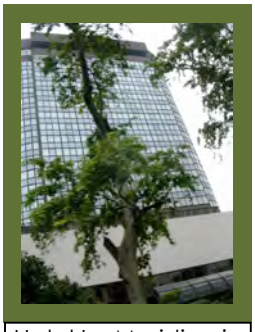
March 2009
Issue Number:22
Editor: Joyce Van Eck

The Sol Newsletter

In this issue.....

Community News

Invitation to the Sixth Solanaceae Genome Workshop, November 2009



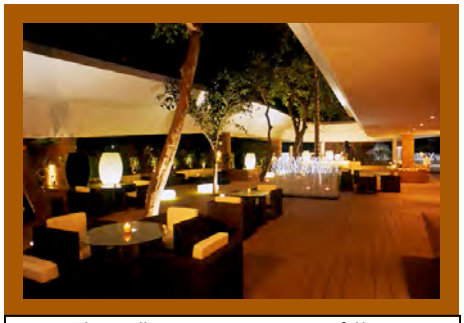
Hotel Le Meridien in New Delhi, India

After a lively SOL 2008 in Cologne, Germany, it is time for all of us to gear towards the next SOL meeting in 2009. The SOL 2009, as we announced at Cologne, will be held at the Hotel Le Meridien in New Delhi, India, from November 8 - 13, 2009. As in past years, SOL 2009 will bring together a spectrum of scientists working on different aspects of the Solanaceae ranging from biodiversity, genetics, plant-pathogen interactions, genomics and bioinformatics. SOL 2009 will be a forum to discuss and present new information generated by the study of Solanaceae species, including progress in the sequencing of various Solanaceae genomes. The conference will also provide a forum for us to sit together and create a roadmap for the future. The official SOL 2009 website (http://www.sol2009.org) will provide you with up-to-date information as the workshop approaches. The website will enable you to register for the workshop, submit an abstract, get information about hotel accommodations and information for pre/post conference tours in India.

November is the best season to visit New Delhi as well as the rest of the country. This time of the year brings greenery on the face of New Delhi, and you can expect plenty of sunny weather, fairly low levels of rainfall and pleasant temperatures. We look forward to seeing you all in New Delhi in November 2009.

Don't hesitate to contact us at sol2009.sharma@gmail.com.

Rameshwar Sharma, Jiten Khurana and Renu Swarup, SOL 2009 Co-chairs.



The Allure open area of the Hotel Le Meridien

Completion of a Genetic Map of Pepper

Provided by Charles Pick

DNA LandMarks announced its collaboration with Cornell University, New York, on the release of its new genetic map in pepper. For its part in the collaboration, DNA LandMarks contributed a series of key genetic markers including DNA primer sequences and assay conditions that allowed the map to be anchored.

"This is the first complete genetic map of the pepper genome based on a set of common genes shared by tomato, potato, eggplant and other species in the nightshade family, as well as the model plant *Arabidopsis thaliana*," commented Prof. Steve Tanksley of Cornell University, "The availability of this map should facilitate both applied and basic research in pepper".

"This collaborative endeavor will help molecular scientists and plant breeders around the world to be more successful", stated Dr. Joachim Richert, CEO of DNA LandMarks "A reliable, well-anchored genetic map is the foundation for effective marker-assisted breeding in any crop."

The genetic map, the key markers and primer sequences will be publicly available at http://www.sgn.cornell.edu/cview/map.pl?map_version_id=58.

The two organizations started the collaboration five years ago when DNA LandMarks shared its library of DNA markers in pepper to support the effort of Cornell University to create a genetic map of this important vegetable crop.

For additional information contact: Charles Pick, MBA, Business Development Manager – charles.pick@dnalandmarks.ca.

The Netherlands and India to Sequence on the *Solanum pennellii* IL

by René Klein Lankhorst

The Dutch Centre for Biosystems Genomics (CBSG) together with the National Institute for Plant Genome Research in Delhi, India have received a grant from the Netherlands Organization for Scientific Research (NWO) to start a joint research project.

