

Physcomitrella genome project by NIBB & MEXT, Japan

1. Full-length cDNA libraries and ESTs 2000-2005

- (1) Protonemata (chloronemata, caulonemata, bud, young gametophores)
13 to 14 days after inoculation
- (2) Auxin treated protonemata
8-11 days after inoculation
- (3) Cytokinin treated protonemata
8-13 days after inoculation
85,000 end sequences for both 5' and 3': 14,000 genes:
Database: PHYSCObase (NIBB), distributed from RIKEN BRC
- (4) Regenerating protoplasts
- (5) Early stages of developing sporophytes
in 2004: both 5' and 3' end sequences
- (6) Late stages of developing sporophytes
- (7) Inducted and differentiating gametangia
- (8) Protonemata
in 2005: both 5' and 3' end sequences

2. Full-length cDNA sequencing (~30 Mb) 2005-2006

- (1) Protonemata (chloronemata, caulonemata, bud, young gametophores)
- (2) Auxin treated protonemata
- (3) Cytokinin treated protonemata
in 2005: 14,000 cDNAs
- (4) Regenerating protoplasts
- (5) Early stages of developing sporophytes
in 2005
- (6) Late stages of developing sporophytes
- (7) Inducted and differentiating gametangia
- (8) Protonemata
in 2006

3. BAC and fosmid libraries: 2004

20X BAC libraries

fosmid libraries

in 2004: Asao Fujiyama's lab

4. BAC end sequencing: 2005

100,000 clones: 100Mb

in 2005

5. Assemble: 2005 ?

in 2005 depending on data release from JGI

6. Annotation: 2006 ?

cDNA to scaffold mapping

blast search for uncovered region

in 2006

Physcomitrella post-genome project by NIBB & MEXT, Japan

1. Tagged and gene/enhancer trap lines: 1998-2000

15,000 lines in NIBB

2. Microarray (oligo array) for all annotated genes: 2006

in 2006

3. GFP/GUS insertion lines at 3' ends: 2006-2009

2,000 lines

transcription factors

receptors

kinases

etc.

from 2006-2009