

by Luigi Guarino 5 years ago

CWR Genomics Meeting

Asilomar Conference Grounds, 11-13 December 201

It's germplasm evaluation, Jim, but not as we know it

Next generation sequencing (NGS) holds the promise for a more efficient approach to germplasm evaluation whereby a carefully selected sub...



And finally something for the weekend...



Luigi Guarino

AgroBioDiverse @AgroBioDiverse

@foodimprover Many thanks indeed to @GenomeBC @GenomePrairie for supporting the meeting of CWR genomics experts #cwrgenomics



5 YEARS AGO



PAG Meeting

PAG Meeting @PAGmeeting

#PAGXXI Attendee Newsletter #6 - Plenary Speakers Spotlight: Monday conta.cc/Zgif5x5x



5 YEARS AGO

Plant & Animal Genome Conference

International Plant and Animal Genome Conference Future Dates. Plant & Animal Genome XXI - January 12-16, 2013 - San Diego; Plant &...



Luigi Guarino

AgroBioDiverse @AgroBioDiverse

See you all at PAG? #CWRGenomics



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Luigi Guarino

AgroBioDiverse @AgroBioDiverse

McCouch wrapping up and thanking everyone #CWRGenomics



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AgroBioDiverse

Rieseberg: plan to develop white paper on the use of genomics and CWR use in breeding. Repository for CWR genomics data! [#CWRGenomics](#)

5 YEARS AGO



Luigi Guarino

AgroBioDiverse

Minor crops could be empowered by genomics. In some cases they are closer to the wild anyway. [#CWRGenomics](#)

5 YEARS AGO



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AgroBioDiverse

[@SandyKnapp](#) Need to keep track of metadata on experiments. [#CWRGenomics](#)

5 YEARS AGO



Luigi Guarino

AgroBioDiverse

Whatever its called, how do you do it? And who does it? Need best practices. And biggest challenge is phenotyping. [#CWRGenomics](#)

5 YEARS AGO



Benjamin Edge

edgeben

[@AgroBioDiverse](#) don't see problem w/ "pre-breeding", but how about population development? CIMMYT has done this well for years. [#CWRGenomics](#)

5 YEARS AGO



Luigi Guarino

AgroBioDiverse

Back to the prebreeding discussion. Germplasm enhancement? Even worse. Base broadening? Too narrow. [#CWRGenomics](#)

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Buckler: We now have the technology to intelligently work around linkage drag. [#CWRGenomics](#)

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**Luigi Guarino**

AgroBioDiverse

Nelson: dont like the word pre-breeding. Yeah but what's the alternative? Subject kinda dropped, alas. [#CWRGenomics](#)



5 YEARS AGO

**Karen James**

kejames@kejames

Some good tweets coming from the crop wild relative (CRW) genomics meeting – [#CWRGenomics](#) – including pearls of wisdom from [@SandyKnapp](#).



5 YEARS AGO

**Luigi Guarino**

AgroBioDiverse

[@SandyKnapp](#) Dont focus on climate change only, many policy makers dont believe in it! [#CWRGenomics](#)



5 YEARS AGO

**Luigi Guarino**

AgroBioDiverse

Ehlers: Our crops missed out on a bunch of variation that has survived climate change [#CWRGenomics](#)



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**Luigi Guarino**

AgroBioDiverse

Buckler: We have so much to learn from diversity, & our capacity to understand it has improved 23 million fold. [#CWRGenomics](#) You heard him!



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**Toby Bruce**

Toby_Bruce

[@AgroBioDiverse](#) [#CWRGenomics](#) sounds like interesting meeting. Thanx for tweets. Have any strategies to overcome linkage drag been discussed?



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**Luigi Guarino**

AgroBioDiverse

McCouch: We want to emphasize the use of natural variation, using all available tools
[#CWRGenomics](#)

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AgroBioDiverse

Burke: goal is not to mine CWR, goal is food security [#CWRGenomics](#)

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**Luigi Guarino**

AgroBioDiverse

[@SandyKnapp](#) "Sometimes easier to reinvent things in a halfassed way rather than use what's already there." I guess thats bad. [#CWRGenomics](#)

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**McCouch RiceLab**

The McCouch Lab investigates natural variation in the genus *Oryza*, focusing on how it evolved, how it is distributed in both domesticated and wild *Oryza* species, how it conditions complex phenotypes and how it can be efficiently utilized in rice improvement.

