



Ingeniería Química
y Biotecnología
FACULTAD DE CIENCIAS
FÍSICAS Y MATEMÁTICAS
UNIVERSIDAD DE CHILE



Identification, heterologous expression and characterization of novel cellulases from white rot fungi

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SEMINARIO DE CLAUSURA

**“OPTIMAL TREATMENT PROCESSES OF LIGNOCELLULOSES
FOR BIOETHANOL – CONSORTIUM: OPTBIO”**

November 15, 2010

Outlook

- **Introduction**

- Cellulose hydrolysis in the bioethanol process
- Enzymes for cellulose hydrolysis
- White rot fungi as source of cellulases

- **Main Goals**

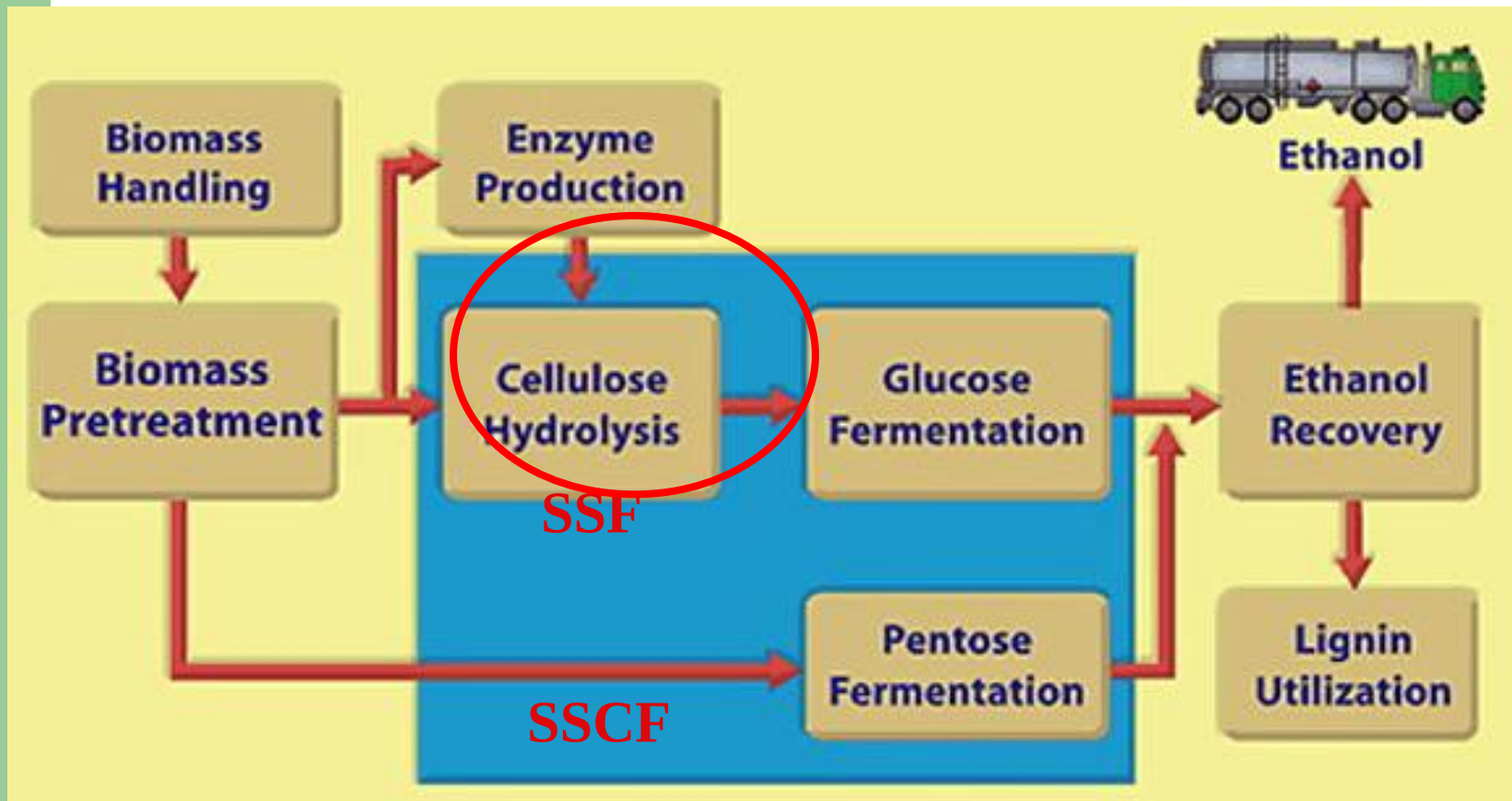
- **General Methodology**

- **Results**

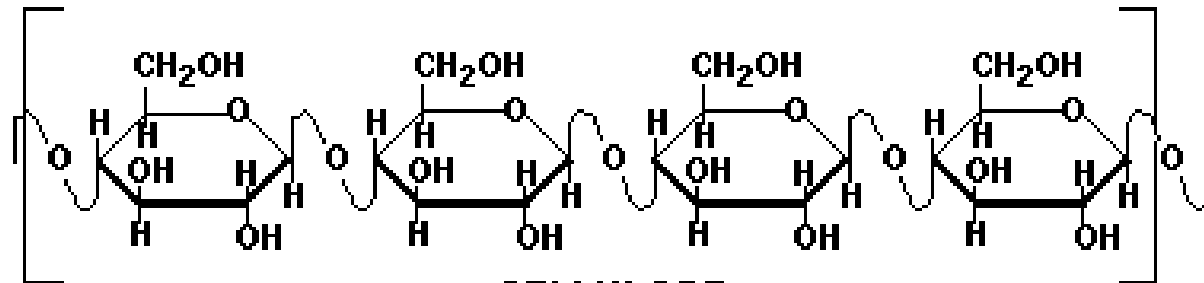
- Identification of cellulolytic fungi
- Identification of novel cellulases and characterization
- Cellulase gene cloning and recombinant expression