In this project, expertise in the field of plant sequencing, bioinformatics, comparative genomics, introgression breeding and crop improvement will be brought together in order to study introgression of wild tomato DNA within the genome of the cultivated tomato (*S. lycopersicum*). Introgression breeding has proved to be one of the most important tools that plant breeders have to improve cultivated tomato. However, a detailed molecular analysis of this fundamental process has never been performed and the underlying sequence-level mechanisms are therefore still largely unknown. Tomato is one of the most popular vegetables in India. The major reason for yield and storage loss of tomato in India is due to fungal infection. The tropical environment of the country aggravates this problem. A rigorous effort has been underway for years to clone the QTL for fungal disease resistance and to introgress that from the wild species to the cultivated varieties, but has had little success.

With the onset of next generation sequencing technologies, it is now feasible to use DNA sequencing to address key questions in introgression breeding. In the project, a draft sequence of the genomes of the two parents of the well-studied introgression line population, *S. lycopersicum* M82 and *S. pennellii* LA716, and the draft sequence of one offspring line expressing QTLs for quality traits will be determined. The comparative bioinformatic analyses of the parents and of the offspring will yield novel insights in the molecular mechanisms underlying introgression in plants in general. In addition, practical information will be gained, like novel SNPs, which can be used directly to introduce QTLs from *S. pennellii* into cultivated tomato. Also, this research will expedite the molecular cloning of genes underlying quality traits in *S. pennellii*.

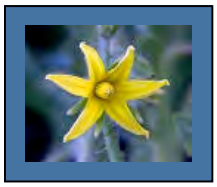
The research project will be carried out in the form of a sandwich PhD program involving 2 PhD students, one supervised by Prof. Akhilesh K. Tyagi and Dr. Debasis Chattopadhyay, and 1 supervised by Dr. Roeland van Ham and Dr. René Klein Lankhorst.

FAO Releases Book on the 'Humble Tuber'

from CropBiotech Net
(http://www.isaaa.org/kc)

The United Nations Food and Agriculture Organization (FAO) has released *New Light on a Hidden Treasure*, a 144-page illustrated book which records the achievements of the International Year of the Potato and underscores its essential message: that the potato is a vital part of the global food system, and will play an ever greater role in strengthening world food security and alleviating poverty. The review also provides the most recent FAO statistics on world potato production and consumption, and profiles of fifty-two major potato-producing countries.

The book is available in Arabic, Chinese, English, French, Russian and Spanish editions at http://www.potato2008.org/en/events/book.html.

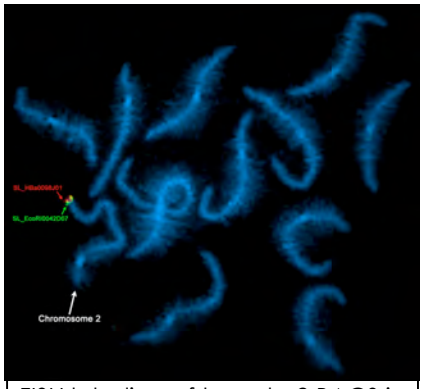



Tomato Sequencing Updates

Chromosomes 1, 10 (US)

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

Recently, the Stack lab at Colorado State University has been engaged in determining the limit of resolution for FISH labeling of tomato pachytene synaptonemal complex (SC) spreads and obtaining an updated estimate of DNA density (megabases per micrometer) along the chromosomes in these preparations. This project has involved performing FISH experiments using probes prepared from BACs contained within a large contig on the long arm of chr2. This contig was sequenced by Korea and the BACs were provided by Sunghwan Jo. Data are currently being analyzed and will be available soon on SGN. The fluorescence micrograph below shows an SC spread with FISH labeling of two such BACs (indicated by red and green arrows) in this contig on chr2. These BACs are separated by approximately 198 kb.



FISH labeling of two chr 2 BACS in a contig on a tomato pachytene synaptonemal complex spread.

Chromosome 2 (Korea)

Contact: Sunghwan Jo (shjo@kribb.re.kr)

To date, 181 BAC clones (20,202,853 bp) whose positions were confirmed on chr2 have been sequenced. 167 BAC clones were completed as HTGS phase 3 and fourteen were completed as HTGS phase 1. Due to the limitation of finding extension BACs, we will not persist in the minimum tiling path for extending the contig size. We examined fosmid end sequences (FES) on SGN and Selected BAC Mixture (SBM) shotgun data (from Dr. Sato, KAZUSA) for walking forward from contig ends. The markers not applied in sequencing yet were also examined, including SSR markers (KAZUSA) and Syngenta markers. We chose ninety-six fosmid clones and seventy-three BACs and ordered the ninety-six fosmid clones from Dr. Giovannoni. We will determine the sequence with GS FLX Titanium after making a pool. Although many of the clones are redundant, we expect that the sequences will serve as a bridge for searching for the next clones. We will continue searching syntenic regions of other reference genomes for the gap closing of chr2.

