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## Community News

### **The 2nd SOL-China Workshop Beijing, China May 23, 2007**

by Sanwen Huang

Institute of Vegetables and Flowers, Chinese Academy of Agricultural Sciences (IVF-CAAS)

Several events related to *Solanaceae* research have occurred since the 1<sup>st</sup> SOL-China workshop held in 2005 at IVF-CAAS. These events include the startup of the Tomato Cooperative Network (affiliated with the Chinese Society of Horticultural Sciences) and the initiation of sequencing tomato chr 3 and potato chr 10 and 11. In order to further promote solanaceous research and establish the *Solanaceae* community in China, the 2<sup>nd</sup> SOL-China Workshop was held on May 23, 2007 at IVF-CAAS. Participants included Prof. Dani Zamir and ten researchers from eight institutions in China.

After Dr. Rifei Sun, Deputy Director of IVF-CAAS, gave the opening remarks, Prof. Dani Zamir gave a plenary talk entitled "Introgression line resolution of complex traits in tomato". He briefly introduced the history and latest developments of the SOL project and systematically reviewed the outstanding investigation on dissecting quantitative traits using the *S. pennellii* introgression lines. Furthermore, he gave enthusiastic advice on how to define the scope of the SOL-China project and suggestions on how to build a strong SOL community in China.

Chinese scientists have been working on various aspects of solanaceous research. Dr. Eileen Ying Wang (Wuhan Botanical Garden, Chinese Academy of Sciences) presented her work on the genomics and genetics of two Chinese herbal medicinal plants, *Lycium* and *Epimedium*. Wencai Yang (China Agricultural University, CAU) introduced his research on identification of the intraspecific genetic variation of tomato and resistance breeding for bacterial spot disease. Guoping Wang (South China Agri. Univ.) reported on the development of SSR markers from tomato EST and BAC end sequences with a goal to develop 2,000 SSR markers in 2008 and to identify a set of highly polymorphic and evenly distributed SSRs for breeders. Junhong Zhang (from Zhibiao Ye's lab in Huazhong Agri. Univ.) shared their exciting progress in the cloning of genes related in abiotic/biotic stress in tomato. Guoyong Jiang (Qingdao Agri. Univ.) reviewed his study on Tm-2<sup>2</sup> anti-viral specificity and interaction with ToMV-MP in transgenic tobacco. He also works on marker-free transformation of tomato. Zhengguo Li (Chongqing Univ.) reported his work on the mechanism of plant hormones in the process of fruit ripening. His lab plans to develop 10,000 mutants using activation tagging. Yanmei Guo (IVF-CAAS) presented the progress on cultivar development, especially on molecular breeding for high lycopene content. Sanwen Huang (IVF-CAAS) presented the progress of seed BAC sequencing of potato chr 10 and 11. Eleven BACs have been sequenced to the 2<sup>nd</sup> phase and *in silico* mapped to the expected positions, which confirmed the quality of the integrated genetic and physical map of potato using the AFLP technique. Comparative sequencing of two BACs from the *nor*

gene region of tomato and potato indicated parallel sequencing in tomato and potato can facilitate assembly and gap filling. Weiwei Jin (China Agri. Univ., CAU) and Yang Gao (Beijing Genomics Institute, BGI) demonstrated the great potential for using their FISH and Hapmap platforms in future sequencing and genetics programs of the SOL-China project, respectively. In addition to the studies of all the participants, the work of other Chinese scientists involved in solanaceous research was discussed. These scientists included Chuanyou Li, Hongqing Ling, and Conghua Xie.

Dr. Yongchen Du (DG of IVF-CAAS) hosted the closing dinner and showed strong support for the SOL-China project while discussion continued during and after the dinner.

The conclusions of the workshop were:

- 1) SOL-China will set up a steering committee and convene a scientific advisory board of international and national leaders.
- 2) SOL-China will identify cutting edge opportunities in *Solanaceae* research to better meet the needs of agriculture and biology in China.
- 3) SOL-China will arrange a meeting with speakers from the other SOL projects in 2008.