- **Conclusions**

The process of bioethanol production from lignocellulosic biomass

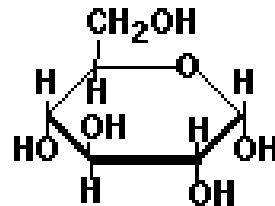


Cellulose hydrolysis

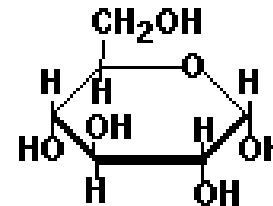


CELLULOSE

HYDROLYSIS



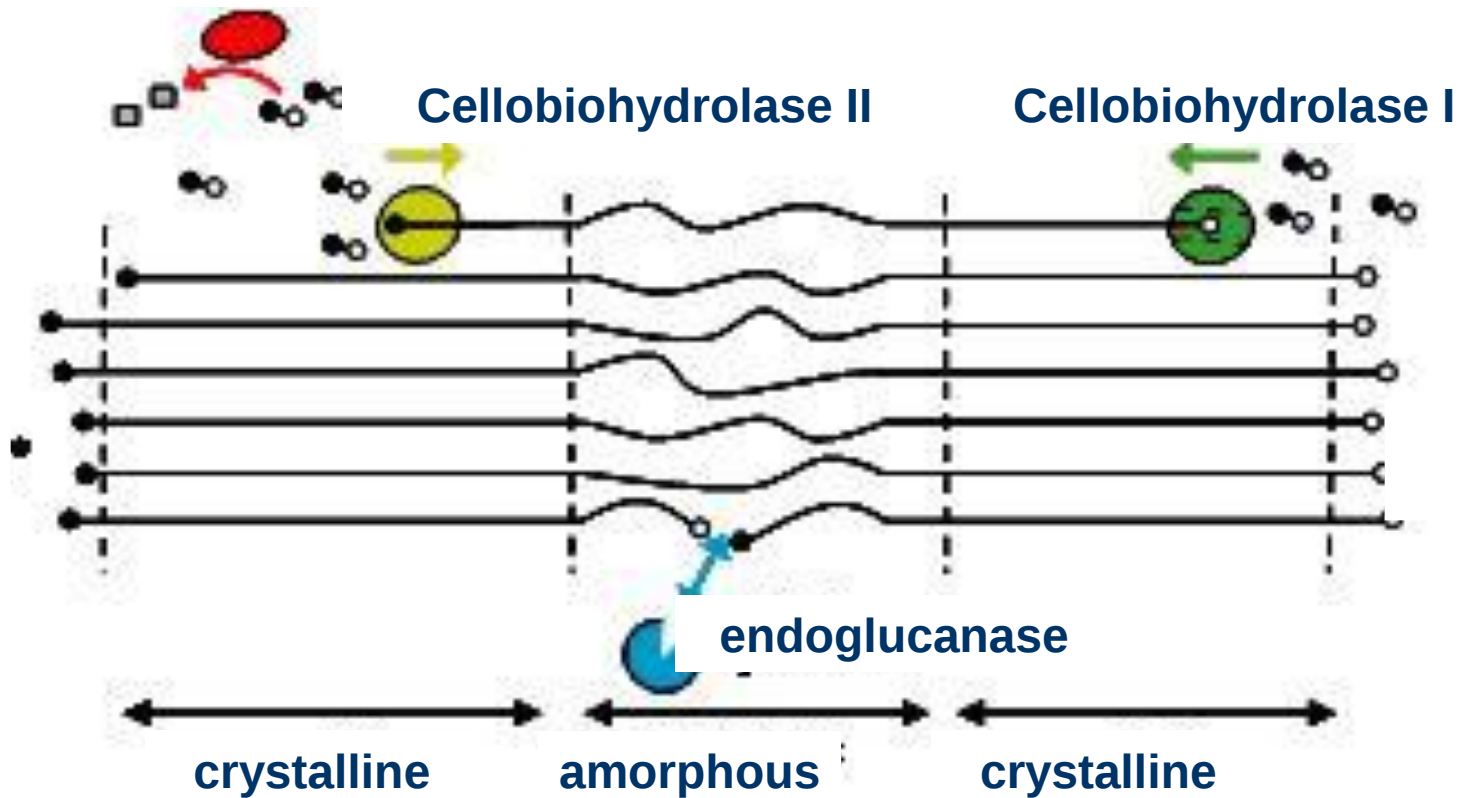
GLUCOSE



GLUCOSE

Cellulose hydrolysis is carried out by an enzymatic complex, cellulase

β -glucosidase

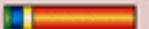


What are the requirements for cellulases to be used for lignocellulose biomass degradation?

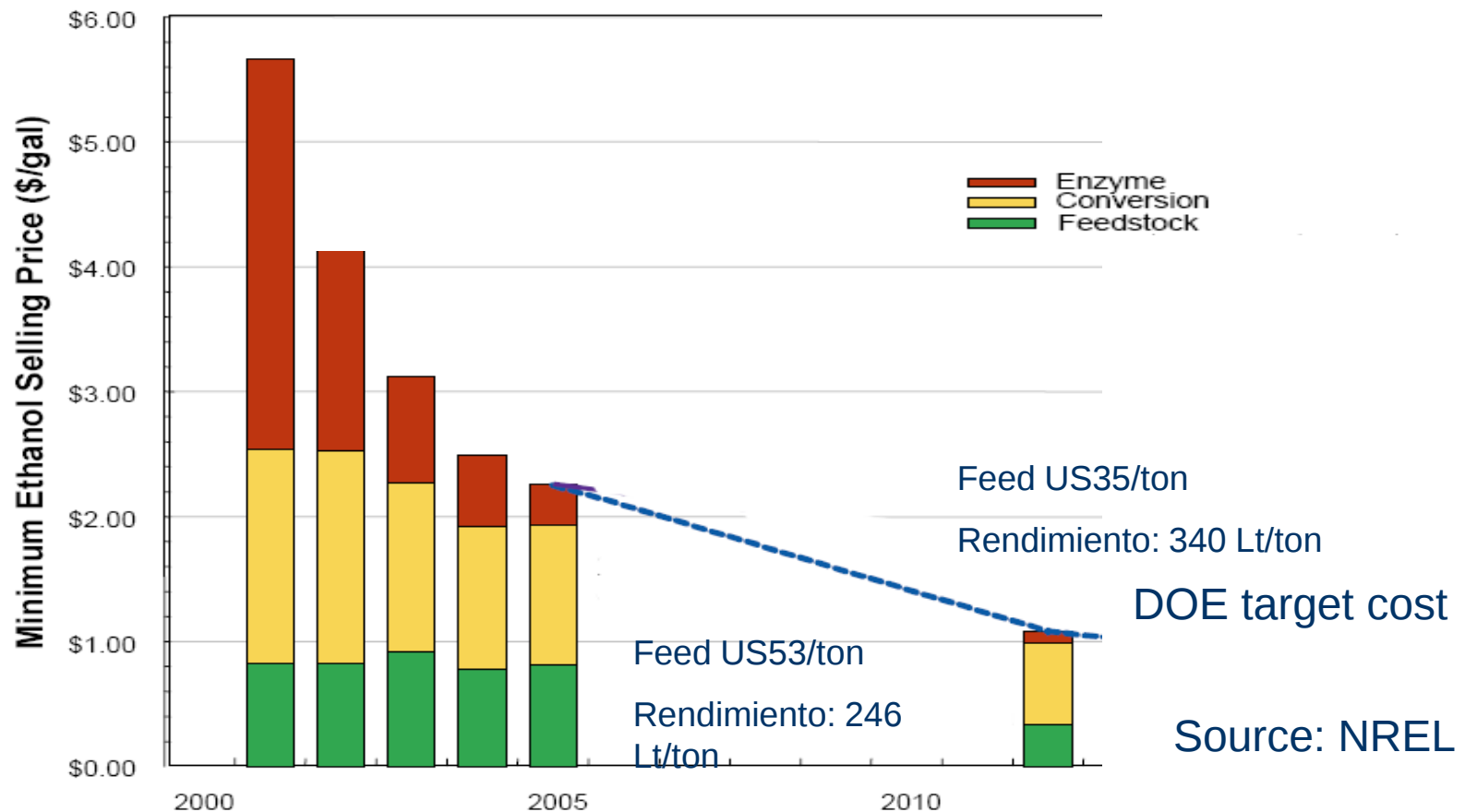
- High activity for extensive hydrolysis and low loading in reactors
- Thermostability for long-time (days) operation at 50°C.
- Tolerance to inhibitors (chemicals, glucose, ethanol, etc)
- High capacity to adsorb to cellulose and low adsorption to lignin

