

JD4.1 Lignin biosynthesis gene orthologs from maize, miscanthus and sugar cane

Objectives:

To identify the enzyme-coding genes involved in lignin biosynthesis in maize, miscanthus and sugar cane.

Procedure:

Arabidopsis genes that are involved in lignin biosynthesis were previously identified by P12 (VIB). Orthologs of these genes will be identified by sequence similarity and (previously generated) expression data in miscanthus by P13 (WU), in maize by P4 (Biogemma) and P6 (INRA) and in sugar cane by CeProBIO Proj. 4 coordinator (UFV).

Results:

Concerning the gene discovery in miscanthus, the current status of the miscanthus sequencing genome project is still not allowing the identification of gene sequences relevant to the lignin biosynthetic pathway. The available data consist of very short sequences of very poor quality and unassembled. To circumvent this problem, P13 focused on quantitative expression analyses to identify ortholog genes in miscanthus. Up to date, the amplification of nine genes has been tested (*COMT*, *PAL*, *LAC*, *4CL*, *CCoAOMT*, *CAD*, *PER*, *C4H* and *CCR*), and partial sequences were obtained for four of them (*C4H*, *CCoAOMT*, *PER* and *CAD*). Further steps consist in adopting alternative approaches to help in the identification of key genes, such as 454 high-throughput sequencing and hybridization with the sugarcane microarray in collaboration with Glaucia Sousa (IQ/USP, CeProBIO).

Concerning gene discovery in maize, putative orthologs of Arabidopsis genes involved in lignin biosynthesis pathway from P12 were identified by P4 based on the B73 Maize Genome (release RefgenV1, FilterGeneSet Genes). Links between Arabidopsis genes and Maize genes are summarized in the table below.

Concerning the gene discovery in sugar cane, a total of 28 unigenes were identified, which were four PALs, two C4Hs, three 4CLs, one HCT (and one HCT-like), two C3Hs, three CCoAOMTs, two CCRs, one F5H, one COMT and four CADs.

Arabidopsis		Maize		
Gene_Arabidopsis	AGI_ID	FilterGeneSet_ID	Position_FGS pseudomolecule_v1	Chromosome
PAL1	At2g37040	GRMZM2G170692	185,977,246-185,979,822	Chr5
PAL2	At3g53260	GRMZM2G118345	27,970,073-27,973,176	Chr2
C4H	At2g30490	GRMZM2G010468	169,132,976-169,135,367	Chr8
4CL1	At1g51680	GRMZM2G055320	104,704,696-104,711,290	Chr9
HCT	At5g48930	GRMZM2G035584	182,823,899-182,828,887	Chr5
		GRMZM2G158083	32,319,457-32,325,547	Chr2
C3H1	At2g40890	GRMZM2G138074	185,986,961-185,989,921	Chr3
		GRMZM2G140817	155,804,205-155,808,669	Chr6
CCoAOMT1	At4g34050	GRMZM2G127948	78,034,306-78,036,491	Chr6
		GRMZM2G099363	16,220,992-16,223,368	Chr9
CCR1	At1g15950	GRMZM2G131205	210,936,172-210,942,246	Chr1
		GRMZM2G131836	49,863,312-49,865,680	Chr7
COMT	At5g54160	AC196475.3_FGT004	32,103,468-32,105,339	Chr4
F5H1	At4g36220	AC210173.4_FGT005	223,425,233-223,428,388	Chr1
		GRMZM2G100158	22,553,064-22,556,468	Chr5
CAD2	At3g19450	GRMZM2G110175	98,298,526-98,302,880	Chr5

discussion/conclusions.

For maize and sugar cane, orthologs of all genes known to be involved in lignification in Arabidopsis have been found, and those that are most likely involved in lignification of maize have been identified. The quality of the genome data did not allow this for miscanthus. Further steps for miscanthus consist in adopting alternative approaches to help in the identification of key genes, such as 454 high-throughput sequencing and hybridization with the sugarcane microarray in collaboration with Glaucia Sousa (IQ/USP, CeProBIO).