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Gramene Tip:

Send Queries to the Gramene development team by using the "Feedback" link at the top of every page. To send queries to other Gramene users, join the Gramene list serve, accessible under "About Us" on the navigation bar.

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Introduction to Gramene contributor project: Panzea

The ultimate germplasm resource to date for localizing QTLs in maize!

The Panzea project (NSF DBI 0321467) is a five-year NSF project headed by John Doebley, and involves eight additional investigators at seven institutions (University of Wisconsin, Cornell University, North Carolina State University, University of Missouri, University of California-Irvine, Cold Spring Harbor Laboratory and USDA-ARS). Our overall objectives are to address two major questions: 'How has selection shaped molecular diversity?' and 'How does this molecular diversity relate to functional trait variation?' We have completed our objectives relating to our first major question, and you can read more about the results to date from this project (and from its five-year forerunner) at <http://www.panzea.org/lit/publication.html>.

Now we are devoting our focus to the characterization of functional diversity in both teosinte and maize. We are engaged in QTL and association mapping experiments both in modern maize and in crosses between teosinte and maize. We are currently working with two teosinte association mapping populations, three teosinte-maize backcross QTL mapping populations, a maize association mapping population and a maize 'Nested Association Mapping' (NAM) population.

The maize NAM population is the centerpiece of our project - we expect this population to be the most significant to the maize research community. Nested Association Mapping is a powerful new method for localizing QTL which uses a multifamily RIL mapping population derived from crosses to a common parent (i.e., B73) in order to perform a joint QTL and association analysis. By employing a genomic scan of common parent-specific SNPs in the progeny RILs combined with high density genotyping (or sequencing) of the parental lines, the NAM strategy captures the best of both worlds: the statistical power of QTL analysis is combined with the high chromosomal resolution of association analysis.

We are pioneering the NAM approach in maize. Our NAM population consists of >5000 RILs from 25 families, with 200 RILs per family, all being genotyped at 1500 SNP loci. It forms a permanent QTL mapping resource for the benefit of the maize and grass communities. The families were generated by crossing 25 diverse maize inbred lines with B73 as the common parent, and the well-known IBM mapping population is included as the 26th family. Finally, a collection of 280 diverse maize inbreds from around the world has been included to serve as an association mapping

platform for maize. We have recently demonstrated the power of our NAM population for detecting higher order epistatic interactions among QTL, using simulated data based upon actual SNP genotypes from our 25 NAM parents (Stich et al., Genetics 176:563-70, 2007).

This summer we planted out all of these RILs in three locations (Raleigh, NC; Aurora, NY; Champaign-Urbana, IL). The parental lines are being sequenced over the next year and a half - making it possible to analyze all populations as one unified experiment, potentially with gene-level QTL resolution.

We are scoring a several obvious agronomic and developmental traits in these populations, but are unable to score some of the more complex traits. We are hoping that maize and grass researchers working on complex, specialty traits will score their own phenotypes of interest in one or more of our NAM 'Fields of Dreams'. We also have extensive experience

in creating barcoding tools for phenotyping, and can provide help with this. For further details or to arrange your phenotyping visit(s), please contact Ed Buckler (esb33@cornell.edu), Jim Holland (James_Holland@ncsu.edu), or Torbert Rocheford (trochefo@uiuc.edu). Our only stipulation is that your data set must be deposited in our project database, Aztec, where it will be held privately for two years (members of the Panzea group will not be allowed to analyze it either, without prior permission from you), and then released to the public via www.panzea.org.

If you are unable to make it to one of our fields this summer, do not fret! Plans are afoot to have public grow-outs of the NAM population for as many as four more years, but at this point funding support is guaranteed only through the summer of 2008. For educators focusing primarily on undergraduate teaching, the NAM resource provides an ideal opportunity for research involving undergraduate or Masters students, potentially funded via the NSF's 'Research Opportunity Awards'. Resources from these awards could potentially be pooled with those from other sources to fund one or more future 'public' grow-outs of the NAM population. In addition, for researchers interested in growing out all or part of the NAM population themselves, seed from the entire, fully-genotyped NAM population will be available from the Maize Stock Center in 2008.