Microorganisms producing cellulases

- *Clostridium*, *Cellulomonas*, *Trichoderma*, *Penicillium*, *Neurospora*, *Fusarium*, *Aspergillus* etc, have cellulolytic and hemicellulytic activity.
- Main producer is *Trichoderma reesei*, containing
 - 8 endoglucanases
 - 2 exoglucanases
 - 1 cellobiase
- **Enzyme properties and productivity have been enhanced but further improvement is still needed**

Enzyme	GHF	Domain structure	Molecular weight (kDa)	
			Calculated	<i>T. reesei</i>
Cellobiohydrolase				
CBH I	7		58	68
CBH II	6		47	58
Endoglucanase				
EG I	7		46	54
EG II	5		42	50
EG III	12		25	25
EG IV	61		34	56
EG V	45		23	36
EG VI	74		85	N.D.
EG VII	61		25	N.D.
EG VIII	5		45	N.D.
			N.D.; not determined	

Cost of cellulase in the bioethanol process



Strategies used to reduce cellulase cost

Enzyme production

- Choice of Organism
- Regulation of Expression
- Induction
- De-repression
- Genomics



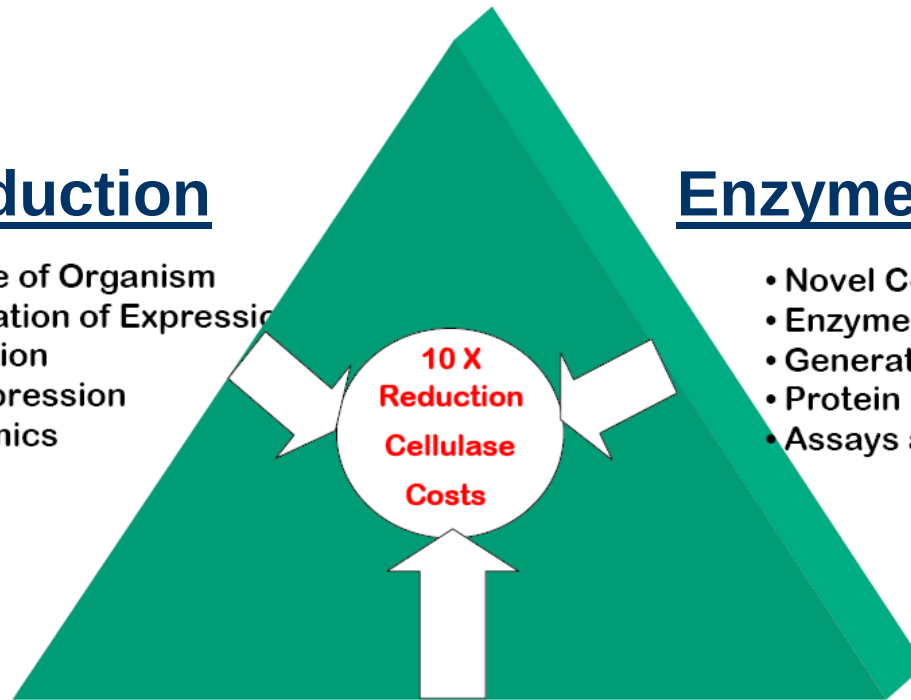
Reduced
\$/gm enzyme

Enzyme performance

- Novel Cellulolytic Activities *
- Enzyme Discovery
- Generation of Diversity
- Protein Engineering *
- Assays and Screens



Reduced
gm enzyme/vol EtOH



Production
process

White Rot Fungi (WRF)