CORNELL

**Luigi Guarino**

AgroBioDiverse

McCouch: genomic data has catalytic role, and also links crops (good for NUS?) [#CWRGenomics](#)

5 YEARS AGO

High-throughput phenotyping and genomic ... [J Integr Plant Biol. 2012] - PubMed - NCBI

PubMed comprises more than 22 million citations for biomedical literature from MEDLINE, life science journals, and online books. Citations may include links to full-text content from PubMed Central and publisher web sites.

NIH

**Luigi Guarino**

AgroBioDiverse


Ehlers: high throughput phenotyping of CWR? Couldnt catch if he was for it or agin it :)
[#CWRGenomics](#)

5 YEARS AGO

**CGIAR GCP Programme**

GCP Programme


RT @soyshadow: Follow #CWRGenomics for latest and interesting updates on the future of plant breeding and the making of our crops.

 5 YEARS AGO

**Luigi Guarino**

AgroBioDiverse

Buckler: Why now though? Fact is that we have never had the computational etc resources we have now to fully explore genome. #CWRGenomics

 5 YEARS AGO

**UCR Newsroom: A Genetic Map for Cowpea**


October 13, 2009: Map also facilitates genetic improvement of several other legumes

 UCR

**Luigi Guarino**

AgroBioDiverse


Ehlers: history of underfunding of CWR use, which nevertheless led to some significant advances #CWRGenomics

 5 YEARS AGO

**Luigi Guarino**

AgroBioDiverse

Rieseberg: challenges: funding and institutional home for prebreeding, germplasm sharing, databases #CWRGenomics

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**Luigi Guarino**

AgroBioDiverse

Rieseberg: plan to develop white paper on the use of genomics and CWR use in breeding. Repository for CWR genomics data! #CWRGenomics

 5 YEARS AGO

**Ruairidh Sackville Hamilton Interview - Part 5**

Ruairidh talks about the creation of IRRI and the impact of their early work.

[YOUTUBE](#)



Luigi Guarino
AgroBioDiverse

S Hamilton IRRI: data collected by genebank users should stay attached to their sample, but trace back to original sample [#CWRGenomics](#)

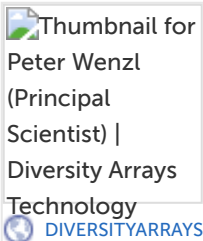
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AgroBioDiverse

Wenzl: looking at allele frequencies within maize landrace accessions too [#CWRGenomics](#)

5 YEARS AGO



Peter Wenzl (Principal Scientist) | Diversity Arrays Technology

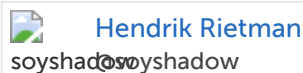
I'm a molecular biologist with experience in abiotic-stress physiology, high-throughput genotyping and gene cloning. My main focus during the last few years has been to advance DArT from the proof-of-concept stage to a mature technology.



Luigi Guarino
AgroBioDiverse

Wenzl: genotyping service being set up in Mexico will survive the project [#CWRGenomics](#)

5 YEARS AGO



Hendrik Rietman
soyshadow

Follow [#CWRGenomics](#) for latest and interesting updates on the future of plant breeding and the making of our crops.

5 YEARS AGO

CIMMYT's Blog " Seeds of Discovery (Seed)

National Service Seed Inspection and Certification (SNICS) and National Plant Genetic Resources for Food and Agriculture (SINAREFI) organized the first Agro-biodiversity and Agroproducts Fair in Xochitla Ecological Park, Tepozotlan, Mexico, during 7-8 September 2012, to promote conservation and sustainable use of genetic resources of crop species which originated in Mexico (maize, squash, bean, avocado, tejacote, poinsettia, and vanilla).


[CIMMYT](#)




Luigi Guarino
AgroBioDiverse


Wenzl of Seeds of Discovery: using GBS to characterize whole maize and wheat CIMMYT collections [#CWRGenomics](#)

5 YEARS AGO


 **Greg Baute**
gregbaute@gregbaute


#Sequence #data is always linked to genbank IDs. They are almost never linked to a gene bank IDs. #CWRGenomics

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 **Luigi Guarino**
AgroBio@AgroBioDiverse


Richards: has developed a schema for legacy AFLP data in literature etc to link back to genebank accessions #CWRGenomics

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 **Luigi Guarino**
AgroBio@AgroBioDiverse


@SandyKnapp The new digital world presents scary challenges we all share, need to collaborate more #CWRGenomics

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 **Luigi Guarino**
AgroBio@AgroBioDiverse


Buckler: point about skill set of curators also applies to breeders; cant just dump the data on them! #CWRGenomics

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 **Luigi Guarino**
AgroBio@AgroBioDiverse


Genebank curators dont want/need raw data, they want answers o specific curatorial and other questions #CWRGenomics