## The African Leafy *Solanaceae* Vegetables with a Potential to be Exploited

By Mary O. Abukutsa-Onyango  
Maseno University, Kenya



**Figure 1:** *Solanum scabrum* (most promising African vegetable nightshade).

For many of the popular *Solanaceae* vegetables known and consumed in many parts of the world, it is the fruit that is normally consumed and rarely the leaves. In Africa, there is a group of *Solanaceae* vegetables whose leaves have been consumed for many centuries by communities on this continent ranging from West, Central, East, and Southern Africa. This group of leafy vegetables has recently been grouped as the African vegetable nightshades, which for a long time have been confused with the deadly nightshade (*Solanum nigrum*). The vegetable nightshades, whose leaves are normally cooked and consumed traditionally by the African people, include the following species: *Solanum scabrum* (Fig. 1), *Solanum americanum* (Fig. 2), and *Solanum villosum* (Fig. 3). Vegetable nightshades are currently widely consumed in Eastern, West, and Central Africa where they have been earmarked for promotion through research and

development due to their potential to confer nutritional and economic benefits to marginal and nutritionally vulnerable populations. *Solanum scabrum*, popularly known as broad-leafed African nightshade, normally has ovate leaves with large purple berries and it is not bitter. *Solanum villosum*, common in Eastern Africa, has lanceolate leaves with small orange colored berries and *Solanum americanum* has lanceolate leaves, but the berries are small, black in color and shiny.

Traditionally in Africa, vegetable nightshades were collected from the wild, but as their domestication progressed, nightshades have come to be increasingly cultivated in small kitchen gardens for domestic use and sale in markets. Their leaves provide a useful green vegetable that is consumed after boiling. Of the three species, *Solanum scabrum* is the most promising and preferred by consumers probably due to its larger leaves that result in higher leaf yields compared to the other two species. The broad-leafed scabrum also has a much-liked and good unique flavor.

In East Africa, the demand for the broad-leafed vegetable nightshade has increased tremendously and the crop has found its way to the major food stores in the region. In order to meet the increasing demand of this vegetable, there is a need to develop production packages to increase the yield and total production not only for local consumption, but also for export. A number of initiatives have been established to promote the production and consumption of vegetable nightshades in Kenya in particular and in Africa at large. Some of these initiatives include: the International Plant



**Figure 2:** *Solanum americanum*

Genetic Resources Institute (IPGRI) African Leafy Vegetables Program funded from 2002 - 2005 that included Kenya, Tanzania, South Africa, Zambia, Cameroon, and Senegal; the SIDA-SAREC project funded in three East African countries (Kenya, Uganda, and Tanzania) from 2004 - 2008; and the EU project "IndigenoVeg" funded from 2006 - 2008.



**Figure 3:** *Solanum villosum*

Despite what is already in place, there is still a lot yet to be done in terms of research to be able to develop the African vegetable nightshades into commercial crops. If they are promoted, they can play a major role in alleviating poverty in Africa because they can be consumed by everyone and have a high nutritional value in addition to medicinal properties. We need support and your indulgence to promote the vegetable nightshades that are **NOT deadly**.

**Contact Information**

Prof. Mary O. Abukutsa Onyango (PhD)  
 Department of Botany and Horticulture  
 Maseno University  
 P.O Private Bag - 40105  
 Maseno - KENYA

Tel: +254-57-351620/2  
 Cell: +254 722 676907  
 Email: mabukutsa@yahoo.com,  
 abukutsa@maseno.ac.ke  
 Fax: +254-57-351221 / 351153

*Note from Joyce Van Eck:* It would be good to have more representation of *Solanaceae* researchers from Africa in our SOL community. One place to start would be for any of you who collaborate with someone in Africa to send e-mail addresses to me (jv27@cornell.edu), and I can add them to the newsletter list.

**Tomato Sequencing Updates**



**Chromosomes 1, 10, 11 (US)**

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

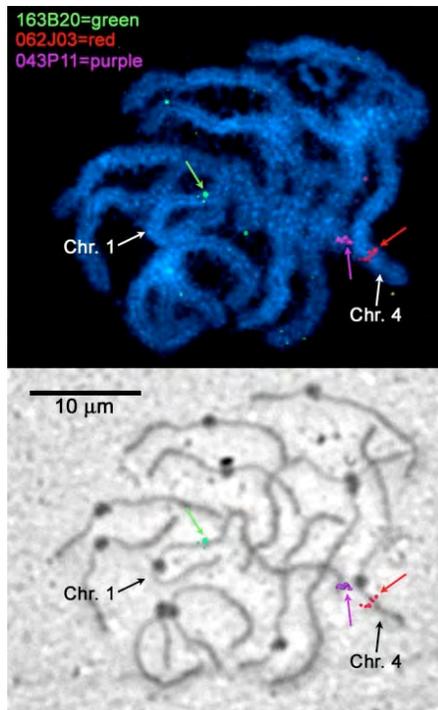
We completed the overgo hybridizations on the MboI filters for the marker sets (ten – twenty markers per set) sent from India, the Netherlands, France, Japan, and Spain. These hybridizations were done in an effort to generate additional sequencing resources.