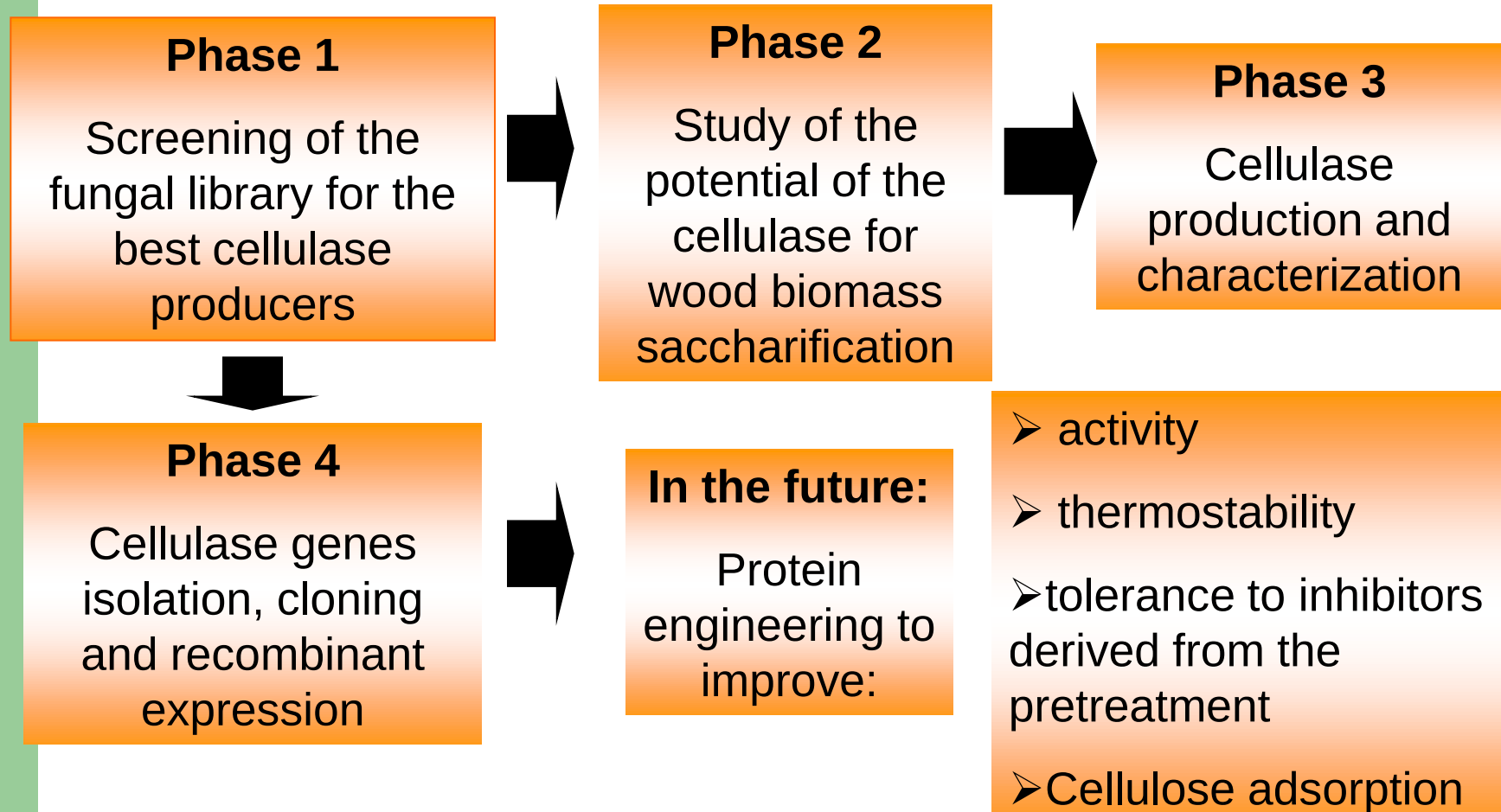
- Grow in the forests
- Degrade wood of trees
- Posses a enzyme system of ligninases, oxidases, peroxidases, hemicellulases and cellulases
- Very low number of cellulases from WRF have been cloned and tested for industrial degradation of cellulose



Main Goals

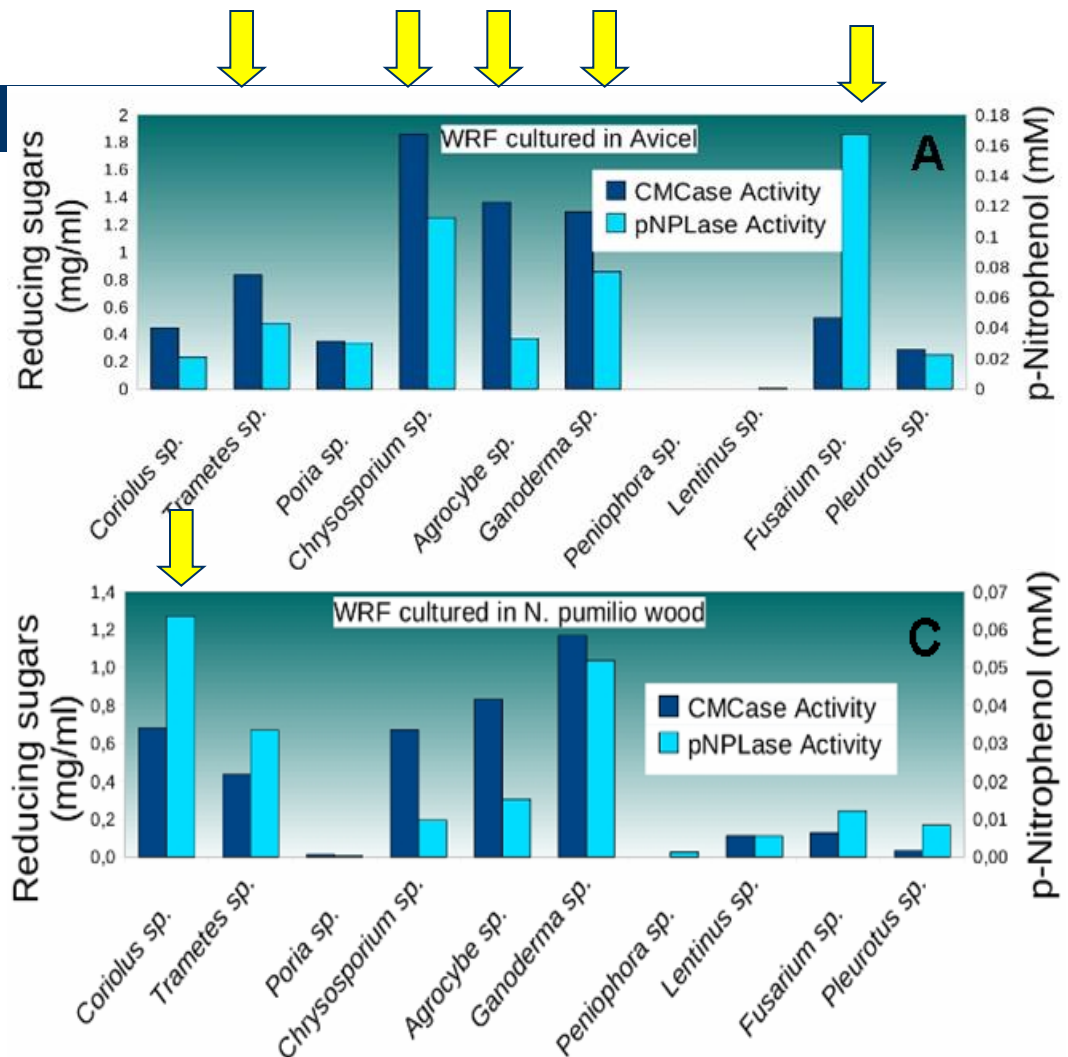
- To evaluate the efficiency of diverse enzymatic complexes previously isolated from WRF fungi.
- To isolate and clone cellulase genes from WRF
- To evaluate the recombinant enzymes performance on the degradation of cellulosic substances to fermentable sugars.
- To study the characteristics of the interaction between cellulose and the wild type and recombinant cellulolytic enzymes.