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 **Chris Richards**
Chris Richards

Dr. Chris Richards Molecular Geneticist USDA-ARS Plant Germplasm Preservation National Center for Genetic Resources Preservation (formerly National Seed Storage Laboratory) crichard@lamar.colostate.edu

 COLOSTATE

 **Luigi Guarino**
AgroBio@AgroBioDiverse

Richards: how to encourage feedback loop of genomic info so that genebanks can make use of it? #CWRGenomics

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**Luigi Guarino**

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Richards: genomics data not getting back to genebank curators in usable form [#CWRGenomics](#)



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**Luigi Guarino**

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Richards: genomics will help you resolve important questions, but skill set needed to use these data uncommon in genebanks [#CWRGenomics](#)



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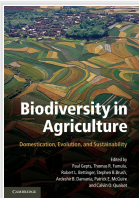
**Luigi Guarino**

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Chris Richards of Ft Collins: if genebanks are libraries, the card catalogue is very limited [#CWRGenomics](#)



5 YEARS AGO



Crop Evolution, Domestication, and Biodiversity - Paul Gepts Lab at UC Davis

Since the beginning of agriculture, some 10,000 years ago, humans have molded the diversity of crop plants around them to suit their diverse needs for food and beverage, feed, clothing and other numerous uses. Starting with the process of domestication, crop biodiversity results from the fascinating interactions among humans, plants, and their

environment.



UCDAVIS

**Luigi Guarino**

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Gepts: pure lining accessions means you could lose out on some genotypes, as well as increasing your genebank management costs [#CWRGenomics](#)



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Perennial Glycine: A new source of genetic diversity for soybean improvement " Agronomy Day 2010, Crop Sciences,U of I

Justin Ma, Graduate Research Fellow, Department of Crop Sciences, 217-333-3155, ma16@illinois.edu Soybean by *G. tomentella* hybrid plant growing in culture in the laboratory Perennial Glycine species are very distant relatives of soybean. Unlike soybean that is native to China, all 26 perennial Glycine species are native to Australia and have been genetically isolated from soybean for several million years.



ILLINOIS



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Nelson: we pure line every visually distinct plant in a soya accession at USDA; not doing this is a false economy #CWRGenomics

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Have to change culture of genebank curators to make them easier to use. One thing is to keep outcrossers as homozygous lines. #CWRGenomics

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#CWRGenomics Valls: Can now truly use best genebank material in best way.

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#CWRGenomics Valls: genomics just the latest step in genebank management, maybe the ultimate step?

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Roundtable on genebanks and genomics. Does all these data mean a change in role for genebanks? #CWRGenomics

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Qui: soya core being used for GWAS; there are 14 soya breeding programs in China! #CWRGenomics

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Qui: soya core and minicore collections based on morphology, SSR and SNPs #CWRGenomics

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CAAS Genebank, Beijing



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**Luigi Guarino**

AgroBioDiverse

Qiu Li Juan of CAAS genebank: Lots of wild and cultivated Glycine, but <2% of accessions used as parents in breeding #CWRGenomics



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AgroBioDiverse

Tomooka: marked differences in environmental adaptation in Vigna luteola complex #CWRGenomics



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Welcome to NIAS Genebank

News Temporary suspension of service (Dec 4, 2012) Our website will be was unavailable from 10:00 to 20:00 19:42 on Dec 6, 2012 (JST:UTC+9) due to electrical outage. NIAS Core Collection (Nov 8, 2012) NIAS Japanese Soybean Core Collection and NIAS World Soybean Core Collection are available now.



AFFRC


 **Luigi Guarino**
AgroBioDiverse @AgroBioDiverse


Quick brief on the Japanese national genebank #CWRGenomics

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 **Luigi Guarino**
AgroBioDiverse @AgroBioDiverse


@SandyKnapp But how to get data from private sector? #CWRGenomics

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 **Sandra Knapp**
SandyKnapp @SandyKnapp


value of CWR will be a big number.. very big number.... #cwrgenomics

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 **Sandra Knapp**
SandyKnapp @SandyKnapp


Someone needs to write a paper on the economic value of crop wild relatives #cwrgenomics

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 **Sandra Knapp**
SandyKnapp @SandyKnapp


\$64K Q - how to enhance and/or control recombination? #cwrgenomics

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 **Sandra Knapp**
SandyKnapp @SandyKnapp

Good plant science integrates across domains - it always amazes me to see disjunctions
#cwrgenomics

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 **Sandra Knapp**
SandyKnapp @SandyKnapp