Measuring Traits @ Aurora Field near Ithaca, NY. Back row (L-R): Zhiwu Zhang, Sara Larsson, Mike Gore, Nick Lepak, Dallas Kroon, Peter Bradbury. Front row (L-R): Jason Peiffer, Elhan Ersoz, Ed Buckler

Cornell Maize Geneticists and "The McClintock Shed"

Meet the amazing team of researchers who set a high standard of excellence for future geneticists, here pictured in front of their field house in 1929, the building that still stands next to the Pounder Heritage Garden in the Cornell Plantations.

Charles Burnham (1903-1989)

Burnham was a maize cytogeneticist and breeder. He came to Cornell as a postdoctoral fellow to work with Emerson and McClintock. Later, he spent 34 years as a faculty member at University of Minnesota and authored 255 scientific papers.

1929 – Completed Ph.D. under Dr. Brink at the University of Wisconsin
1962 – Published *Discussions on Cytogenetics*

Marcus Rhoades (1903-1991)

Rhoades made important contributions to the fields of maize genetics and cytogenetics. He unselfishly shared unpublished information, exchanged seed stocks, and revealed new techniques in order to advance the knowledge of maize genetics. Dr. Rhoades was also interested in non-Mendelian genetics, and made several breakthroughs in this subject.

1977- Became Foreign Fellow of the Royal Danish Academy of Science and Letters

1981- Awarded the Thomas Hunt Morgan Medal of the Genetics Society of America

1982- Received an honorary Sc.D.

Material originally presented as a Poster at Cornell's Plant Breeding & Genetics Centennial Celebration, July 2007. Contributed by: Denise E. Costich^{1,2}, Michelle Denton², Max Kraft², Sara Larsson², Michael Oak², Erin Ploetz², Michael Ryskin², Grisha Temnykh², Stephen Wu² and Edward Buckler^{1,2}

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The Sixth International Genetics Congress was held in August of 1932 in Ithaca, NY. Here, over 800 people attended, 101 members of which were from other countries of the world, including some of the most famous geneticists of the time. At the congress, scientific abstracts were presented, social activities organized, and a variety of exhibits presented. [Reference: J. Heredity 23:355-360 (1932)]



Outside the plant breeding shed near Cornell's Ag Quad in 1929 are (standing, from left) researchers Charles R. Burnham and Marcus Rhoades, Professor Rollins A. Emerson, and Barbara McClintock, later a Nobel laureate. Kneeling is George W. Beadle, also to be a Nobel laureate, with Emerson's dog Pudgie.

George Beadle (1903-1989)

Beadle worked with R.A. Emerson and L.W. Sharp as a graduate student. He studied Mendelian asynapsis in maize, and received his Ph.D. for this work.

1958 – Received the Nobel Prize together with E. L. Tatum for their work with the *Neurospora* fungus and their theory that each gene controls the reproduction, function, and specificity of a particular enzyme

1961 - Elected Chancellor of the University of Chicago, and later that year became President of the University

Barbara McClintock (1902-1992)

McClintock was a leader in the field of maize cytogenetics with her studies on the changes of maize chromosomes during reproduction. This made it possible for her to develop techniques to visualize the chromosomes and demonstrated fundamental genetic ideas such as recombination by chromosomes crossingover during meiosis.

1927 – PhD in botany from Cornell University

1944 – Member of the National Academy of Sciences

1983 – Received the Nobel Prize in Physiology or Medicine for the discovery of genetic transposition (jumping genes)

Rollins Adams Emerson (1873-1947)

Emerson published many papers on maize including the following topics: sex expression, plant color inheritance, quantitative inheritance and mutations. Founded the Maize Genetics Cooperation, an organization which sponsored a newsletter and a mutant stock center.