General strategy

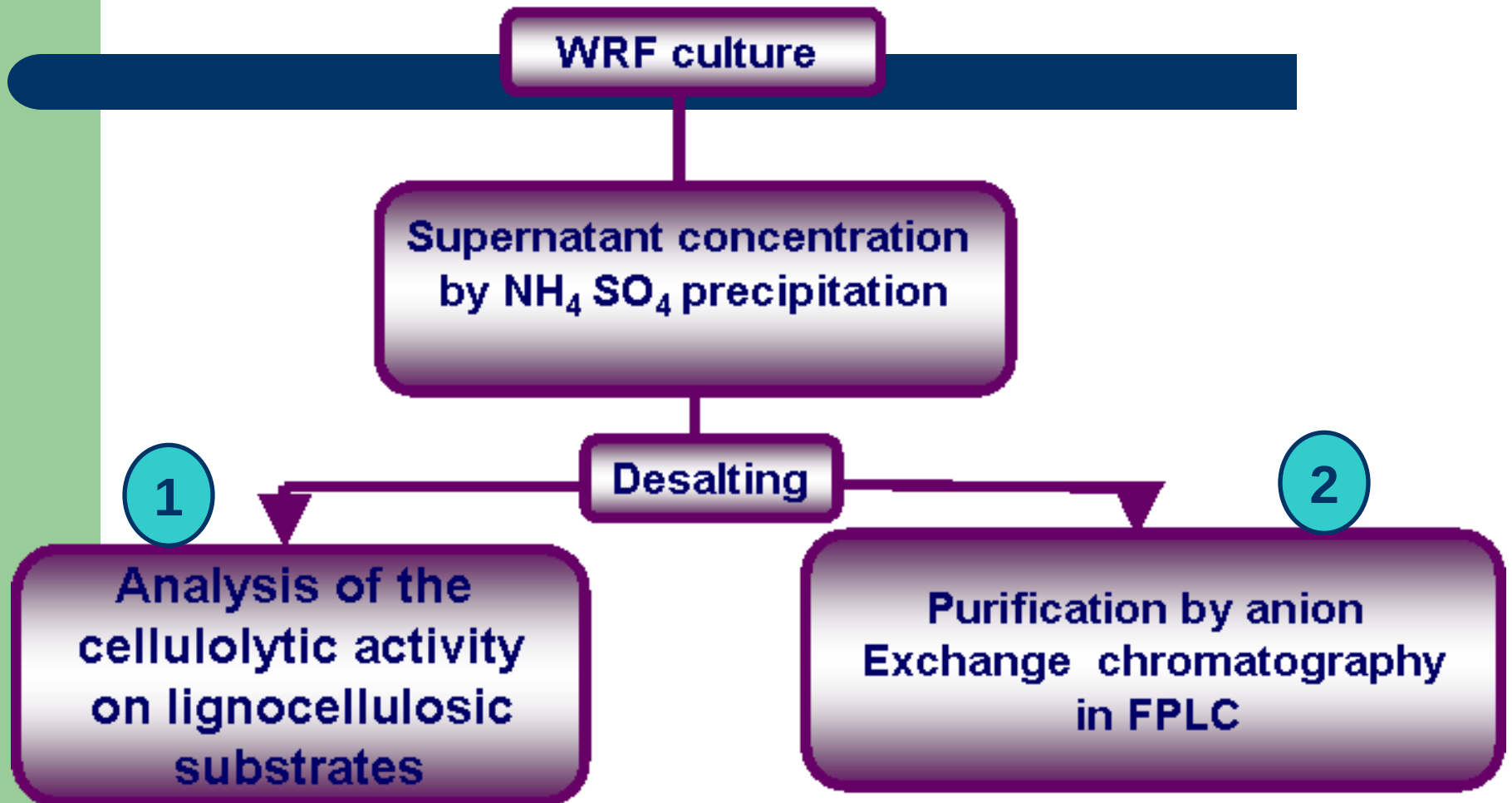


Phase I: Identification of the best WRF producers of cellulase activity

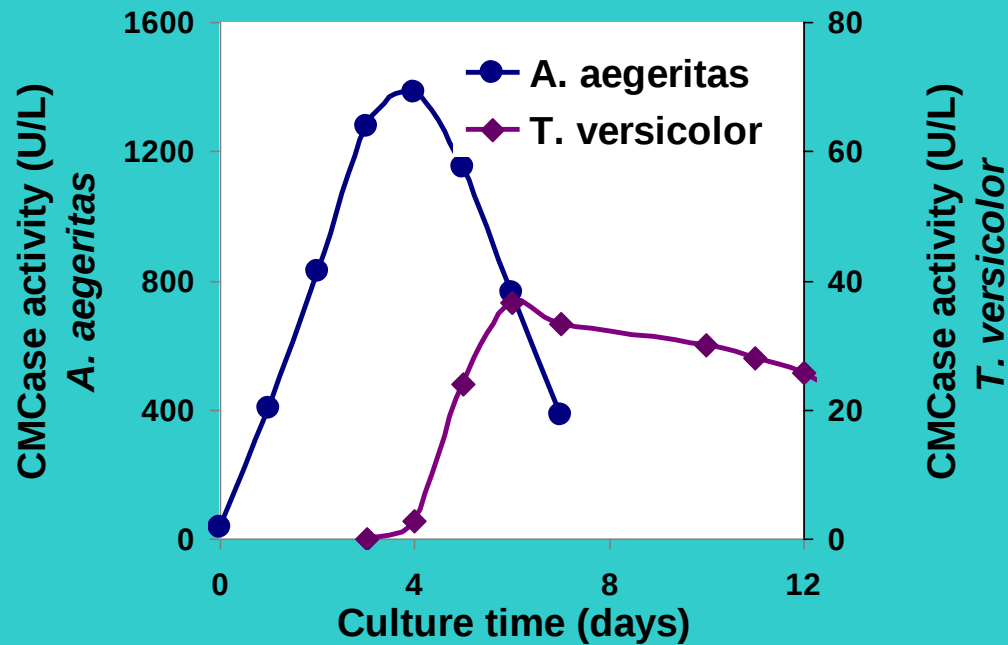
- Fungi were cultured in saline medium with cellulose as the only carbon source
- Production of endoglucanase and exoglucanase activity was evaluated using specific substrates for endoglucanases (CMC) and exoglucanases (pNPL)
- Six fungal isolates were selected for the next step



Phase II: Cellulolytic activity of WRF cellulases for wood biomass saccharification