Lots of missing information like passport info, documentation, but not made public or accessible
- need aggregation! #cwrgenomics

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 **Sandra Knapp**
Sandy Knapp @SandyKnapp


Darwin Core as example of good use of standards - biodiversity informatics is leading the way!
[#cwrngenomics](#)

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 **Sandra Knapp**
Sandy Knapp @SandyKnapp


I hate acronyms.... [#cwrngenomics](#)

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 **Luigi Guarino**
AgroBioDiverse @AgroBioDiverse


[@SandyKnapp](#) Seeds Exposed Every Day [#CWRGenomics](#)

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 **Sandra Knapp**
Sandy Knapp @SandyKnapp


SEED (sustainable exploration and exploitation for development) [#cwrngenomics](#)

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 **Sandra Knapp**
Sandy Knapp @SandyKnapp


Databases need to be easy in, easy out! [#cwrngenomics](#)

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 **NEON**


Laura was the NEON project's first official engineer. She earned her electrical engineering degree from Colorado State University and worked for a Loveland, Colo. water analysis company and Los Alamos National Laboratory before coming to the National Science Foundation-funded National Radio Astronomy Observatory as a subsystem engineer.


 [NEONINC](#)

 **Sandra Knapp**
Sandy Knapp @SandyKnapp

How about a Trait Observation Network (TRON?) for phenotyping of crops and wild relatives - like NEON or GEOBON but for food [#cwrngenomics](#)

 5 YEARS AGO


 Thumbnail for **Gbif.org: Home Page**
 Gbif.org: Home Page No Description Available

 GBIF


 **Sandra Knapp**
 SandyKnapp@SandyKnapp


CWR community talking about the GBIF model for exposing data - good concurrence of global public good outputs and objectives [#cwrgenomics](#)

 5 YEARS AGO


 **Sandra Knapp**
 SandyKnapp@SandyKnapp


Crop Wild Relatives are weeds.... but weeds only flowers in disguise! [#cwrgenomics](#)

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 **Sandra Knapp**
 SandyKnapp@SandyKnapp


Good Phenotyping Practice (GPP) = databases, standards, ontologies, all linked to methods [#cwrgenomics](#)

 5 YEARS AGO


 **Dr Sandra Knapp | Natural History Museum**


Merit Researcher, Head of Division Life Sciences department LS Plants Division
 Natural History Museum Cromwell Road London SW7 5BD Email Dr Sandra Knapp
 Biography *Solanum dulcamaroides* Poiret, a Mexican canopy liana related to the
 European woody nightshade. Ph.D., Cornell University, Ithaca NY, dissertation in
 Botany (1986). B.A.

 NHM


 **Sandra Knapp**
 SandyKnapp@SandyKnapp

International phenomics network needs to be more visible! [#cwrgenomics](#)

 5 YEARS AGO

 **Greg Baute**
 gregbaute@gregbaute

Needed infrastructure for phenotyping? Apps for mobile devices. Web-based platforms. [#CWRGenomics](#)


 5 YEARS AGO


Greg Baute

gregbaute@gregbaute

Phenotyping not as sexy as genomics. Need to raise its profile? build community?


[#CWRGenomics](#)

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Sandra Knapp

SandyKnapp@SandyKnapp

End of an amazing second day talking crop wild relatives in Asilomar - whole new worlds opening up for sharing across crops [#cwrgenomics](#)


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Luigi Guarino

AgroBioDiverse@AgroBioDiverse

"There is a pleasure in the pathless woods. There is a rapture on the lonely shore." [#asilomar](#)

[#CWRGenomics](#)


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Wild lupin on sand dunes at [#Asilomar](#). Apt scenery for a CWR meeting. [#cwrgenomics](#)


pic.twitter.com/ieRVqC6MqC6M

 LUIGI GUARINO @AGROBIODIVERSE · 5 YEARS AGO


 **Luigi Guarino**
 AgroBioDiverse @AgroBioDiverse

“@lab_ri: @AgroBioDiverse e.g. More noncoding variation. But I have little evidence for it (yet).” #CWRGenomics

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 **Luigi Guarino**
 AgroBioDiverse @AgroBioDiverse


“@lab_ri: Yeah I wasn't clear. Point was genetic architecture of adaptive traits in complex genomes may be different. 1/2” #CWRGenomics

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 **Luigi Guarino**
 AgroBioDiverse @AgroBioDiverse

Ross-Ibarra: Complicated point about whether adaptation is different in complex genomes. Dont really follow :(#CWRGenomics

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 **Greg Baute**
 gregbaute @gregbaute


Session3: Key crop specific challenges? Depends on the species. Phenotyping and databases needed for all. #CWRGenomics

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 **Greg Baute**
 gregbaute @gregbaute


Minor crops? learn from related major/model crops #CWRGenomics

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 **Myles Lab**
 foodimprover @foodimprover

Discussing with experts from around the world: How do we integrate wild relatives into breeding programs? Tricky stuff! #CWRGenomics

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 **Virginia Gewin**
 VirginiaGewin @VirginiaGewin

@AgroBioDiverse @gregbaute @geneticmaize Keep the #asilomar tweets coming. Any of you going to INTLPAG in January? Chat there if so?