Last month, we sent 1,000 fosmid ends for sequencing to obtain preliminary information on the potential utility of the fosmid library. Sequence information will be available soon.

The Stack lab at Colorado State University has localized an additional ten BAC clones using fluorescence in situ hybridization (FISH), bringing the total number of clones that we have positioned on tomato chromosomes to ninety-two. The recently positioned BACs include:

Chromosome Arm	BAC ID
1Q	LE_HBa0163B20
	LE_HBa0043P11
3Q	LE_HBa0031P17
4P	LE_HBa0062J03
4Q	LE_HBa0208L16
	LE_HBa0171B19
	LE_HBa0094K06
5P	LE_HBa0298C03
7Q	LE_HBa0059P18
	LE_HBa0082D04

same arm. The red signal for LE\_HBa0062J03 (red arrows) lies within the heterochromatin near the eu-/heterochromatin border on the short arm of chr 4.



**Figure 1:** FISH labeling with two BACs on chr1 and one on chr 4 in fluorescence (upper) and phase (lower) images of tomato SC spread.

FISH labeling with two BACs on chr 1 and one on chr 4 is illustrated in the fluorescence and phase images of a tomato SC spread (Fig. 1). The fluorescent signals have been superimposed on the phase image to illustrate their positions on the chromosomes. The green signal for LE\_HBa0163B20 (green arrows) is located at the eu-/heterochromatin border on the long arm of chr 1, and the purple signal for LE\_HBa0043P11 (purple arrows) is located near the end of the

## **Chromosome 2 (Korea)**

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

As stated in our previous report, when we have accumulated more and more BAC sequences, we are facing some segmental duplication on the specific areas, which eventually interfere with BAC extension. At some point we stopped BAC extension and are waiting for more finished BAC sequences. Currently, we have finished nine additional BAC clones (total 118 BACs). In addition, sixteen BACs are in the sequencing pipeline. I also want to mention that we are using IL mapping for selection of our next BAC clones.

## **Chromosome 3 (China)**

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

Update pending.

## **Chromosome 4 (UK)**

Contact: Karen McLaren (kb1@sanger.ac.uk) or Helen Beasley (hr1@sanger.ac.uk)

9,908,019 bp of sequence have been generated at the Wellcome Trust Sanger Institute for chr 4 as of June 25<sup>th</sup>, 2007. Of this figure, 9,760,982 bp are unique. The sequence has been produced from eighty-two BACS originating from the LE\_HBa and SL\_MboI libraries. We intend to finish all BACS that will contribute to chr 4 to HTGS phase 3 and currently fifty-four BACs that correspond to 6,051,651 bp of sequence have been deposited in the public databases at EMBL/GenBank/DDBJ as phase 3. All other chr 4 BACs with EMBL/GenBank/DDBJ accessions are currently active in our sequencing pipeline at HTGS phases 0 to 2.

## **Chromosome 5 (India)**

Contact: Akhilesh Tyagi (akhilesh@genomeindia.org)

The Indian Initiative on Tomato Genome Sequencing is currently working on fifty BAC clones from chr 5. Eleven BAC clones have reached Phase III level of sequencing, while twenty and eight BAC clones are at Phase II and Phase I, respectively. Eleven BAC clones are in the early phase of sequencing. We have received overgo results on MboI filters for the entire set of twenty markers that we sent to the Cornell group, which has enabled us to pick BACs on new nucleation points. Some of these BACs are already in the sequencing pipeline while others are in the screening process to confirm their position on chr 5 using the Introgression Lines. In addition, certain BACs sequenced to different levels have been found to be redundant in the MTP or have been confirmed on other chromosomes using Introgression Lines and/or FISH data. Screening for more BACs on new markers as well as a search for extension BACs on BACs that are already being sequenced is in progress by performing overgo hybridizations on the filters available for the three tomato libraries.