Chromosome 3 (China)

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

Update pending.

Chromosome 4 (UK)

Contact: Gerard Bishop (g.bishop@imperial.ac.uk)

Since the transfer of sequencing activities from Wellcome Trust Sanger Inst. to Imperial College, we have been focusing on ensuring that all BACs in the AGP and TPF files are on chr4. We have generated new TPF and AGP files in which 127 BACs are now on chr4, verified either by 1) FISH data; 2) presence of a chr4 marker sequence; 3) IL-mapping data; or 4) by having contiguous sequence with a BAC that has been mapped using at least one of the previous three methods. In summary, we now have 123 HTGS3 BACs on chr4 AGP and have placed approximately fifty-eight BACs to chr0, seventeen of which are definitely on chr0 based on IL mapping results.

The following BACs are likely to be on the respective chromosomes due to the presence of the appropriate markers. LE_HBa0203P08.1 on chr2 (two markers and information from Sunghwan Jo); LE_HBa-34P15 on chr5 (two markers); LE_HBa-244P17 on chr5 (three markers).

There is a possibility that certain BACs placed on chr0 will return to chr4 as they were selected to be in a chr4 FPC contig. However, as our IL mapping was suggesting that many were not on chr4, and in case other groups find that they extend into these BACs, we felt it more useful to the community to place these on chr0.

Our current focus is to use the 3D BAC pools to isolate BACs for the approximately seventy-seven chr4 markers for which we do not have a BAC.

We are also exploring how the potato chr4 genome sequencing project can inform BAC selection for the tomato project and vice versa. More details of the outcome from this work will be in our next update.

Chromosome 5 (India)

Contact: Akhilesh Tyagi (akhilesh@genomeindia.org)

At the Indian Initiative on Tomato Genome Sequencing, we have confirmed the positions of eighty-five BACs on chr5. Sequencing is in progress on all these BACs, out of which forty-two BACs are in phase III, twenty-two are in phase II and fourteen are in phase I. The remaining seven BACs are either in the early phase of sequencing or library preparation. A search is on to find new extension BACs by performing overgo hybridizations on the filters available for the three tomato libraries, PCR screening on the 3-D DNA pools of the HindIII and MboI BAC libraries, analysis of the fosmid end sequences and SBM (Selected BAC Mixture) shotgun data. In addition, new nucleation points are also being identified by developing CAPS markers for the 200 BACs assigned to India for mapping purposes.

Chromosome 6 (The Netherlands)
Contact: Sander Peters (sander.peters@wur.nl)

Please see the Next Gen Initiative Update following the chromosome updates.

Chromosome 7 (France)
Contact: Murielle Philippot (murielle.philippot@ensat.fr)

To date, 174 BACs and seven fosmids have been selected and validated on chr7. Among these there are ninety "seed BACs" and ninety-two overlapping BACs and fosmids. 106 BACs have been sequenced to phase 2 or 3 and seventy-five are in phase 0 or 1. In the last period, we exclusively obtained BAC sequences using the NextGen 454 sequencing method (GS-FLX using Long Paired End Tag reads and Multiplex Identifiers /MIDs). We submitted a total of 135 BAC sequences anchored to chr7 and three BACs allocated to chr0 to Genbank and SGN.

Overall, 17.7 Mb of sequences were generated of which 14.7 Mb are non-redundant (55% of the total estimated euchromatin of chr7). The BACs are organized in forty-one contigs on chr7. Our largest contig contains nineteen BAC members and covers 1.75 Mb. It is situated in the distal portion of the long arm of chr7 and is covering a genetic distance of 22.5 cM. We continue to join megacontigs of BACs, and the last one we obtained covers 58 - 68 cM. It contains nine BAC members and is 780 kb long.