 5 YEARS AGO

**Myles Lab**foodimprover
foodimprover

Shift of breeding from public to private threatens food supply - Global Crop Diversity Trust meeting sponsored by [@GenomeBC](#) [@GenomePrairie](#)

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**Luigi Guarino**AgroBioDiverse
AgroBioDiverse

Ross-Ibarra: have lost diversity in some genes not involved in domestication but close to genes that were [#CWRGenomics](#)

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**Luigi Guarino**AgroBioDiverse
AgroBioDiverse

Ross-Ibarra [@lab_ri](#): havent lost much var in maize as a whole, but have in some breeding programmes [#CWRGenomics](#)

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**Luigi Guarino**AgroBioDiverse
AgroBioDiverse

Ross-Ibarra: Some traits clearly adaptive in teosinte completely absent in domesticated maize [#CWRGenomics](#)

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**Luigi Guarino**AgroBioDiverse
AgroBioDiverse

Ross-Ibarra: 20% of highland maize genome comes from teosinte, specific introgressions associated with high alt adaptation [#CWRGenomics](#)

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**Luigi Guarino**AgroBioDiverse
AgroBioDiverse

Ross-Ibarra: Bunch of inversion polymorphisms show up as environmental outliers [#CWRGenomics](#)

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R-I Lab

Dept. Plant Sciences Genome Center * Center for Population Biology University of California One Shields Ave. * Davis, CA. 95616 530 752 1152 * rossibarra at ucDavis dot edu



**Luigi Guarino**

AgroBioDiverse

Ross-Ibarra: Lots useful adaptation in teosinte, have identified candidate loci by relating SNPs with environmental variables [#CWRGenomics](#)

 5 YEARS AGO
**Benjamin Edge**


edgeben@edgeben

[@AgroBioDiverse](#) Hard enough to work with a specific trait from one exotic. Problematic to follow w/ multiple wilds. [#CWRGenomics](#)

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**Luigi Guarino**

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Breakout session on grasses: breeders dont want too much diversity up front, ie pops combining crosses with multiple wilds [#CWRGenomics](#)

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Breakout sessions on different plant families. Including one called Others... [#CWRGenomics](#)

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Roundtable: 1 beyond CWR: domesticate rest of the flora 2 quantify CWR use in \$ 3 its the products, stupid, not the tools! [#CWRGenomics](#)

 5 YEARS AGO
**Faculty of Agriculture, Food and Environmental Quality Sciences, HUJI**

Dr. Daniel Zamir The Hebrew University of Jerusalem Faculty of Agriculture P.O. Box 12, Rehovot 76100 Israel Tel: 972-8-9489092 Fax: 972-8-9468265 e.mail: zamir@agri.huji.ac.il Personal Date of Birth: Jan 6, 1950, Jerusalem, Israel Marital Status: Married, five children Education Ph.D. University of California, Davis, Genetics (1978-1981). M.S. University of California, Davis, Vegetable Crops (1977-1978) B.S.

 HUJI
**Luigi Guarino**

AgroBioDiverse

Zamir: lets go back to standard deviation, I like to see big bars on a graph, they represent variation that could be exploited [#CWRGenomics](#)

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AgroBioDiversBioDiverse

Zamir: people should not just publish mean values #CWRGenomics

5 YEARS AGO



Daniel Zamir in full flight about yield stability in changing environments #cwrgenomics
pic.twitter.com/vLEibM5xbM5x

LUIGI GUARINO @AGROBIODIVERSE · 5 YEARS AGO



Luigi Guarino
AgroBioDiversBioDiverse

Shaw: genetic variation can increase under changing environments #CWRGenomics

5 YEARS AGO



Luigi Guarino
AgroBioDiversBioDiverse

Shaw: modelling adaptation in changing env: genetic variance for fitness rises, halting plummet in fitness #CWRGenomics

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Luigi Guarino
AgroBioDiversBioDiverse

