SOL NEWSLETTER

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COMMUNITY NEWS

Tomato field in Indonesia

INDOSOL

Contributed by Sjaak van Heusden

High Quality Solanaceous Vegetables by Exploration of Natural Biodiversity

There is a long-term co-operation between The Netherlands and Indonesia in the field of agriculture. This cooperation was based on the notion that agriculture and agricultural research is of prime importance for the economic and social development of Indonesia. The cooperation led to research programs for training, extension, applied research, agri-business driven research and fundamental research and capacity building. The various programmes led to an extended network to the benefit of Dutch and Indonesian scientists, policy makers and companies.

In 2006, a new program was submitted and granted by the Royal Dutch Academy of Sciences. To have maximal synergy between the projects, all partners will work with fruit-bearing solanaceous crops. These crops are of primary importance in both countries. The program will focus on optimal growth and development of tomatoes with a high nutritional quality. For optimal growth we need varieties that can grow under adverse conditions. Pests and diseases readily attack the crops and large amounts of chemical protection agents are used. For sake of focus, the program will only address pests and not diseases. For a high nutritional quality we need plants with a specific metabolic composition. Metabolomics allows us to measure these compounds and unravel the pathways.

The main research topics are:

1. *Solanaceae* and environment: understand and exploit mechanisms for pest-resistance of fruit-bearing *Solanaceae*.
2. *Solanaceae* and health: understand and exploit the biochemical pathways in fruit-bearing *Solanaceae* of carotenoids, flavonoids and terpenoids.

These topics were chosen from a long list by Dutch and Indonesian partners with advice from private companies. Coherence, scientific challenge and economic importance led to the choice of topics.

This program named INDOSOL will be linked to other *Solanaceae* initiatives (like EUSOL), such that the Indonesian candidates can take part in the EUSOL meetings to get access to the state-of-the-art in their research field, to establish networks and to present their work.

INDOSOL will consist of five different PhD projects. One project, dealing with the characterization and exploitation of biodiversity will host two PhD-candidates. The other projects will employ one PhD-candidate. All PhD projects will be executed by an Indonesian PhD fellow.

The projects are:

1. Quality attributes to pepper metabolites: a systems approach
2. Components of whitefly resistance in tomato and hot pepper
3. Candidate genes for thrips resistance in pepper (Capsicum spp.)
4. Nutritional value and 'attack' resistance in wild Indonesian *Solanum* species

At the end of 2006, a number of PhD candidates will be interviewed and 10-12 candidates will be chosen. In the first year, this group will be further educated in Indonesia. A number of scientific courses will be organized and supplemented by other, more general courses. At the end of year one, five candidates will be selected for the five, four-year PhD sandwich projects.

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Nomenclature for Wild and Cultivated Tomatoes

Contributed by Iris E. Peralta

This is an abbreviated version of a much longer article that will soon be published in the Tomato Genetics Cooperative Newsletter complete with many historical and interesting references.

The names of wild tomatoes

Recently, we (Peralta, Knapp, and Spooner) completed an in-depth study of tomatoes and their wild relatives to provide new species definitions, revise and update the nomenclature, and synthesize knowledge about these plants. We treated tomatoes in the large genus *Solanum*, rather than as the segregate genus *Lycopersicon*, based on evidence coming largely, but not exclusively, from studies of DNA sequences. In the past decade, several molecular phylogenetic studies of the *Solanaceae* have unambiguously shown tomatoes to be deeply nested within *Solanum*. We propose a phylogenetic classification philosophy that simply states the hypothesis that tomatoes may have more "predictivity" under *Solanum*, and also apply a Linnaean nomenclatural system (hierarchical) to provide the valid names of wild species under *Solanum* and their equivalents in *Lycopersicon* for ease of comparison to the literature.

Based on morphological characters, phylogenetic relationships, and geographic distribution, we proposed the segregation of four species within the highly polymorphic green-fruited species *S. peruvianum* sensu lato (sensu lato refers to a broad concept of a species): *S. arcanum*, *S. huaylasense*, *S. peruvianum*, and *S. corneliomulleri*. The first two have been described as new species from Perú, while the latter two had already been named by Linnaeus and MacBride, respectively. We recognize yet another new yellow- to orange-fruited species, *S. galapagense*, segregated from *S. cheesmaniae*; both are endemic to the Galápagos Islands. In total, we recognize thirteen species of wild tomatoes, including the cultivated tomato (*Solanum lycopersicum*) and its weedy escaped forms that are distributed worldwide. This is an increase from the nine species of tomatoes traditionally recognized.