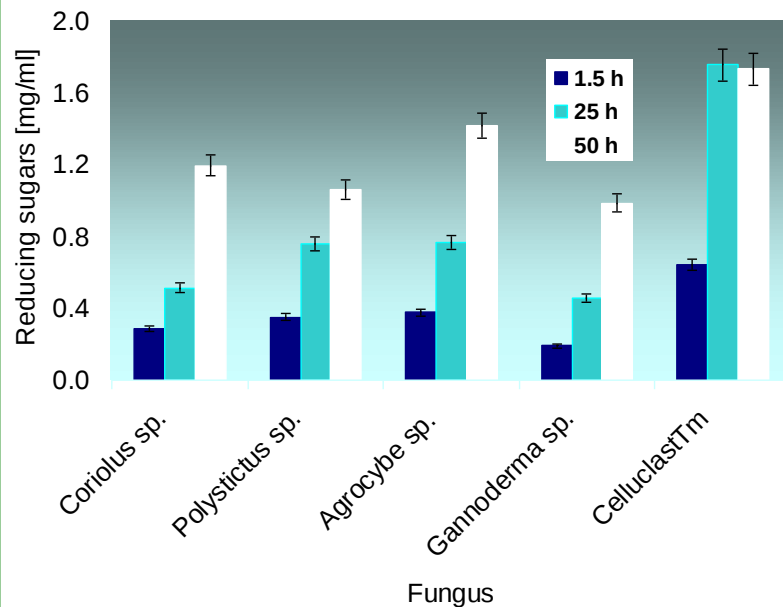


Cellulase production by WRF

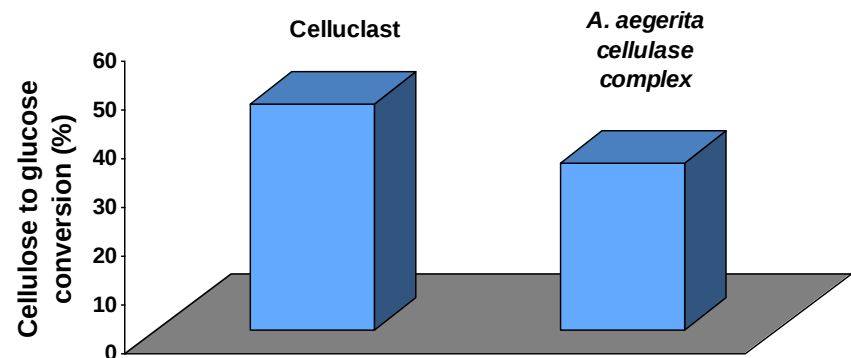
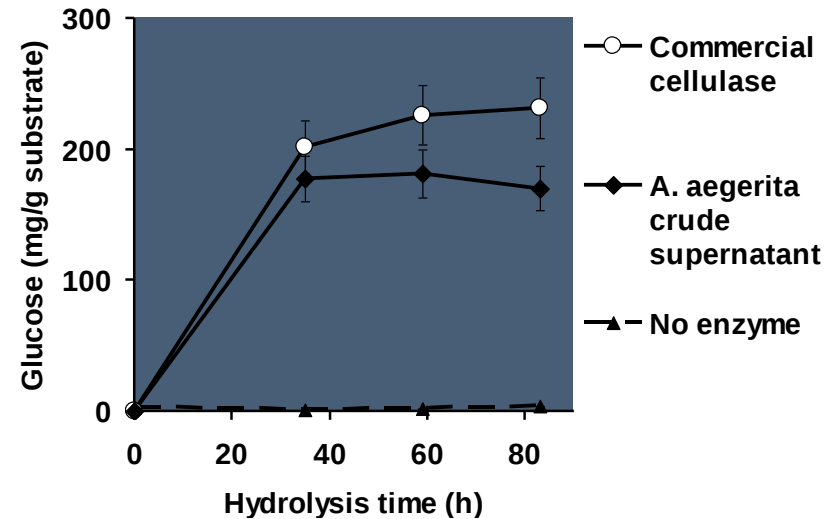


Phase II. Cellulolytic activity in WRF crude extracts on lignocellulosic substrate

Degradation of *N. pumilio* (Lenga) wood chips by enzymes from WRF



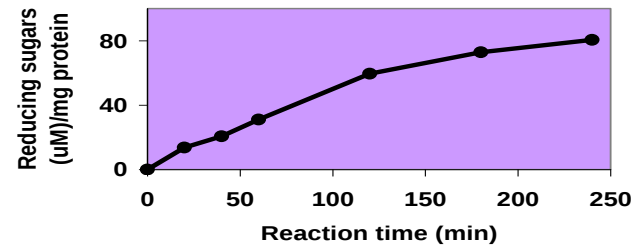
Fungal cultures supernatants were incubated with wood chips (1%) at 50 °C at pH 5 for 1.5, 25 or 50 hours.



Phase III. Cellulases production and characterization

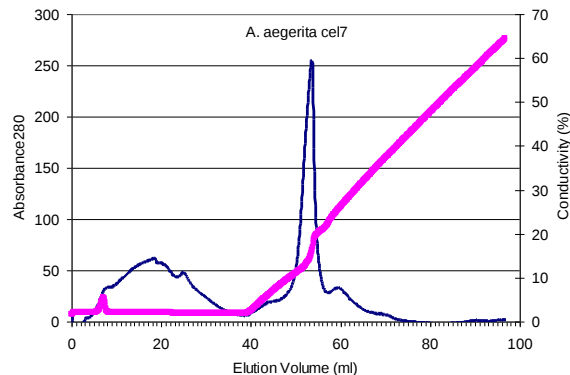


Activity of cel7 on microcrystalline cellulose

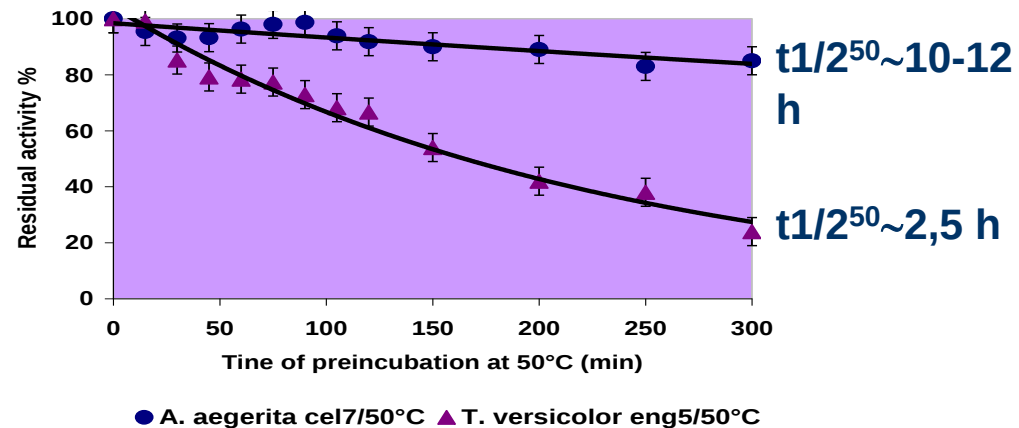


Specific activity = 0,5 U/mg prot.