1910 – First paper on maize genetics

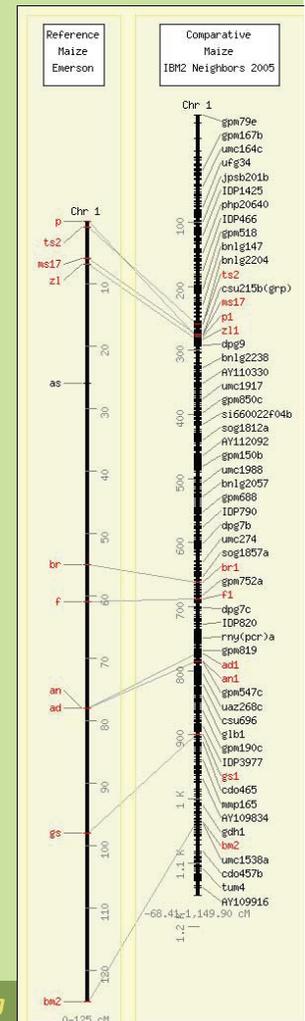
1914 – Head of Department of Plant Breeding at Cornell

1925-31 – Dean of Cornell University Graduate School

1939 – Delegate to Seventh International Genetics Congress Cornell Maize Genetics

75 years of Mapping the Maize Genome

- Emerson's map of Chromosome 1 (on left), showing the approximate locations of 11 genes, compared to a modern-day map. Map contributed by Immanuel Yap, Gramene



Upcoming Outreach:

Gramene plans to participate at these upcoming meetings. You may attend these workshops and posters to learn about Gramene or get answers to questions. See the Calendar below for dates and locations.

Aug. 29-31. Environmental ontology workshop. Oxford, England

Sept 21-22. Eighth Agricultural Ontology Service (AOS) Workshop on "7 years of AOS: Achievements and Next Steps", Rome, Italy.

"Rice: Research to Production" course launched last May at the International Rice Research Institute (IRRI) in the Philippines

Community Calendar

2007

Aug. 13-17. Computational Systems Bioinformatics. UC San Diego

Aug. 20-31. 2007 Rice Breeding Course: Laying the Foundation for the Second Green Revolution. Philippines

Aug. 29-31. Environmental ontology workshop. Oxford, Engl.

Sept 21-22. Eighth Agricultural Ontology Service (AOS) Workshop on "7 years of AOS: Achievements and Next Steps". Rome, Italy

Oct. 9-14. 4th International Rice Blast Conference. Vaya Huatian International Hotel, Changsha, Hunan, China

Oct. 15-17. 5th International Symposium for Rice Functional Genomics. Tsukuba, Japan

Oct 22-24 ACPFG Genomics Symposium - The Genomics of Drought. Adelaide, SA

Nov 4-8. Crop Sciences International Meeting (ASA-CSSA-SSSA). New Orleans, LA, USA

Nov 5-9. 11th International Symposium on Pre-harvest Sprouting in Cereals. Mendoza, Argentina

Dec 2-4. 2007 National Fusarium Head Blight Forum. Kansas City, Missouri USA

2008

January 6-11. 8th Annual Long-Oligonucleotide Microarray Workshops. Tucson, AZ

January 12-16. PAG-XVI. San Diego, CA, USA

Feb 18-21. RTWG Meeting. San Diego, CA, USA

April 5-10. 10th International Barley Genetics Symposium (IBGS). Alexandria, Egypt

August 24-29. 11th International Wheat Genetics Symposium. Brisbane, Australia

Gramene FAQ

Contact Gramene through the "Feedback" link at the top of any page to ask questions. Here are some recent questions that have been answered.

Q: I have run RM1109 several times with 12 different accessions, and always get the size between 105-115bp. In Gramene, it is 198. How can I explain the difference?

A: The number reported in Gramene is straight out of the original publication, which is based on electronic results. If you look at our own ePCR results, you'll see that RM1109 has two different positions on the TIGR genome: the longer position is 198 bp, exactly that estimated. The shorter position is 111 bp, which is closer to your actual results. Another possibility could be that your sample did not include Nipponbare germplasm - the sequence the ePCR is based on. For some SSR markers, there are quite dramatic differences in SSR product sizes between indica and japonica subspecies.

Q: What is the suitable method/procedure for identifying candidate genes within QTL regions?

A: Currently there is no standard method/procedure to do that. It's more an art than science. Basically you should use all integrated information/data within those QTL regions, such as gene models, together with GO term annotations, associated EST or expression data, biochemical pathways, the informatics from other species, etc.