Solanum chilense

Nomenclature of cultivated tomato and the history of their scientific naming

Different names in different languages were used to name tomatoes in the time before standardized scientific naming. Tomatoes were introduced into Europe from the Americas and became known to botanists about the middle of the sixteenth century.

Pietro Andrea Matthioli (1544) described tomatoes for the first time with the common Italian name "Pomi d'oro" (Golden Apples). Early botanists recognized the close relationship of tomatoes with the genus *Solanum*, and commonly referred to them as *Solanum pomiferum*. Tournefort (1694) was the first to name cultivated tomatoes as *Lycopersicon* ("wolf peach" in Greek). He placed forms with large multilocular fruits in the set of plants he called *Lycopersicon,* but kept the plants with bilocular fruits as *Solanum*. Linnaeus (1753) began to consistently use Latin binomials. He classified tomatoes in the genus *Solanum* and described *S. lycopersicum* (the cultivated tomato) and *S. peruvianum*. The very next year Miller (1754) followed Tournefort and formally described the genus *Lycopersicon*, which for him was defined on fruit characteristics and included the potato.

Today, based on evidence from molecular phylogenetic studies and more in-depth studies of plant morphology and distribution, there is general acceptance of the treatment of tomatoes in the genus *Solanum* by both taxonomists and breeders alike. These names in *Solanum* are being incorporated in germplasm bank databases as in the C.M. Rick Tomato Genetic Resources Center (http://tgrc.ucdavis.edu/).

In conclusion, the generic status of tomatoes has been in flux since the eighteenth century, reflecting two main and often competing goals in taxonomy, that of: 1) predictive natural classifications (treatment in *Solanum*) and 2) the maintenance of nomenclatural stability (treatment in *Lycopersicon*). The economic importance of tomatoes has stimulated discussion amongst taxonomists and breeders about the relative value of classifications that emphasize predictivity versus stability.

For tomato cultivars, we support a taxonomy treatment under the Code of Nomenclature for Cultivated Plants (ICNCP), which provides a framework more appropriate to name the great diversity of cultivated tomatoes, all members of the single biological species *S. lycopersicum*, generated by breeding. This taxonomy has yet to be developed on a global scale, but would be useful to standardize the naming and exchange of the wide variety of tomato cultivars in use today.

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TOMATO SEQUENCING UPDATES

SOL 2006 – Genomics Meets Biodiversity – Update on Tomato Genome Sequencing

Provided by Jim Giovannoni

The International Solanaceae Meeting was held in Madison, Wisconsin July 23 – 27 and was a great success. Sincere thanks are due to David Spooner and his colleagues for organizing a highly productive meeting! For the first time, the SOL conference was joined with the International Solanaceae meeting and the International Potato Society meeting resulting in a gathering of over 500 academic and industry scientists, students and funding agency representatives from all corners of the world. Participants had the opportunity to explore the incredible diversity of the family *Solanaceae* which encompasses over 3000 species, learn about and view the progress of the International Tomato Genome Sequencing Project consortium, and examine some of the more applied aspects of *Solanaceae* genomics via the activities of the potato breeding participants. The meeting was kicked off with an informative perspective of the tools and lessons learned from Arabidopsis genomics provided by the keynote speaker, Joe Ecker of the Salk Institute. Subsequent morning sessions provided a mix of genomics and biodiversity talks followed by afternoon sessions and workshops that delved into the details of targeted research topics.

Of particular interest to the SOL Newsletter audience was the workshop on tomato genome sequencing. Representatives of all ten participating countries were present and made it clear that the project is well out of the starting gate. All ten countries have provided finished BACs to date with South Korea completing over one quarter of the expected BACs for chromosome 2. Japan and The Netherlands also reported substantial numbers of completed BAC sequences and the UK project led by the Sanger Center reported fingerprinting of the MboI BAC library and initial integration of the resulting data with that available from the HindIII library. This data is available for download from Sanger. All project participants are forwarding sequence data to the SGN database for which Lukas Mueller provided an update including new anchor BACs revealed through an in silico screen of mapped marker sequences to the BAC end sequence database. The workshop was followed by a sequencing lunch discussion where the topics of central focus included strategies for walking from anchor/seed BACs and end-game strategies to insure sequencing by all participants meets agreed standards. Additional discussion centered on using available data to address the genome size estimates on which the project plan is based. Both the UK and South Korea representatives stated that their activities to date indicate that the size estimates for the euchromatin space on their respective chromosomes were consistent with predictions. The goal of having more than 50% of sequencing completed by next year was set by the chairs of the International Steering Committee, Dani Zamir and Sandy Knapp.