Anionic Exchange chromatography

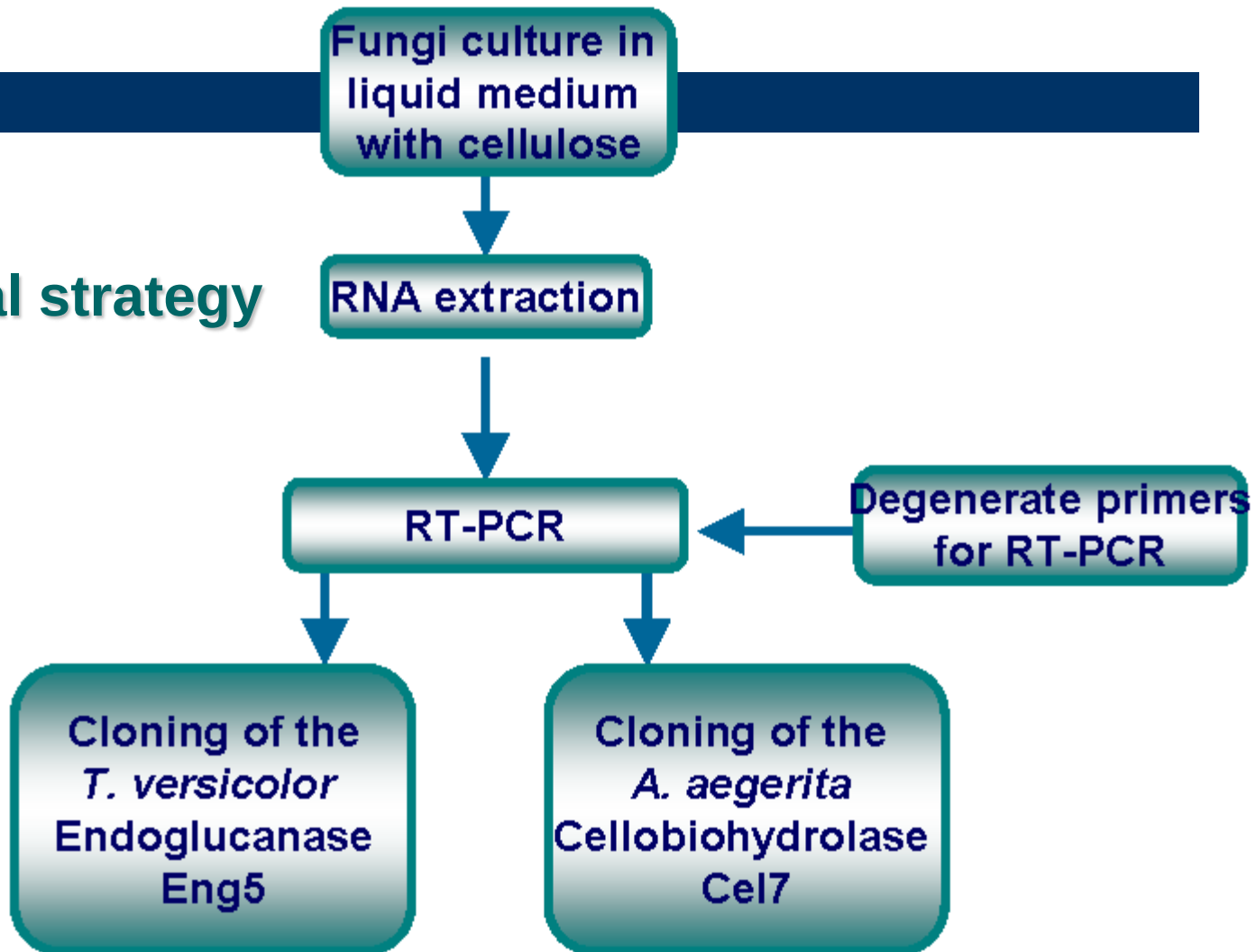


Thermal stability of purified cellulases



Phase IV. Identification of the cellulase genes, and recombinant expression

General strategy



Partial sequences for several cellulase genes were identified using molecular techniques

Comparison of WRF cellulase sequence to described cellulases

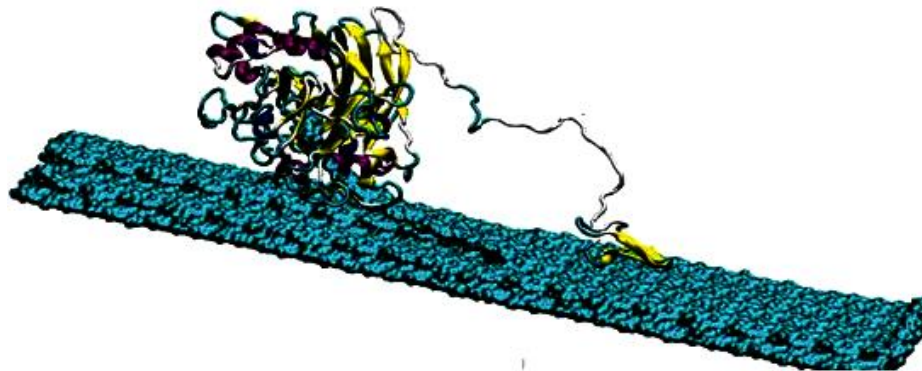
Fungus	Enzyme specificity	Sequenced (%)	Identity ^a (%)
<i>Trametes versicolor</i>	GH5 endoglucanase	46	33
	GH6 exoglucanase	58	89
	GH7 exoglucanase	49	79
<i>Fusarium oxysporum</i>	GH7 endoglucanase	25	47
	GH61 endoglucanase	29	54
<i>Ganoderma applanatum</i>	GH61 endoglucanase	29	37
<i>Phanaerochaete chrysosporium</i>	GH7 exoglucanase	60	100
<i>Coriolus versicolor</i>	GH7 exoglucanase	20	100
<i>Agrocybe aegerita</i>	GH7 exoglucanase	42	89

Symbols



Gene fragments selected to complete the sequence

Domain architecture of the cellulases isolated from *Trametes versicolor* and *Agrocybe aegerita*