Shaw: Numbers important. Well, doh. #CWRGenomics

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[#cwrgenomics](#) Genomics and crop wild relatives pic.twitter.com/rssw4H514H51


 LUIGI GUARINO @AGROBIODIVERSE · 5 YEARS AGO



Luigi Guarino

AgroBioDiverse

Shaw: iconic work by Lenski in natural selection in bacteria. But where is this going? Breath bated here. [#CWRGenomics](#)


 5 YEARS AGO




Luigi Guarino

AgroBioDiverse

Shaw: key points: nothing better than individual selection, better to have large pops, expression depends on environment [#CWRGenomics](#)

 5 YEARS AGO



Thumbnail for
Professor Ruth
G. Shaw |
College of
Biological
Sciences
 UMN

Professor Ruth G. Shaw | College of Biological Sciences

University of Minnesota College of Biological Sciences <http://www.cbs.umn.edu/>



Luigi Guarino

AgroBio@AgroBioDiverse

Ruth Shaw: what can we learn from evolutionary biology about breeding for climate change?

[#CWRGenomics](#)

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Greg Baute

gregbaute@gregbaute

Rieseberg via a cartoon: "Its all about recombination, deal with it" [#CWRGenomics](#)

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Luigi Guarino

AgroBio@AgroBioDiverse

Zamir: cold temperatures on young plants increases recombination rates [#CWRGenomics](#)

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Luigi Guarino

AgroBio@AgroBioDiverse

Rieseberg: my hope is to find variation in recombination rates in natural populations

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Buckler: chemical approaches to increasing recombination rates [#CWRGenomics](#)

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Rieseberg: if you overdo recombination you might get sterility [#CWRGenomics](#)

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AgroBio@AgroBioDiverse


Rieseberg: no need to redomesticate sunflower, but could be useful to bring in branching genes

[#CWRGenomics](#)

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 **Luigi Guarino**
AgroBio@AgroBioDiverse


Rieseberg: So what to do? Exploit variation in crossability. Increase recombination rates (modifiers). #CWRGenomics

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 **Luigi Guarino**
AgroBio@AgroBioDiverse

Rieseberg: sunflower improvement significantly impacted by linkage drag from wild relatives #CWRGenomics

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 **Luigi Guarino**
AgroBio@AgroBioDiverse


Rieseberg: chromosomal rearrangements limit introgression from wild to cultivated sunflower lines #CWRGenomics

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 **Luigi Guarino**
AgroBio@AgroBioDiverse

Rieseberg: Ecological genes may be important to agriculture for very weird reasons eg flowering time in sunflower #CWRGenomics

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 **Luigi Guarino**
AgroBio@AgroBioDiverse


Rieseberg: genome scans of wild sunflowers show divergen regions, can relate these to contrasting environmental conditions #CWRGenomics

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 **Luigi Guarino**
AgroBio@AgroBioDiverse

Rieseberg: wild sunflowers very strongly isolated by reproductive barriers #CWRGenomics

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 **Luigi Guarino**
AgroBio@AgroBioDiverse

Rieseberg: genes of ecological importance may also be of agricultural significance #CWRGenomics

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**Luigi Guarino**

AgroBioDiverse

Rieseberg: topdown vs bottomdown approaches to understanding genetic mechanism of adaptation #CWRGenomics



5 YEARS AGO

Faculty Profile : Department of Biology : Indiana University Bloomington

Research Description The Rieseberg lab integrates high-throughput genomic methods, bioinformatics, ecological experiments, and evolutionary theory to study the origin and evolution of species, domesticated plants, and weeds. Some of the problems we are currently working on are described below: Speciation - Our primary research interest concerns how new plant species arise (Science 317:910-914) - one of the most fundamental questions in biology.



INDIANA

**Luigi Guarino**

AgroBioDiverse

Morning from #asilomar, 2nd day of CWR genomics smackdown. Loren Rieseberg on reproductive barriers, ecological genomics etc #CWRGenomics



5 YEARS AGO

**Eve Emshwiller**

EveEmshwiller

Anyone going to publish proceedings of "meeting of #crop wild relative #genomic experts"? @AgroBioDiverse @gregbaute #genome #CWRGenomics



5 YEARS AGO

**Greg Baute**

gregbaute

Genome selection with CWRs using recombination in low recomb areas, diversity or geographic variation as the selected phenotype #CWRGenomics



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**Greg Baute**

gregbaute

Session2: Identify/predict which parts of CWR genomes are useful with... Local adaptation? Gene expression? Candidate genes? #CWRGenomics