Chromosomes 1, 10, 11 (US)

Contact: Joyce Van Eck (jv27@cornell.edu)

To date, we have sequenced a total of fifteen BACs for all three chromosomes, and four BACS are in the sequencing pipeline. We are in the process of confirming and selecting additional BACs for sequencing. Efforts are underway by SGN in collaboration with other bioinformatics groups to determine parameters for annotation by working with ten tomato test BACs.

Since our last report, the Stack lab has localized an additional seven BACs, bringing the total number positioned by FISH to fifty. Among these new BACs are the first two to be localized on chr 10 (Fig. 1) and one located at the centromere of chr 6 (Fig. 2). The recently positioned BACs include:

Chromosome Arm	BAC ID
1P	262O22
	069E17
3Q	157P11
4Q	106F07
6P	057J04
10P	041K23
10Q	234C10

In other news, we report that Dr. Song-Bin Chang has left the Stack lab to take an Assistant Professorship in the Department of Agronomy at the National Taiwan University in Taipei. We rejoice with Song-Bin on his professional appointment in his native country and wish him great success, but we miss his pleasant personality and excellent work on FISH here at Colorado State University.

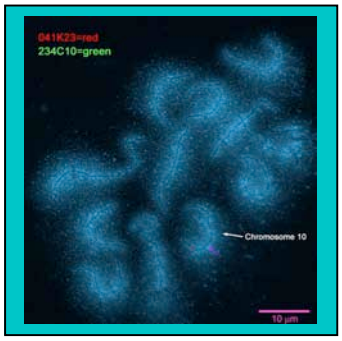

Figure 1: FISH labeling of two BACs on chr 10, 041K23 (red) and 234C10 (green). The purple arrow points to the centromere.

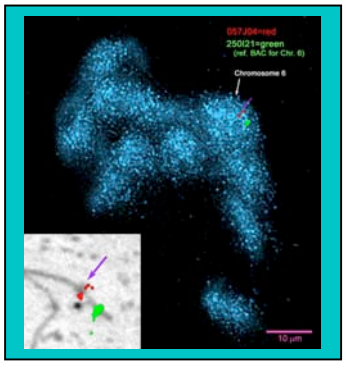

Figure 2: FISH labeling of two BACs on chr 6, 057J04 (red) and 250I21 (green). The purple arrow indicates the position of the centromere. The inset shows the fluorescent signals superimposed on the phase image of chr 6. The signal for 057J04 lies partly over the kinetochore.

Chromosome 2 (Korea)

Contact: Sanghyeob Lee (sol6793@kribb.re.kr)

To date, we have completed the sequence for eighty-six BACs (twelve additional BACs since our last report in June). Six BACs are in the pipeline and waiting for finishing. Three BACs are in the sequencing pipeline. We have tried the new SL_MboI FPC data (from the Sanger Center) for BAC extension. When we searched this new database, it gave us more BAC clones as compared with the results from our previous search of the HindIII FPC database. However, we did not find any additional extension BACs in this new database as compared with the HindIII database at this time.

Chromosome 3 (China)

Contact: Chuanyou Li (cyli@genetics.ac.cn)

Update pending

Chromosome 4 (UK)

Contact: Christine Nicholson (ckb@sanger.ac.uk)

To date, we have sequenced 3,010,682 bp for chr 4, of which 2,827,932 bp are unique (excluding overlapping sequence). 1,090,890 bp of this sequence have been fully finished to HTGS phase 3 and the remaining sequence is in Finishing. All sequences from HTGS phase 1 to phase 3 are available via the EMBL/Genbank/DDBJ public databases. Additional, BACs have been selected and verified to confirm clone identity and these are currently pre-accessioned in our sequencing pipeline. BAC statuses are updated at the BAC Registry.

