Genomic Arabidopsis Resource Network

Issue 2
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Update on GARNet Resources at ATIS - January 2000

Jonathan Clarke

ATIS has now established all the protocols required for the amplification and sequencing of dSpm and Ds insertion sites. Quality assurance strategies have been defined and implemented and a data management system will be installed early in 2001. Existing SLAT line and ACTIVATE line SINS have been subjected to our QAs and corrections made where required. 100 QA SINS from the ACTIVATE collection are ready for release, but are awaiting seed bulking which should be complete in January.

ATIS has established close links with NASC to ensure consistency of information and stock management. A sequence release strategy has been implemented to link SINS and NASC seed stock numbers. All SINS/NASC stock numbers will be submitted to GenBank/EMBL as an STS. This will ensure instant access to line information after BLAST search alignment. ATIS's database, ATIdb has been commissioned and is available at http://stein.cshl.org/~h-liu/atidb/index.html. The ATIS web site was released in September and includes a gateway to tagging resources (http://jic.bbsrc.ac.uk/STAFF/michael-bevan/ATIS/index.htm).

Recovery of viable lines from the ACTIVATE collection have been disappointing due to poor seed viability. We expect to recover only 50% (1000 lines) from the collection and the rate of SINS production has been slow while GA treatments were refined to recover the collection. We hope to release the SINS and bulked seed by February. We have received a donation from David Twell of 5000 single seed decent lines from the SLAT collection which complements our own collection of 2000 lines. Generation of the SINS from these lines has been initiated.

GARNet Metabolomics update (31/01/01)

Mike Beale

All equipment is installed and running well.

Specific metabolite profiling

Ten or so applications have been approved by the steering committee. The first three analyses (carotenoids by HPLC-DAD and fatty acids by GC-MS) are in progress. In other cases plants are being grown for bulking of seed to give enough plants for analysis. There is a queue forming and more involved analyses, such as for cytokinins will take time, please be patient.

Metabolomics

Optimisation of GC-MS and NMR methods for maximum information from crude samples is proceeding and a comparative study of a set of ecotypes is in its early stages.

Update on GARNet Proteomics Resource.

Cambridge Centre for Proteomics.

Kathryn Lilley

- The following staff have been appointed to positions within the facility (start dates in parentheses):

manager	dr. kathryn lilley ksl23@cam.ac.uk or proteomics@bioc.cam.ac.uk	(1st november 2000)
2d gel post doc.	dr. azam razzaq ar251@cam.ac.uk	(1st october 2000)
mass spectrometry post doc.	dr. michael deery	(3rd january 2001
2d gel technician	margaret evans	(3rd january 2001)
mass spectrometry technician	julie howard	(15th january 2001)

- Amersham Pharmacia DIGE system (differential protein labelling using Cy dyes) is installed and is currently being optimised for use in conjunction with *Arabidopsis* protein samples.

- A MALDI-Tof mass spectrometer (Micromass TofSpec2E) has been installed, a second mass spectrometer, Micromass Q-Tof, is due to be installed at the beginning of February.

The Cambridge Centre for Proteomics expects to be in a position to accept samples sometime in March. A website charting the progress of the facility will soon be linked to the GARNet site. In the meantime, please feel free to contact Kathryn Lilley (01223 765255) or Paul Dupree (01223 333340 or pd101@cam.ac.uk) if you have any questions about the facility or wish to discuss relevant submissions to the GARNet steering committee.

Karin van de Sande.