5 YEARS AGO

**Greg Baute**

gregbaute@gregbaute

Session2: [#databases](#) - How to make them collaborative? How to make people contribute? Focus on Metadata and flexibility [#CWRGenomics](#)

 5 YEARS AGO
**Luigi Guarino**

AgroBioDiverse@AgroBioDiverse

Michael: colleagues at Monsanto have asked what is the product that comes genomes. Not the only ones to ask, I suspect. [#CWRGenomics](#)

 5 YEARS AGO


Thumbnail for
Oxford
Nanopore
Technologies


Oxford Nanopore Technologies

Oxford Nanopore Technologies® is developing the GridION™ system and miniaturised MinION™ device. These are a new generation of electronic molecular analysis system for use in scientific research, personalised medicine, crop science, security/defence and more. The platform technology uses nanopores to analyse single molecules including DNA/RNA and proteins.

**Luigi Guarino**

AgroBioDiverse@AgroBioDiverse

Michael: solid state nanopore sequencing in 5 years, sampling directly from the field, no prepping samples [#CWRGenomics](#)

 5 YEARS AGO
**Luigi Guarino**

AgroBioDiverse@AgroBioDiverse

Michael: CouchDB document-based database increases flexibility, but need solid ontologies [#CWRGenomics](#)

 5 YEARS AGO
What is NoSQL, and why do you need it? | ZDNet

Summary: NoSQL is a whole new way of thinking about a database. Though NoSQL is not a relational database, the reality is that a relational database model may not be the best solution for all situations. Imagine that you have coupons that you wanted to push to mobile customers that purchase a specific item.

**Luigi Guarino**

AgroBioDiverse@AgroBioDiverse

Michael: getting away from pre-defined database schemas noSQL [#CWRGenomics](#)

 5 YEARS AGO



Luigi Guarino

AgroBioDiversBioDiverse

Michael: structured databases and hardwired analysis pipelines not conducive to data sharing
[#CWRGenomics](#)



5 YEARS AGO



Luigi Guarino

AgroBioDiversBioDiverse

Michael: we still dont have good genome visualization [#CWRGenomics](#)



5 YEARS AGO

List of sequenced plant genomes - Wikipedia, the free encyclopedia

This list of sequenced plant genomes contains all the plant species known to have publicly available complete genome sequences that have been assembled, annotated and published; unassembled genomes are not included, nor are organelle only sequences.

[WIKIPEDIA](#)



Luigi Guarino

AgroBioDiversBioDiverse

Michael: Gone from 3 to 50 plant genomes in last 5 years. [#CWRGenomics](#)



5 YEARS AGO



Luigi Guarino

AgroBioDiversBioDiverse

Michael: solution is not integration but sharing [#CWRGenomics](#) he'll have to unpack that, I suspect



5 YEARS AGO



Luigi Guarino

AgroBioDiversBioDiverse

Todd Michael of Monsanto on data management and integration [#CWRGenomics](#)



5 YEARS AGO



Luigi Guarino

AgroBioDiversBioDiverse

Loren: alternative is to retrain more frequently, maybe thats way to make progress in minor crops [#CWRGenomics](#)



5 YEARS AGO



Genomic Selection

MAIN MENU Articles Drafts Software Contact us Genomic Selection Traditional plant breeding programs rely mainly on phenotypes being evaluated in several environments; selection and recombination are based solely on the resulting data plus pedigree information, when available. Marker assisted selection (MAS) uses molecular markers in linkage disequilibrium (LD) with QTL.



Luigi Guarino

AgroBioDiverso @AgroBioDiverso

Loren: every time, GS numbers go up. Is it going to be useful for minor crops? #CWRGenomics

5 YEARS AGO

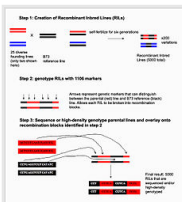


Luigi Guarino

AgroBioDiverso @AgroBioDiverso

Buckler: If doing NAM again, would use different numbers. #CWRGenomics

5 YEARS AGO



Nested association mapping - Wikipedia, the free encyclopedia

Nested association mapping (NAM) is a technique designed by the labs of Edward Buckler, James Holland, and Michael McMullen for identifying and dissecting the genetic architecture of complex traits in corn (Zea mays).