Our tilepath selection strategy makes use of marker and BAC end sequence (BES) data in association with fingerprint data to select BACs to sequence in FPC. We generated >43,000 fingerprints from the SL_MboI library. These fingerprint data are publicly available at ftp://ftp.sanger.ac.uk/pub/tomato/map/. With the addition of the added fingerprint data, we are continuing to assess and refine the chr 4 FPC contigs as a way of generating a reduced number of longer contigs from which to select the tiling paths. As discussed at the recent meeting in Madison, we will provide regular monthly updates of our chromosome status in the form of TPFs and AGPs.

In order to identify additional BACs along chr 4, we would like to anchor markers from the Tomato EXPEN-2000 map to the FPC contigs. We aim to achieve this by screening the SL_MboI library with missing markers. The library has been gridded in-house to generate filters for the hybridizations.

We have additional BAC and contig candidates, however, we need to confirm that they are indeed on chr 4, or overlap with established contigs. We hope to attain this information by FISH localizations, genetic mapping and colony PCR verification using BES probes. In addition, we look forward to gaining further insight from the FISH data into the euchromatin/heterochromatin distribution along the chromosome.

Chromosome 5 (India)

Contact: Akhilesh Tyagi (akhilesh@genomeindia.org)

The Indian Initiative on Tomato Genome Sequencing is currently involved in sequencing thirty-four BAC clones anchored to chr 5 specific markers (CT101, C2-At1g60440, T1252, C2-At1g60200, cLET-8-B23, T0564, cLED-8-G3, T1592, Bs4, T1360, cLEX-13-G5, T1746, T1777, T1541, T1584, TG69, CT130, TG185, TG597 and CT138). BAC sequencing has progressed to various stages. Seven BACs are at phase 1,

fourteen BACs are at phase 2, and five BACs have reached phase 3. Nucleation points have been confirmed using IL lines. The marker T0876 and its associated BACs (C05MBa0077G20, C05HBa0179K09 and C05MBa0032F07) at 12.0 cM were reallocated to chr 7 by using chr 5 and chr 7-specific IL lines.

Chromosome 6 (The Netherlands)

Contact: Sander Peters (sander.peters@wur.nl)

We completed phase 2 sequencing for twelve extension BACs. To investigate the overlap in more detail, we determined the sequence homology between seed and extension BACs. We found twelve overlapping domains with a 100% sequence match between seeds and their extension BACs (Table 1). This result further validates our BAC walking strategy using an automated STC approach. (H153G23 was a kind gift from Barbara Baker, Dept. of Plant and Microbial Biology, University of California-Berkeley; USDA, Plant Gene Expression Center, USA).

Table 1:

Extension BAC	Seed BAC	Overlap (nts)	Sequence match
H019E05	H073H07	3520	100%
H023D12	H125P18	11392	100%
H023D12	H002C17	1294	100%
P066P09	H304P16	1099	100%
P103P06	H120H21	2966	100%
H118O07	H106K23	12996	100%
H128E05	H002C17	4449	100%
H144J05	H054K13	3081	100%
H146A12	H012A08	7555	100%
H197N20	H153G23	42339	100%
E008G21	H054K13	4432	100%
M009E16	H024L21	4000	100%

Small contigs consisting of overlapping BACs started to emerge. For example, H023D12 overlaps at both its SP6 and T7 ends, and bridges the gap between seed BACs H002C17 and H125P18. The other side of seed BAC H002C17 is extended by H128E05. The 4 overlapping BACs have been merged into a contig of ~350 kb which lands on the long arm of chr 6 at approximately 60cM. Likewise, for the short arm, we now have a contig of ~440 kb consisting of 4 overlapping BACs (H112G05, H250I21, H073H07, H019E05) which lands onto the chr 6 KFG Mi marker. In the near future, the number of seed, extension, and STC screening data will grow and we intend to construct a dedicated database to manage these data sources.

The uneven distribution of seed BACs for chr 6 is of general concern. Although, some thirty-five seeds serve as islands from which the BAC walking is initiated, their relatively small number leaves unfavorable large oceans yet to be walked. This is suggested by genetic marker positions that are associated with these seeds (Table 2) and additional FISH experiments.