## **Chromosome 6 (The Netherlands)**

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

BACs H215M16, H059D21, H086B01, and E129O21 have been closed. H023B17, H040F08 have been FISHed on chr 6 and identified as seed BACs for extension BAC walking. These BACs have entered the sequencing and finishing pipeline together with extension BACs H015I15, H020O17, H049I02, H066D13, H095I22, H116O16, H218N05, H221G10, E014B21, E039G15, M022H01, M047K24, M060G16, M067G18, M074G21, M115P13, M135H21, and M142B16. In addition, we are

currently fishing twelve candidate seed BACs. Seven BACs have been found by the new overgo screens done by Cornell and five BACs have been selected from the latest Syngenta FPC build. A rough gap size estimate on the short and long arm has been made. The short arm gap at the 0 - 3 cM region is estimated to be 500 - 1000 kb. Currently, we are fishing five additional BACs that have a plausible match with markers T1928 (0 cM) and CT216 (0 cM) in order to produce a start position for extension walking north of the short arm gap. Furthermore, three gaps on the long arm were identified based on a pooled BAC experiment for which thirty-five seeds were used, as reported in issue number 11 of the SOL Newsletter. Based on this experiment, the gaps are estimated to be 1500 - 2000 kb each. A new pooled BAC experiment is planned to determine whether seed and extension BACs have filled these long arm gaps in addition to the original set of thirty-five seed BACs.

## **Chromosome 7 (France)**

Contact: Farid Regad (regad@ensat.fr)

Four new BACs are in the sequencing pipeline: LE\_HBa0040A11, LE\_HBa0162L12, LE\_HBa0025K09, LE\_HBa0028J09. Five BACs have been completed: LE\_HBa0103N02, LE\_HBa0006H17, LE\_HBa0012N15, LE\_HBa0114J16, SL\_EcoRIO020F06. Twelve BACs are in phase 3 and will be submitted to GenBank.

Moreover, four BACs have been FISH localized on chr 7 (data from Steve Stack's lab): LE\_HBa0111F22--94.3% +/- 1.5% on 7P (in euchromatin), LE\_HBa0095C18--98.5% +/- 2.0% on 7P (near telomere), LE\_HBa0082D04--15.4% +/- 1.9% on 7Q (in heterochromatin), LE\_HBa0188B22--29.9% +/- 2.0% on 7Q (in heterochromatin, not far from border).

## **Chromosome 8 (Japan)**

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

We finished sixty-five clones to Phase 3 (total non-overlapping length 6,749,334 bp). In our effort to develop new EST SSR-derived microsatellite markers to map them on the EXPEN-2000 genetic map, we have so far mapped 220 markers successfully. For markers newly mapped on chr8, PCR screening of the BAC DNA pool is being performed to find corresponding BACs. We are expecting to obtain up to fifty additional seed points on chr 8 for the sequencing.

Shotgun sequencing of the selected low-copy BACs is in progress, and we have already generated 580,000 reads producing 420 Mb in length.

## **Chromosome 9 (Spain)**

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

Since the last sequencing report to the SOL Newsletter, we have made some progress concerning the number of finished BACs (from thirty-one to thirty-eight) and now have seventeen in progress. Out of the thirty-eight finished ones, nineteen are seed BACs and nineteen are extension BACs. Out of the seventeen BACs in progress, nine are seed BACs and eight are extension BACs. Currently, only two are in the process of verification of the amount of overlapping in the case of two extension points. That is, extension continues to be a problem. Indeed, most of our progress in the last two months comes as the result of incorporating new seed BACs to the sequencing pipeline. These new BACS came from the

in silico study against the BAC end sequence (BES) database, FPC from Syngenta, new markers from Syngenta, and overgo hybridizations conducted for us by the group at Cornell.

From the "in silico" study carried out by Cornell, we had initially selected seven seed BACs, which we reported in the latest SOL Newsletter. We have received the results of FISH from Hans de Jong for the three BACs where the marker was detected but no polymorphism was detected between *S. lycopersicum* and *S. pennellii*, therefore the ILs approach was not possible. Two of them were confirmed and mapped to chr 9 and therefore selected as seed BACs. They are currently in the sequencing pipeline. The other one is not on chr 9 (Fig. 2).

From the overgo hybridizations conducted at Cornell, we received a list of BACs for ten markers, but we could only confirm a BAC-marker association in two cases. They were localized on chr 9 by sequencing the corresponding allelic variant in the ILs spanning chr 9 regions. One of them was finally discarded (the one located at 9 cM) because upon sequencing of its BES we could see that it overlaps almost completely with BACs recently sequenced that extended from a seed BAC located at 11 cM. The Cornell group conducted additional overgo hybridizations for chr 9, and we recently received new candidates.