Chromosome 8 (Japan)
Contact: Shusei Sato (ssato@kazusa.or.jp)

As of February 20, 2009, 177 BAC clones (101% of initial target) have been completed as Phase 3 that produced a non-redundant length of 17,465,737 bp, and an additional eleven BAC clones are in the sequencing pipeline.

We are continuing the accumulation of Selected BAC Mixture (SBM) shotgun data, which reached 3.7 million files generating 2.1 Gb of total length. These shotgun sequences have been assembled into 205,091 contigs covering approximately 580 Mb regions of the genome.

Chromosome 9 (Spain)
Contact: Antonio Granell (agranell@ibmcp.upv.es)

Several strategies have been used to overcome the initial lack of seed and extension BACs. New seed BACs came from computational association BAC end-anchor markers, Syngenta data (FPC and markers), new overgo hybridizations done by the Tanksley group at Cornell Univ. (MboI library), Kazusa Institute markers, Italian group mapping, etc. The success of the various strategies tested has been limited: thirty-eight seed BACs have been extended by fifty-five extension clones, forty-five BACs, and ten fosmids.

The present status of the sequencing covers a total of 8.9 Mb, which corresponds to 56% of the chr9 euchromatin. Currently, additional extension BACs are being pooled for 454 sequencing.

Chromosome 11 (China)
Contact: Zhonghua Zhang (zhangzh.ivf@caas.net.cn) or Sanwen Huang (huangsanwen@caas.net.cn)
Update pending.

Chromosome 12 (Italy)
Contact: Mara Ercolano (ercolanao@unina.it)

Currently, eighty-six BACs belonging to chr12 are in various steps of the sequencing process. Of these, twenty-three are in HTGS3, fourteen are in HTGS2, and twenty-one are in HTGS1 and have been submitted to GenBank/SGN. In order to identify new sequencing starting points, forty-five free markers (SSR markers provided by the Japanese member of the sequencing consortium and other markers that were found in the SGN repository) have been IL-verified to map in chr12. We are proceeding with FISH, both to map seed BACs and some BACs that are probably located close to telomeres but cannot be mapped by IL methodology. A total of sixty-four unannotated BACs using IL strategy have been mapped on various chromosomes to find new seed points for the community. Moreover, thirteen out of ninety BACs that have been completely sequenced and then found not to map on the correct chromosome have been mapped on the proper chromosome. This will help those projects fill gaps and increase their sequence shared with little effort. Mapping data have been uploaded onto SGN and the mapping protocol has been distributed to the SOL consortium.

Next Gen Initiative Update

by René Klein Lankhorst

At the SOL Genome Workshop in Cologne, Roeland van Ham (CBSG), René Klein Lankhorst (CBSG), Giovanni Giuliano (ENEA), Giorgio Valle (University of Padua), Shusei Sato (Kazusa) and Mark van Haaren (Keygene) presented their plan to boost the sequencing of the Heinz genome by starting the Next Gen Initiative.

It was proposed to produce a whole genome sequence coverage of Heinz 1706 using next generation sequence technology. The Italian and Dutch groups will each produce a 10 X coverage of the genome using 454 sequencing (on the Titanium platform, Roche) plus a 15 X coverage on the SOLID system (ABI). For the purpose of assembling the next generation sequencing data, Keygene will produce a new physical map of the Heinz genome. This new map will be made with Keygene's novel WGP technology, which they recently presented at the PAG meeting in San Diego and which they successfully applied to generate the sequence of the melon genome.

In the assembly of the Next Gen data, the SBM (Selected BAC Mixture) sequencing data from Kazusa will also be included, as well as all available BACs, BAC ends and fosmid ends from the entire SOL consortium.

Since the meeting in Cologne, the number of participants in this initiative has increased considerably: the French (Mondher

Bouzayen) will contribute another 10 X 454 coverage from the French national tomato sequencing project, and India (Akhilesh Tyagi) will contribute a 5 X 454 coverage. Through the Spanish national sequencing project (Toni Granell) another 30 X SOLID coverage will be produced, whereas from the EU-SOL partners involved in tomato sequencing (The Netherlands, Italy, Spain, France and UK) resources will be made available for bioinformatics and, if needed, additional 454 coverage. Also, the EU-SOL together with the US team (Jim Giovannoni) will construct a novel BAC library, which will further improve the quality of the physical map that Keygene will construct.