To further nucleate the oceans, we started FISH screening twenty-two additional candidate seed BACs in collaboration with Dr. Hans de Jong from the laboratory of Cytogenetics of the Wageningen University and Research Centre. We will FISH near genetic locations directed by associated marker positions as shown in the following table.

Table 2:

Candidate seed	Marker	Type	Chr 6 position
H003K02	TG178	RFLP	53 cM
H032F01	T1049	COS	72 cM
H044J22	T0805	COS	43 cM
H109C03	TG365	RFLP	56 cM
H155K09	T1500	COS	10 cM
H167M06	cLET-4-G23	EST	28 cM
H194N16	cLET-5-C8	EST	45 cM
H222I23	T1079	COS	27 cM
H246E15	T0798	COS	69 cM
H251G05	T1198	COS	5 cM
H261A18	cLET-4-G23	EST	28 cM
H267C16	T0244	COS	10 cM
H271F05	T1049	COS	72 cM
H271L05	TG178	RFLP	6 cM
H286N17	cLET-5-C8	EST	45 cM
H288L16	cLET-2-H1	EST	10 cM
H295L11	T0244	COS	10 cM
H301C21	T0834	COS	32 cM
H302A23	T0774	COS	18 cM
H307T13	T0834	COS	32 cM
H309D09	TG356	RFLP	56 cM
H309K01	cLET-5-A4	EST	10 cM
H310B09	T1556	COS	59 cM
H336O09	T1636	COS	5 cM

Chromosome 7 (France)

Contact: Farid Regad (regad@ensat.fr)

Update pending

Chromosome 8 (Japan)

Contact: Erika Asamizu (asamizu@kazusa.or.jp)

We finished sequencing thirty-one BACs and all sequences have been uploaded. We came to the conclusion that the finished clone HBa0076J13, which was selected because it was anchored to cLET-5-O24 on chr 8, actually locates to chr 3 by the results of FISH and fingerprint analyses. To date, we have produced 3,226,822 bp of non-redundant nucleotide sequence (excluding overlap and HBa0076J13 sequences). Currently, six BACs are being assembled, and nine of the fourteen new seed BACS, which were selected from the 3D DNA-pool, are in the sequencing pipeline.

Chromosome 9 (Spain)

Contact: Antonio Granell (agranell@ibmcp.upv.es)

Update pending

Chromosome 12 (Italy)

Contact: Mara Ercolano (ercolano@unina.it)

To date, sixteen seed BACs associated to eleven markers mapping on the short arm and five on the long arm of chr 12 have been selected for validation and sequencing. Four seed BAC sequences have been submitted to SGN. Four BACs were completed to phase 3 and an additional eight BACs are currently in phase 1 or 2. In order to identify new BACs to move out from finished seed BACs, BAC-end libraries were screened by BLASTn. Significant BLAST hits originated from the three BAC libraries. For each seed BAC, multiple hits ranged from one to six with an average of three hits. Good candidates were selected on the basis of the program Backend Extension v 0.1‰ complementary to the SGN Online BLAST Interface. The overlaps were confirmed by PCR and IL mapping. However, some difficulties were found with respect to minimal overlapping. A total of twenty-seven BACs are currently at different phases in the sequencing pipeline. The sequencing of seven BACs selected for extension has been completed to phase 1, four BAC clones are in the production phase, and verification of eight additional BACs is in progress.

WHAT'S NEW ON SGN?

(1) A user updatable gene database: The recently introduced Gene database with information on genes, alleles, phenotypes, literature, and sequence data can now be updated by SGN users. Every locus has an associated editor. To update a gene entry and become its editor, locate the gene detail page using the search, and click on the link "Request Editor Privileges". You will be assigned as the locus editor by SGN. Other users can still add new allele and synonym information. Newly created information is owned by the respective submitters. User updating of gene and plant ontology annotations will follow soon. For an example of a locus detail page, see http://sgn.cornell.edu/phenome/locus_display.pl?locus_id=428.

(2) BLAST-Watch: Submit a BLAST search to SGN that will be run every Sunday at midnight and you will be notified of newly matched sequences by email. To use BLAST-Watch, log in to SGN by clicking on the login link in the upper right corner of any page. There should be a link "submit sequence to BLAST Watch". This brings up the BLAST interface. Enter the sequence you would like to watch, adjust all parameters, and click on "submit".