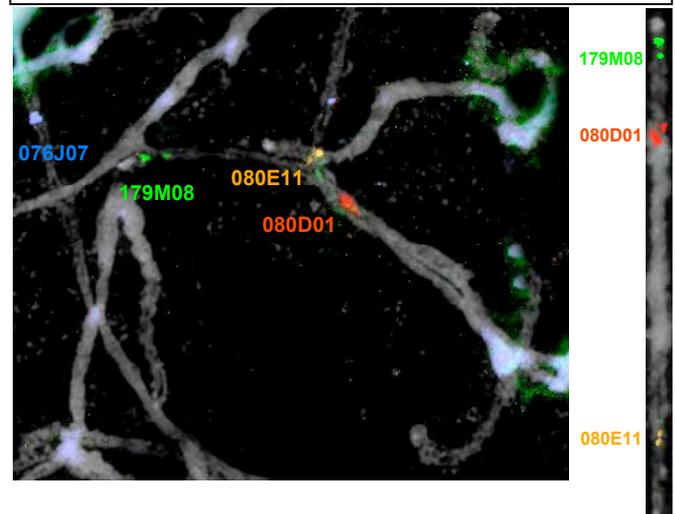
We were not able to select many markers from the information provided by Syngenta, including from the FPC. We have conducted PCR analysis for eleven markers and found the markers in the corresponding BACs, but only two seed BACs were confirmed by polymorphism in the ILs. We are currently PCR amplifying another region to see if we are able to detect polymorphism in the ILs. In case we fail, we will send them for FISH.

We have clearly identified the euchromatic-heterochromatic borders for both arms of chr 9. The one corresponding to the long arm was defined with a BAC sent for FISH by the Italian group that ended up on chr 9. We have recently received the FISH localization from Hans de Jong corresponding to a sequenced BAC where several repeats and Ty3 sequences (normally found in regions close to the centromere) were identified. FISH confirmed it is

located in the euchromatin-heterochromatin transition on the short arm (Fig. 2).

We are currently searching for additional seed BACs for chr 9 by PCR using BAC pools. We will also use this strategy for the BES for our "dead" ends (BACs we cannot extend from).

**Fig. 2:** BACs localized by FISH.



### **Chromosome 12 (Italy)**

Contact: Mara Ercolano ([ercolano@unina.it](mailto:ercolano@unina.it))

Currently, sixty-four BACs of chr 12 originating from the LE\_HBa, SL\_EcoRI and SL\_MboI libraries are in different stages of the sequencing pipeline. Fifteen contigs using the sequences of forty-eight BACs have been established. Some difficulties were encountered in selection of extending BAC clones as in some cases candidates match large parts of their sequence with the anchoring BAC. We are also focusing on filling large chr 12 gaps by selecting new SGN seed BACs and confirming BACs from the Syngenta initiative. Ten new SGN seed BACs were validated and fifty-one Syngenta candidate BACs have been confirmed by BAC-end sequencing. The chromosome location of these clones will be verified by IL mapping.

## **Announcements**

### **Jobs**

#### **Post-doctoral Researcher at the Max-Planck-Institute of Molecular Plant Physiology in Potsdam**

The Max-Planck-Institute of Molecular Plant Physiology in Potsdam invites applications for a Post-doctoral researcher to study metabolic pathways underlying tomato fruit quality. The position forms part of a DFG funded tri-national project with the Zamir group in Israel and the Ghareeb and Sayed groups in Palestine. The aim of the project is to evaluate the complex relationship between genetic factors, tolerance to irrigation stress in the field, and fruit quality. It is hoped that it will ultimately comprise of both fundamental and applied research with attention for the later being placed on post-harvest physiology and processing aspects.

Applicants should have a PhD in Biology, Biochemistry or Chemistry with a strong background in biochemistry and interest in bioinformatics. Candidates with experience in metabolite profiling and or genetics will be preferred.

For further information, please contact Dr. Alisdair Fernie, phone: +49 331 5678211, e-mail: [fernie@mpimp-golm.mpg.de](mailto:fernie@mpimp-golm.mpg.de).