The industry has expressed great interest in our plans and we have established co-operations now with Roche and ABI to assist in the sequencing and in the assembly of the Next Gen data.

Meanwhile, the Next Gen Initiative has started up successfully and the first results already have been obtained:

-454 random shotgun libraries (The Netherlands and Italy) and 3kb/20kb paired-end libraries (Roche) have been constructed. These libraries have been QC-ed and proven to be of excellent quality (contamination with only 0.7 % mitochondrial DNA and 3.3 % chloroplast DNA, good coverage of a test panel of BACs).

-A 15 X SOLID coverage of the Heinz genome has been produced (The Netherlands, ABI). Together with bioinformaticians from ABI, CBSG will start the assembly of this data.

-Keygene has started the construction of the physical map by making specific pools of the available BAC libraries (HindIII, EcoRI, Mbo1).

-The construction of the novel BAC library with random sheared inserts is underway (The Netherlands, US, Lucigen). First results of a test cloning show that the production of a large insert library with randomly sheared Heinz DNA is feasible.

Finally, as we decided in Cologne, the Next Gen Initiative is open to all SOL consortium members and anyone who would like to join us in this effort is very welcome. Our goal is to complete the first draft of the tomato genome by the end of this year and if you want to be involved, please contact René Klein Lankhorst (rene.kleinlankhorst@wur.nl).

Announcements

Publications

Journal Articles

Chang S-B, Yang T-J, Datema E, van Vugt J, Vosman B, Kuipers A, Meznikova-Skleničková M, Szinay D, Klein Lankhorst RM, Jacobsen E, de Jong H (2008) FISH mapping and molecular organization of the major repetitive sequences of tomato. Genome Res 16: 919-933.

Olmstead RG, Bohs L, Abdel Migid H, Santiago-Valentin E, Garcia VF, Collier, SM (2008) A molecular phylogeny of the Solanaceae. Taxon 57:1159-1181.

Peters SA, Datema E, Szinay D, van Staveren M, Schijlen E, van Haarst J, Hesselink T, Henkens M, Bai Y, de Jong H, Stiekema WJ, Klein Lankhorst RM, van Ham RCHJ (2009) *Solanum lycopersicum* cv. Heinz 1706 chromosome 6: distribution and abundance of genes and retrotransposable elements. Plant J (in press).

Ranc N, Munos S, Santoni S, Causse M (2008) A clarified position for *Solanum lycopersicum* var. *cerasiforme* in the evolutionary history of tomatoes (Solanaceae). BMC Plant Biology, 8:130 doi:10.1186/1471-2229-8-130.

Szinay D, Chang S-B, Khrustaleva L, Peters S, Schijlen E, Stiekema WJ, van Ham RCHJ, de Jong H, Klein Lankhorst RM (2008) High-resolution chromosome mapping of BACs using multi-colour FISH and pooled-BAC FISH as a backbone for sequencing tomato chromosome 6. Plant J 56 (4):627-637.

Tang J, Baldwin SJ, Jacobs JME, van der Linden CG, Voorrips RE, Leunissen JAM, van Eck H, Vosman, B (2008) Large-scale identification of polymorphic microsatellites using an *in silico* approach. BMC Bioinformatics 9:374 doi:10.1186/1471-2105-9-374. Results can be found at http://www.bioinformatics.nl/tools/polyssr.

Tang X, Szinay D, Lang C, Ramanna MS, van der Vossen EAG, Datema E, Klein Lankhorst RM, Jan de Boer J, Peters SA, Bachem C, Stiekema WJ, Visser RGF, de Jong H, Bai Y (2008) Cross-species BAC-FISH painting of the tomato and potato chromosome 6 reveals undescribed chromosomal rearrangements. Genetics 180:1319-1328.

Books

Catalog of Traditional Populations of Pepper, Tomato, and Zapallo Collected in the Andean Valleys of Argentina (2008) Peralta IE, Makuch M, Garcia Lampasona S, Occhiuto PN, Asprelli PD, Lorello IM, Togno L. INTA, Argentina, 128 pp. ISBN 978-987-521-335-7.