At Gramene, you can also use the GrameneMart mining tool at <http://www.gramene.org/Multi/martview>. Begin with a particular chromosome and narrow down to your genomic region of interest. You can get more info about how to use Mart by reading the Mart tutorial and FAQs.

Opportunities

Here are opportunities for researchers and students. Please check with each organization to confirm due dates. (Due dates are in mm/dd/yy format).

- 5th ISRFG abstract for oral and poster presentation. Due **8/15/07**
- *IJPG* call for papers for Bioinformatics Tools for Plant Genomics Due: **9/1/07**
- *RTWG Meeting* Title-Summary due: **11/1/07**, Abstracts due: **12/1/07**
- *Monocots IV*. Abstracts for oral contributions and posters due **5/31/08**.

Plant Sciences jobs @ North Dakota State University, Fargo, ND.

Pre-proposals (PP) for research projects for fiscal year 2008 U.S. Wheat & Barley Scab Initiative (USWBSI) http://www.scabusa.org/research_rfp08.html

GRAMENE



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Genes & Alleles
Maps and CMap
QTL

Ontologies
Pathways
Literature
Proteins
Markers
GrameneMart

Gramene is a curated, open-source, web-accessible free data resource for comparative genome analysis in the grasses. Our goal is to facilitate the study of cross-species homology relationships using information derived from public projects involved in genomic and EST sequencing, protein structure and function analysis, genetic and physical mapping, interpretation of biochemical pathways, gene and QTL localization and descriptions of phenotypic characters and mutations.

email: gramene@gramene.org

For updates on releases and other information, join Gramene's mailing list or view the mailing list archive.

www.gramene.org

Educational Link: Sorghum Research! Learn about current research in sorghum, view photos and explanations of how Ergot affects sorghum, Sorghum Lodging, Greenbug Resistance, and the process of developing new lines.
<http://www.wkarc.org/Arch/Research/sorghum/sorghum.asp>.

Gramene Tip: Researchers who have published data that is not currently in the Gramene database are encouraged to contact Gramene to request curation of their article.

Gramene Tip: The SSR Marker Resource is listed under the Marker database, and offers SSRIT, a list of common markers, and primer information from McCouch lab.

For world-wide rice news, check out IRRI's news page at <http://ricenews.irri.org/>

Recommended Reading

Polyploids, genome halving and phylogeny. Sankoff D, Zheng C, Zhu Q. *Bioinformatics*. 2007 Jul 1;23(13):i433-i439.

Are source and sink strengths genetically linked in maize plants subjected to water deficit? A QTL study of the responses of leaf growth and of Anthesis-Silking Interval to water deficit. Welcker C, Bousuge B, Bencivenni C, Ribaut JM, Tardieu F. *Journal of experimental botany*, 2007, vol. 58, pp. 339-349.

The plant structure ontology, a unified vocabulary of anatomy and morphology of a flowering plant. Ilic K, Kellogg EA, Jaiswal P, Zapata F, Stevens PF, Vincent LP, Avraham S, Reiser L, Pujar A, Sachs MM, Whitman NT, McCouch SR, Schaeffer ML, Ware DH, Stein LD, Rhee SY. *Plant Physiol*. 2007 Feb;143(2):587-99. Epub 2006 Dec 1.

Genome-wide analysis of ABA-responsive elements ABRE and CE3 reveals divergent patterns in Arabidopsis and rice. Gomez-Porras JL, Riano-Pachon DM, Dreyer I, Mayer JE, Mueller-Roeber B. *BMC Genomics*. 2007 Aug 1;8(1):260.

Molecular and pathotypic characterization of new *Xanthomonas oryzae* strains from West Africa. Gonzalez C, Szurek B, Manceau C, Mathieu T, Séré Y, Verdier V. *Mol Plant Microbe Interact*. 2007 May;20(5):534-46.

Diversity of wild and cultivated pearl millet accessions (*Pennisetum glaucum* [L.] R. Br.) in Niger assessed by microsatellite markers. Mariac C, Luong V, Kapran I, Mamadou A, Sagnard F, Deu M, Chantreau J, Gerard B, Ndjeunga J, Bezançon G, Pham JL, Vigouroux Y. *Theor Appl Genet*. 2006 Dec;114(1):49-58. Epub 2006 Oct 18.

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