(3) SolCyc Biochemical Databases have been created for tomato (LycoCyc), potato (PotatoCyc), pepper (CapCyc), and eggplant (SolaCyc) based on the Pathway Tools software from SRI International (http://bioinformatics.ai.sri.com/ptools/). Each database contains extensive information on compounds, enzymes, and pathways that can be browsed graphically and queried with text queries. The Omics viewer allows the overlay of expression and other data on a pathway overview diagram. In addition, comparative queries between species are possible. The SolCyc collection of pathway databases can be accessed at http://sgn.cornell.edu/tools/solcyc/.

(4) We have migrated to a new and much improved marker and map database, and improved the marker search and display. Please take a moment to look at the new interfaces available at http://sgn.cornell.edu/search/direct_search.pl?search=markers. The marker search page also features help tooltips and allows download of results as a text file.

(5) We computationally mapped BAC ends to the F2-2000 maps by BLASTing them against the marker sequences, resulting in an additional 290 anchor points for the physical map. The results are displayed on the F2-2000 map at http://sgn.cornell.edu/cview/map.pl=9&physical=1). In the diagram, the computational matches are shown as a red outline, and the experimental matches are in green. The raw results can be downloaded from the ftp site at ftp://ftp.sgn.cornell.edu/tomato_genome/physical_mapping/computational/.

(6) A database of in-situ images has been added and can be reached through the tools menu or the link http://sgn.cornell.edu/insitu/. The database can be updated by users with image add, delete, and annotation editing functions. The current images were generated by the floral genome project (FGP). For more information on FGP, visit http://floralgenome.org/ and http://pgn.cornell.edu/.

(7) A page describing the ECO-SOL (formerly SOL-ANDINO) project has been added. It can be accessed at http://sgn.cornell.edu/about/ecosol/ or a link on the SGN homepage.

The following new data is now available on SGN:

(1) A new tomato unigene build is available, including 53,000 new tomato ESTs provided by Daisuke Shibata, Eyal Fridman, Giovanni Giuliano, Bin Cong, and their colleagues.

(2) A total of 133 BAC sequences have been reported finished in the BAC registry database. Full-length sequences are available for ninety-two sequences with many more BACs in the pipeline.

(3) A total of forty-two BACs have been FISHed by Stephen Stack and colleagues. They are available from the tomato FISH map at http://sgn.cornell.edu/cview/map.pl?map_id=13.

Other changes:

o Note that the Genome Browser was moved from the Tools menu to the Sequencing menu.

ANNOUNCEMENTS

JOB OPPORTUNITY

POSTDOCTORAL RESEARCH POSITION
COLORADO STATE UNIVERSITY
FLUORESCENCE *IN SITU* HYBRIDIZATION IN SUPPORT OF THE INTERNATIONAL EFFORT TO SEQUENCE THE TOMATO GENOME

An NSF-funded postdoctoral position is available to do fluorescence *in situ* hybridization (FISH) in support of the international effort to sequence the tomato (*Solanum lycopersicum*) genome (see <http://www.sgn.cornell.edu>). For this project, we currently hybridize genomic DNA (inserts from a tomato BAC library) to pachytene chromosomes to keep the sequencing effort concentrated and properly oriented in euchromatin. In addition, we will do fiber-FISH to define the size of gaps between contigs.

Candidates should have a Ph.D. in genetics, biology, or a related field and a background in cytogenetics and molecular biology. Experience with plant chromosomes and FISH is desirable.

Applications will be accepted until the position is filled, but should be received by October 1, 2006 to receive full consideration.

The university is located in Fort Collins, Colorado, a beautiful city of 120,000 people located at the foot of the Rocky Mountains 60 miles north of Denver. The Rocky Mountain National Park and opportunities for hiking, skiing, and fishing are located nearby.

Colorado State University is an equal opportunity/affirmative action employer and complies with all federal and Colorado laws, regulations, and executive orders regarding affirmative action requirements. To assist the university in meeting its affirmative action responsibilities, ethnic minorities, women and other protected class members are encouraged to apply and to so identify themselves.