Petunia - Evolutionary, Developmental and Physiological Genetics (2009) Gerats T, Strommer J (Eds.) 450 pp. ISBN: 978-0-387-84795-5

About this book:

In 1984, when the first edition of this monograph was published, Petunia was well positioned as a classical model system to contribute significantly to the coming explosion in plant molecular biology. Its strength was fostered by years of physiological, biochemical, genetic and cytogenetic research - the contributions of early workers who saw the value and promise of this horticulturally significant representative of the Solanaceae. The present edition encapsulates the state of Petunia-based research a quarter of a century later. It paints a rich portrait of progress, particularly but not exclusively in evolutionary and developmental biology. The wealth of knowledge presented here, and the continued promise of Petunia as a research system, both follow from a combination of that solid early work, the amenability of Petunia to molecular analysis, and the dedication and collegiality of the Petunia research community. All are richly documented in this work.

Originally published as volume 9 in the series: Monographs Theoret. Genetics 2nd ed., 2009, XXII, 450 p. 97 illus., 65 in color. Hardcover 66,95 €. ISBN: 978-0-387-84795-5.

Website Resources

Breeders Toolbox

New tools are now available in the Breeders Toolbox (http://www.sgn.cornell.edu/breeders/). These tools include: On the fly QTL analysis for Solanaceae traits, an Intron Finder, and a CAPS Maker Designer. Feedback on the toolbox is welcome and can be sent to Joyce Van Eck (jv27@cornell.edu).

Job Announcements

BHN Research Immokalee, Florida
www.bhnseed.com

Plant Breeder/Plant Pathologist

A privately-funded vegetable variety development firm is looking for a plant breeder with strength in plant pathology for its research program in South America. Responsibilities include developing tomato varieties, conducting host resistance work, evaluating grower field performance trials and assisting with established breeding program in Florida. Candidate must have a Plant Breeding PhD or MS with experience and a minor in Plant Pathology or vice versa. Breeder will be headquartered in Florida and travel to South America. Computer knowledgeable, detail-oriented and the ability to speak Spanish are preferable. Compensation package will be commensurate with experience and competitive.

Send resume, college transcripts, and three letters of reference to:
Dr. Jim Augustine
BHN Research
PO Box 3267
Immokalee, FL 34142
e-mail: jaugustine@bhnseed.com
Fax: 239-352-1565

Conferences

Xth World Petunia Days
March 28 - April 1, 2009
Universidad Politécnica de Cartagena, Spain
http://www.upct.es/~genetica/xwpd.html

Potato Association of America
August 9 – 13, 2009
Fredericton, New Brunswick, Canada
http://www.paa2009.org

Tomato Breeders Roundtable
June 28 - July 1, 2009
Embassy Suites, Sacramento, CA

SOL 2009, The 6th Solanaceae Genome Workshop
November 8 – 13, 2009
New Delhi, India
http://www.sol2009.org

Solanaceae Recipes

African Leafy Solanaceae Vegetable (*Solanum scabrum*) in Cream

Contributed by Mary O. Abukutsa-Onyango
Department of Hoericulture, Jomo Kenyatta University of Agriculture & Technology
P.O. Box 62000 00200 NAIROBI-KENYA
e-mail: mabukutsa@yahoo.com

Ingredients:

½ kg young tender leaves of *Solanum scabrum*
¼ liter water
50 ml cream
1 medium onion
2 medium ripe tomatoes
2 tbsp vegetable oil
1 tsp table salt

For garnish:
Sliced onions
Sliced ripe tomato

Solanum scabrum growing in the field ready for use in the recipe described.

Preparation:

1. Clean, wash and chop the green leaves of *Solanum scabrum*, onion and tomatoes.
2. Bring water to boil and put the green leaves in the boiling water for 15 minutes.
3. Drain the stock and keep for later use.
4. Heat the vegetable oil and add the onion until golden brown.
5. Add the tomatoes, stir and cook until soft.
6. Add the boiled green leaves, stir, cover and simmer for 2 minutes stirring occasionally.
7. Add the cream and the drained stock, salt to taste, cover and simmer for 3 minutes.
8. Preparation yields four to five servings and is best served with mashed bananas or "*ugali*" (Swahili name for popular Kenyan dish made from maize meal; see picture below).