Luigi Guarino

AgroBioDiverso @AgroBioDiverso

Buckler: nested association mapping eliminates pop structure by design #CWRGenomics

5 YEARS AGO



Luigi Guarino

AgroBioDiverso @AgroBioDiverso

Buckler: Population structure a nightmare for GWAS. Would it be useful to sample hybrid zones? #CWRGenomics

5 YEARS AGO



Luigi Guarino

AgroBioDiverso @AgroBioDiverso

Buckler: can identify adaptive rare alleles through pop genetic analysis #CWRGenomics

5 YEARS AGO

**Luigi Guarino**

AgroBio@AgroBioDiverse

Buckler: CWR have high N_e , so LD decays rapidly, lots rare alleles, expose genetic load via inbreeding #CWRGenomics



5 YEARS AGO

Tocochromanol functions in plants: antioxidation and beyond

1Carlsberg Research Center, 10 Gamle Carlsberg Vej, DK-2500 Valby, Denmark 2Departament de Biologia Vegetal, Universitat de Barcelona, Facultat de Biologia, Avinguda Diagonal 645, E-08028 Barcelona, Spain *To whom correspondence should be addressed. E-mail: smunne{at}ub.edu Received November 15, 2009. Revision received January 24, 2010. Accepted January 26, 2010.



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**Luigi Guarino**

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Buckler: Toco-chromonols? Yesh I dont know what those are either. #CWRGenomics



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**Luigi Guarino**

AgroBio@AgroBioDiverse

Buckler: its all about saving time in the breeding cycle #CWRGenomics



5 YEARS AGO

Home

MaizeGenetics.net - Website of the Edward Buckler lab

[MAIZEGENETICS](#)

**Luigi Guarino**

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The famous Ed Buckler on next: analysis strategies for linking genotypes to phenotype to tap wild diversity #CWRGenomics



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**Luigi Guarino**

AgroBio@AgroBioDiverse


First morning over. Still that dichotomy between targeting specific traits in CWR vs using them for base broadening #CWRGenomics



5 YEARS AGO


 **Greg Baute**
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Repeated point session 1: It depends. [#CWRGenomics](#)

 5 YEARS AGO


 **Greg Baute**
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Repeated point session 1: Need to collect, store and connect data: ecological, phenotypic and genomic for CWRs in genebanks [#CWRGenomics](#)

 5 YEARS AGO


 **Greg Baute**
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Session1: How to phenotype? It depends on trait. Get breeders involved but they do not want wild material in their plots [#CWRGenomics](#)

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 **Greg Baute**
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Session1: How many individuals from each CWR accession? It depends on breeding system and collection history [#CWRGenomics](#)

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 **Greg Baute**
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Session1: Phenotype or Genotype CWRs? Pre-breeding. Phenotype subsets. Subset based on genotype. [#CWRGenomics](#)

 5 YEARS AGO


 **Greg Baute**
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Session1: How to select a subset of CWRs? New material, what can be used, has traits of interest, found in diverse environments [#CWRGenomics](#)

 5 YEARS AGO


 **Greg Baute**
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With CWRs there are concerns with regards to reference [#genomes](#). May not give you the whole picture of CWRs [#CWRGenomics](#)

 5 YEARS AGO


 **Greg Baute**
gregbaute@gregbaute

Session1: How to estimate variation in CWRs? Sequence! Tiered approach, whole #genome seq + #GBS #CWRGenomics

 5 YEARS AGO

 Thumbnail for **Asilomar Conference Grounds - Pacific Grove CA - Asilomar.com**


Asilomar Conference Grounds is located on the Monterey Peninsula in Pacific Grove, CA. A premiere Monterey conference center with overnight lodging.

 VISITASILOMAR


 **Kasia Stepien**
kasiastepien@kasiastepien

@gregbaute one of #UBC researchers at #crop wild relative #genomics meeting in Monterey. Follow meeting w #CWRGenomics

 5 YEARS AGO


 **Myles Lab**
foodimprover@foodimprover

Discussing with experts from around the world: How do we integrate wild relatives into breeding programs? Tricky stuff! #CWRGenomics

 5 YEARS AGO


 **Greg Baute**
gregbaute@gregbaute

At #asilomar for a meeting of #crop wild relative #genomic experts @AgroBioDiverse @lab_ri #genome Stay tuned with #CWRGenomics


 5 YEARS AGO

McCouch, Susan Rutherford

outreach overview 1) The primary focus of my outreach activities is on providing middle and high school students with an opportunity to participate in basic, hands-on laboratory experiments involving plant molecular genetics and to think about how research in the plant sciences contributes to addressing problems of global food production, human nutrition and environmental sustainability.

 CORNELL

Thanks to Susan for being the driving force behind this meeting...

 **Crop Wild Relative Genomics: a Key to Unlocking Diversity**

Session 1: Measuring genotypic and phenotypic variation in CWRs 'Where is the diversity?'

WORDPRESS