon:43648	А	missense_variant	725	242	P/L	cCg/cTg Note=Protein of unknown function;
CQ000008	EMS2427 Contig	2_pilon:123790	Т	5_prime_UTR_vari	ant -			- Note=Similar to BRK1: Protein BRICK 1 (Arabidopsis thaliana OX%3D3702);
CQ000173	EMS3118 Contig	2_pilon:2077208	т	missense_variant	391	131	G/R	Ggg/Agg Note=Similar to At1g65750: Putative ribonuclease H protein At1g65750 (Arabidopsis thaliana OX%3D3702);
CQ000175	EMS2427 Contig	2_pilon:2148447	Т	synonymous_varia	nt 534	178	E	gaG/gaA Note=Similar to RE2: Retrovirus-related Pol polyprotein from transposon RE2 (Arabidopsis thaliana OX%3D3702);
CQ000178	EMS2427 Contig	2_pilon:2208493	Т	missense_variant	649	217	L/F	Ctt/Ttt Note=Similar to SUC3: Sucrose transport protein SUC3 (Arabidopsis thaliana 0X%3D3702);
CQ000197	EMS1849 Contig	2_pilon:2420986	Т	missense_variant	226	76	D/N	Gat/Aat Note=Similar to WRKY72: Probable WRKY transcription factor 72 (Arabidopsis thaliana 0X%3D3702);
CQ000197	EMS1445 Contig	2_pilon:2420897	G	synonymous_varia	nt 315	105	N	aaT/aaC Note=Similar to WRKY72: Probable WRKY transcription factor 72 (Arabidopsis thaliana 0X%3D3702);
CQ000212	EMS3287 Contig	2_pilon:2616807	т	3_prime_UTR_vari	.ant -			- Note=Similar to RAD52-2: DNA repair RAD52-like protein 2%2C chloroplastic (Arabidopsis thaliana 0X%3D3702);
CQ000219	EMS2427 Contig	2_pilon:2652959	А	3_prime_UTR_vari	ant -			- Note=Similar to At1g28120: Ubiquitin thioesterase otubain-like (Arabidopsis thaliana 0X%3D3702);
CQ000227	EMS3118 Contig	2_pilon:2736384	Т	missense_variant	99	33	M/I	atG/atA Note=Similar to CRN: Inactive leucine-rich repeat receptor-like protein kinase CORYNE (Arabidopsis thaliana OX%3D3702);
CQ000232	EMS3299 Contig	2_pilon:2765081	т	missense_variant	257	86	S/F	tCt/tTt Note=Similar to NXD1: Protein NEOXANTHIN-DEFICIENT 1 (Solanum lycopersicum 0X%3D4081);
CQ000233	EMS2427 Contig	2_pilon:2766773	Т	3_prime_UTR_vari	ant -			- Note=Similar to SCPL45: Serine carboxypeptidase-like 45 (Arabidopsis thaliana OX%3D3702);
CQ000234	EMS2077 Contig	2_pilon:2781532	3TTT	5_prime_UTR_vari	ant -			- Note=Similar to SCD2: Coiled-coil domain-containing protein SCD2 (Arabidopsis thaliana OX%3D3702);
CQ000236	EMS3118 Contig	2_pilon:2793407	т	missense_variant	88	30	G/R	Gga/Aga Note=Protein of unknown function;
CQ000240		2_pilon:2830582		missense_variant	610	204	G/R	Gga/Aga Note=Similar to LAX2: Protein LAX PANICLE 2 (Oryza sativa subsp. japonica OX%3D39947);
CQ000240	EMS409 Contig	2_pilon:2830721	Т	stop_gained	471 157	W/*	tgG/tg	A Note=Similar to LAX2: Protein LAX PANICLE 2 (Oryza sativa subsp. japonica OX%3D39947);

Select mutation of interest \rightarrow Research the gene \rightarrow Design experiment

Fundamental lab skills: Basic command line, greenhouse, wet lab

Fundamental research skills: Literature review, hypothesis, experiment, data analysis, troubleshooting

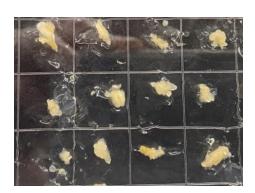
Inducing targeted variation in quinoa

 \rightarrow

Transformation of quinoa

Generate undifferentiated callus tissue \rightarrow transform with exogenous DNA \rightarrow regeneration/embryogenesis







 \rightarrow



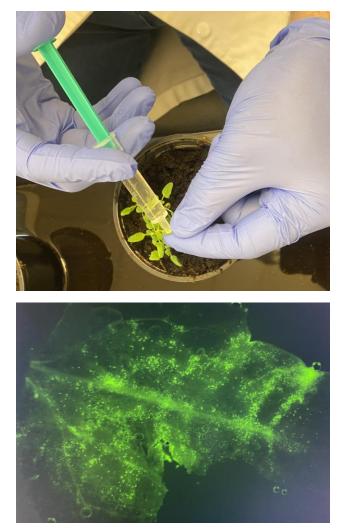


Inducing targeted variation in quinoa

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