Sample of prepared recipe

Samples of mashed bananas-yellow and '*Ugali*'-white

Chili Verde con Pollo y Cashews

Includes modifications by Ruth A. White
November 2006

Ingredients:

6 large chicken breasts
1.5 to 2.5 cups avocado salsa verde (See recipe below)
½ -¾ medium onion, chopped
1 bay leaf
½ teaspoon ground white pepper
1 teaspoon ground cumin
2 cloves crushed, minced garlic
2 – 3 cups chicken stock
2 Serrano chiles, chopped, discard seeds
2 Poblano chiles, roasted, discard seeds & veins, chopped
4 Anaheim chiles, roasted, discard seeds & veins, chopped
1 – 2 Tablespoons Masa Harina (hominy flour as thickener and adds flavor)
12 – 16 ounces whole cashews (or more)
3.5 ounces white chocolate (Lindt is a good brand), add 1 hour before serving
12 ounces sour cream, add 5 minutes before serving
Monterey Jack cheese, shredded (optional)
fresh cilantro, chopped (optional)
blue corn tortilla chips (optional)

Preparation:

1. Combine chicken breasts, salsa verde, onion, bay leaf, white pepper, cumin, garlic, chicken stock, chiles, and cashews in a slow-cooker (See step #6). Cover, set it to low, and let it cook for 8 to 9 hours.
2. Add white chocolate, stir to mix, then cook an additional hour.
3. Take a fork and shred the chicken right in the pot (it will now easily fall apart).
4. Stir it together, and thicken the chili with a little Masa Harina, which also adds a nice flavor to the chili. You can use guar, xanthan, or flour if you cannot find Masa Harina, but you won't have the corn flavor of the Masa Harina.
5. Serve the chili with sour cream (I add it in to the pot about 5 minutes before serving), shredded Monterey Jack cheese (or a similar cheese), and/or fresh chopped cilantro to taste. Blue corn tortilla chips also add a nice flavor and crunch to the chili, but you can use yellow or white corn tortilla chips instead or none as you prefer.
6. If you do not have a slow cooker, bring the first set of ingredients to a boil, then reduce heat to a simmer. Reduce cooking time to around 3 hours, until the chicken easily falls apart. I've only done this recipe in the slow cooker, so I don't have times yet for on the stove.

Avocado Salsa Verde

Includes modifications by Ruth A. White
November 2006

Ingredients:

2 large Anaheim chiles
½ pound tomatillos, husked, rinsed, and coarsely diced
1 ½ cups low-salt chicken broth (preferably home-made)
2 large green onions, chopped
2 Serrano chiles, stemmed, seeded, and chopped
1 clove garlic, crushed and chopped
¼ cups fresh cilantro leaves, chopped, firmly packed
1 Tablespoon whipping cream (or sour cream)
1 Tablespoon fresh lime juice (optional)
1 ripe avocado, pitted, chopped

Preparation:

1. Char Anaheim chiles directly over gas flame or in broiler until blackened on all sides. Enclose in a paper or plastic bag and let stand about 10 minutes. Peel away the blackened skin, seed, and chop chiles.
2. Combine tomatillos, chicken broth, green onions, Serrano chiles, and garlic in a medium saucepan. Bring to a boil over medium-high heat. Reduce heat to medium-low; simmer until mixture is reduced to 1 2/3 cups, stirring occasionally (about 18 minutes.) Transfer mixture to a blender.
3. Add Anaheim chiles, cilantro, avocado, and cream. Puree until smooth. Season salsa with salt and pepper to taste. Add lime juice, if desired. You can make this a day ahead and refrigerate or use right away in Chili Verde con Pollo y Cashews or serve warm over broiled salmon or scrambled eggs. Rewarm before serving.

Tomatillos: green tomato-like vegetables with paper-thin husks.
Anaheim chiles: also known as California or New Mexico chiles. Light green, about 6 - 8 inches long by 1 inch wide at the stem. Mild, approximately 1,000 - 1,500 Scoville heat units.
Serrano chiles: medium to dark green, about 2 inches long and 1 cm in diameter. Hot, between 7,000 - 25,000 Scoville heat units.
Poblano chiles: dark green, triangular shaped, about 4 inches long by 2.5 - 3 inches wide at top. Mild, about 2,500 - 3,000 Scoville heat units.