PublisherInfo		
PublisherName	:	BioMed Central
PublisherLocation	:	London
PublisherImprintName	:	BioMed Central

A green cell-cycle transcriptome

ArticleInfo		
ArticleID	:	4620
ArticleDOI	:	10.1186/gb-spotlight-20021025-01
ArticleCitationID	:	spotlight-20021025-01
ArticleSequenceNumber	:	286
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	2
ArticleHistory	:	RegistrationDate : 2002–10–25 OnlineDate : 2002–10–25
ArticleCopyright	:	BioMed Central Ltd2002
ArticleGrants	:	
ArticleContext	:	130593311

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The transcriptional regulation of the cell cycle in plants has features in common with other higher eukaryotes, as well as potential plant-specific pathways. In the Early Edition of the Proceedings of the National Academy of Sciences Breyne *et al.* describe a genome-wide expression analysis of cell-cycle-modulated genes in the tobacco Bright Yellow-2 (BY2) cell line. They applied a cDNA-amplified fragment length polymorphism (AFLP) technology to overcome the limitations imposed by the lack of extensive genomic and microarray resources for tobacco. Analysis of about 10,000 transcript tags revealed that 10% of transcripts were periodically expressed. Hierarchical clustering identified clusters associated with the phases of the cell cycle. About one third of the tags are homologous to genes of known function. Breyne *et al.* identified genes encoding cyclins, kinases and phosphatases previously associated with cell-cycle progression, as well as novel genes that may provide insights into the regulation of the plant cell cycle.

References

1. When plant cells decide to divide.

2. *Proceedings of the National Academy of Science*s , [http://www.pnas.org]

3. Transcriptome analysis during cell division in plants, [http://www.pnas.org/cgi/doi/10.1073/pnas.222561199]

4. Genome-wide expression analysis of plant cell cycle modulated genes.