Applications including cover letter, curriculum vitae, and the names of two referees should be sent by August 1st, to:

Max-Planck-Institut für Molekulare Pflanzenphysiologie  
Personalverwaltung  
Wissenschaftspark Golm, Am Mühlenberg 1, 14476 Potsdam

## Conferences



### **The 4<sup>th</sup> Solanaceae Genome Workshop**

September 9 – 13, 2007

Ramada Plaza, Jeju Island, Korea

Early registration deadline - July 31, 2007

<http://www.solanaceae2007.org/board/index.php>

#### **Announcement from the organizing committee:**

Dear Participants of SOL2007:

We are sorry for the inconvenience on the online registration and abstract submission for the SOL2007. There were unexpected security problems (fire wall) in our web server. Few days ago, we moved our home page to a new server, which operated independently of the original server with the same web address (<<http://solanaceae2007.org>><http://solanaceae2007.org>).

We also extended the deadline for abstracts submission until July 31, 2007. Now both abstract and registration deadlines are July 31, 2007.

On the matter of hotel reservation, we had a good deal with the Ramada Plaza Jeju (the original prices are about 300 USD/night). The conference prices will be applied to whom reserve before July 31, 2007 through our home page. We blocked around 150 rooms until sold and the block will be released on the 1st of August. Please be hurry for your hotel reservation.

If there are any troubles in the abstract submission or registration, please let us know (mail to Prof. Doil Choi, [doil@snu.ac.kr](mailto:doil@snu.ac.kr)).



### **9<sup>th</sup> World Petunia Days**

October 28 – 31, 2007

Amsterdam, The Netherlands

<http://www.petuniaplatform.net/index.php?page=activities>

### **2007 Tomato Breeders Roundtable**

November 4 - 7, 2007

Nittany Lion Inn

200 West Park Ave, State College, PA, USA

<http://tomatoroundtable07.psu.edu>



## SOL2008

The following is from an e-mail sent by the local organizing committee for SOL2008:

Dear Colleagues in the Solanaceae Research Community,

It is our pleasure to announce that the **Max-Planck-Institute for Plant Breeding Research** (MPIZ), Cologne, Germany, will organize in collaboration with Phytowelt GreenTechnologies GmbH (sender) the 5th Solanaceae Genome Conference (**SOL2008**) from **October 11 to 16, 2008** in **Cologne, Germany**. Cologne is a beautiful and lively city located at the river Rhine in the mid West of Germany, with lots of things to do and to see, with two airports nearby and fast train connections. We cordially invite you to visit us next year and experience an excellent conference with an attractive and stimulating scientific and social program. Please mark this date in your agenda for 2008. Further details concerning this conference will be published in due time on the MPIZ website.

The local organizing committee, represented by:  
Christiane Gebhardt (gebhardt@mpiz-koeln.mpg.de)  
(member of the SOL steering committee)  
MPIZ, Cologne

PS: Please note that the original plan to hold SOL2008 in Latin America had to be abandoned and therefore the conference was moved to Germany.

### Request for Solanaceae Images

The SOL Genomics Network (SGN; [sgn.cornell.edu](http://sgn.cornell.edu)) posts *Solanaceae* images on their homepage. They like to change them periodically and are in need of more images. If you have any *Solanaceae* images that you would like to contribute to SGN, send them to Lukas Mueller at [lam87@cornell.edu](mailto:lam87@cornell.edu).



### Solanaceae Recipes

## Chicken, Eggplant, and Tomato Curry

From <http://www.cookinglight.com>

### Ingredients

1 tablespoon curry powder	1 2/3 cups thinly sliced onion
1 teaspoon salt	1 1/2 cups (1/4-inch-thick) slices green bell pepper
1 teaspoon paprika	3/4 cup tomato juice
8 (4-ounce) skinless, boneless chicken breast halves	1 teaspoon crushed red pepper
3 teaspoons olive oil, divided	1 garlic clove, minced
5 cups coarsely chopped eggplant (about 1 pound)	4 cups hot cooked rice

### Preparation

Combine curry powder, salt, and paprika in a shallow dish. Dredge chicken breast in the curry mixture.

Heat 1 1/2 teaspoons oil in a large nonstick skillet over medium heat. Add half of chicken; cook 5 minutes on each side or until browned. Remove chicken from pan. Repeat procedure with remaining 1 1/2 teaspoons oil and chicken.

Add eggplant, onion, and bell pepper to pan; cook 3 minutes or until vegetables are crisp-tender, stirring frequently. Return chicken to pan. Add tomato juice, red pepper, and garlic; bring to a boil. Cover, reduce heat, and simmer 35 minutes or until chicken is done. Serve with rice.

### Yield

8 servings (serving size: 1 chicken breast half, about 1/3 cup vegetables, and 1/2 cup rice)