To apply, please send a letter of interest (including relevant experience), a current CV, and names and contact information for three references to:

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8th World Petunia Days
October 12-14, 2006
Jacksonville, Florida

The Environmental Horticulture Department and College of Agricultural and Life Sciences at The University of Florida welcome you to the Eighth World Petunia Days in Jacksonville Beach, Florida on October 12-14, 2006. This is the first time the World Petunia Days have been held in the United States, so it is our privilege to host WPD8 in sunny Florida! Details regarding registration, abstract submission, etc. can be found at http://hort.ifas.ufl.edu/petunia.

eusol

The kick-off meeting of the EU-SOL project will take place in Wageningen from November 21 – 22, 2006. For additional information, contact René Klein Lankhorst at rene.kleinlankhorst@wur.nl.

Plant Genomics European Meetings

October 11 – 14, 2006
Venice, Italy
www.plant-gems.org

INTERNATIONAL PLANT & ANIMAL GENOME CONFERENCE

Plant and Animal Genome XV Conference

January 13 – 17, 2007
Town and Country Convention Center
San Diego, California
http://www.intl-pag.org/

Vegetarian Fideuá

Contributed by: Marcos Egea-Cortines & Julia Weiss
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Introduction

I am convinced that there must have been an extremely strong negative selection against little babies and children that were fond of vegetables during our evolution as hunter-gatherers. Otherwise, you cannot explain their tenacious aversion against green stuff across cultures.

This recipe is an evolution of the traditional fideuá from the Levante Region in Spain. It improved our quality of life as postdocs, by downregulating tension during feeding bouts and turned out to become a winner when vegetarians visited us.

The rationale behind this recipe is that by blending vegetables into a cream and coloring the food with saffron, you can obtain impressive dishes in terms of taste, and kids will swallow it in ample quantities without trying to dissect the spaghetti to get rid of the sauce. They just cannot see the metabolomic part integrated into the dish-keeping carbohydrate matrix. Both baseline color obtained by saffron and the cooking procedure make it especially challenging for our dearest little ones in their curator tasks.

Fideuá is a version of the better-known Spanish paella (pallela for UK citizens), but is made with pasta. The noodles are going to be cooked in batch with the sauce that normally contains fish and other stuff. But this one as I said is vegetarian.

Concerning different materials, I have come to appreciate the Picual olive oil variety as especially good for these kinds of dishes, where you make a fried sauce from vegetables. Single variety olive oil is like single malt Scotch. Try it and you will know what I mean.

Materials for two grown-ups plus two F1's

-200 gr of mature red tomatoes
-150 gr of mature red peppers
-150 gr of eggplant
-2 garlic cloves- could be amplified
-1 tablespoon of sweet paprika
-4 tablespoons of Picual first press olive oil. If you cannot get it, go for high quality olive oil.
-1/4 teaspoon of saffron. You might find yellow food color based on turmeric. You get the color but don't get the taste.
-salt
-250 gr of noodles (10 minutes cooking time)
-500 mL of water (ratio of 2ml/gr pasta) or if you have it, use vegetable soup with bouquet garni (see Bocuse, Paul)
-Large shallow pan where you can get the whole thing to boil

Method

1. Put the vegetables into a blender and process them into a smooth cream.
2. In a large pan, put oil and vegetable mix, fry slowly and reduce to approx. 66% original volume.
3. Boil the water on a side pot, and add salt and saffron.
4. Add paprika powder to vegetable sauce, fry one more minute and add the pasta. Stir-fry the pasta with the vegetable cream for about 2 minutes till it is properly mixed.
5. Pour boiling water on the top of the pasta mixture and let boil open.
6. The pasta will be ready in about 13 minutes and it will absorb all the water and vegetable cream. Done this way, it should not get overcooked since like for paella this cooking method is a mixture of evaporation and water absorption by the matrix. It should have a general strong orange-reddish color that helps for the tiny bits of sauce that have not made it into the pasta to get by unnoticed…

Final comments

It might get slightly crispy on the bottom. If you like it crispy all over (kids love it) you can cook the whole thing in the oven, but you should use a shallow form that fits. In this case, just pour the boiling water/soup over the pasta coming from step 4 and incubate at 200-220 ºC for 12-15 minutes depending on the oven model.

I did not forget oregano or Parmesan cheese. This is not Italian pasta, it is a vegetarian version of fideuá. The real fideuá will have 250 gr of fresh tuna, 250 gr of sepia (squid), and the soup will be made with about 1 kgr of fish bones and leftovers sieved through cloth after an incubation at 100ºC for at least 2 hours. But that is another story…