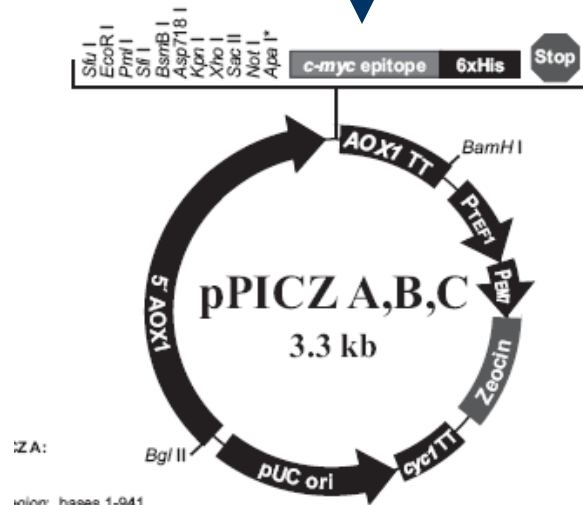
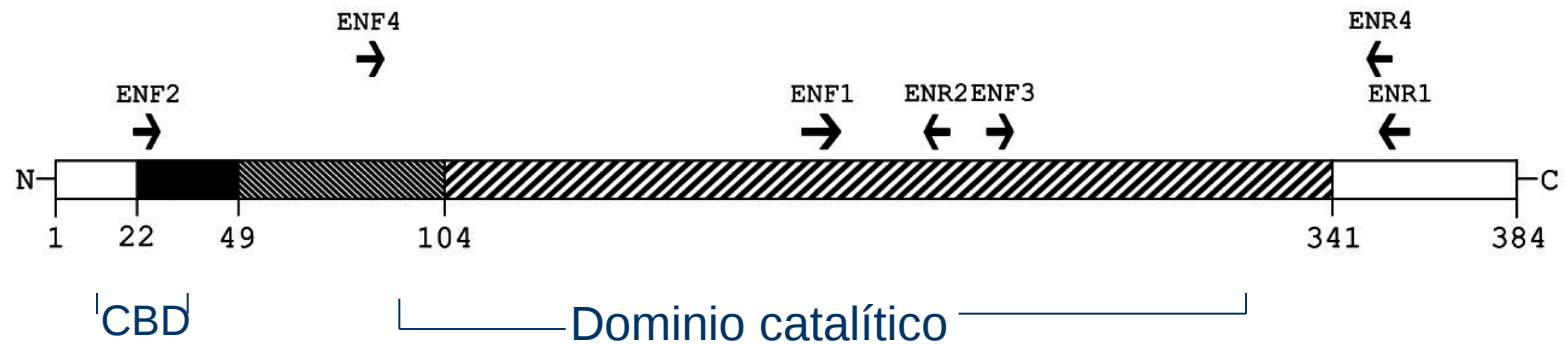
Are these novel cellulases?

Comparison of WRF cellulases amino acid sequence to known fungal cellulases available in databases.

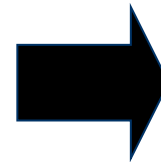
Identity (%)				
	<i>T. hirsuta</i>	<i>T. reesei</i>	<i>H. insolens</i>	<i>A. niger</i>
Eng5	83	26	42	44
	<i>T. reesei</i>	<i>P. chrysosporium</i>	<i>T. emersonii</i>	<i>P. chrysosporium</i>
Cel7	57	78	59	78

According the sequence criterium, genes isolated from *T. versicolor* and *A. aegerita* encode for novel cellulases, not described so far.

Gene cloning and recombinant expression of the two novel cellulases



Yeast
*Pichia
pastoris*



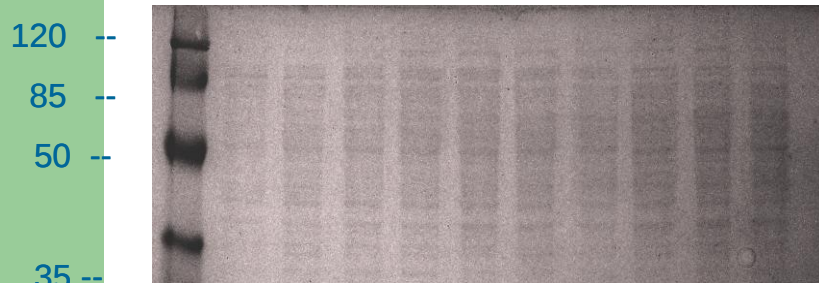
?
Cellulases

Recombinant expression of Eng5 in the yeast *P. pastoris*

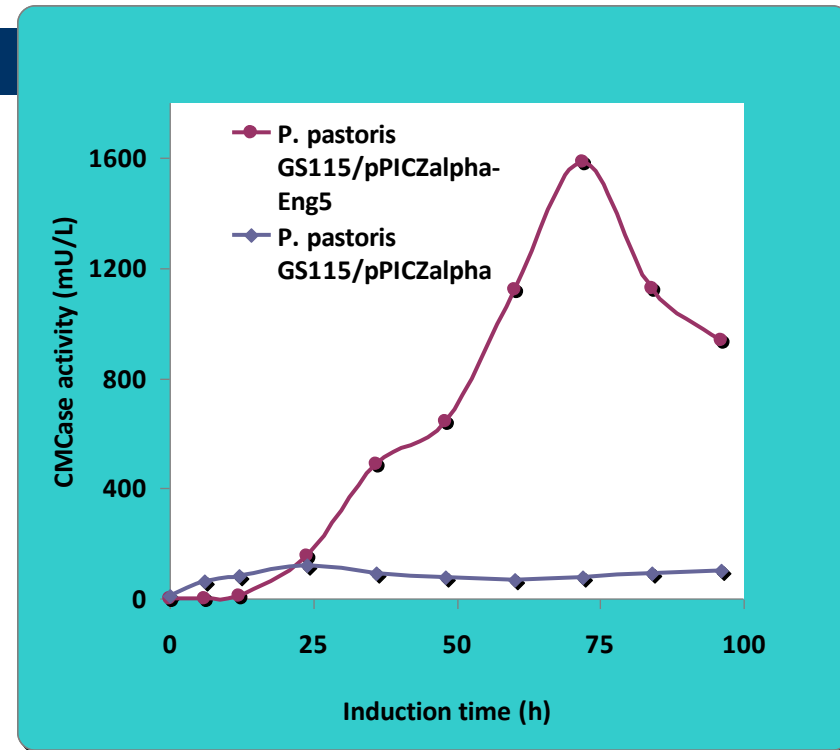
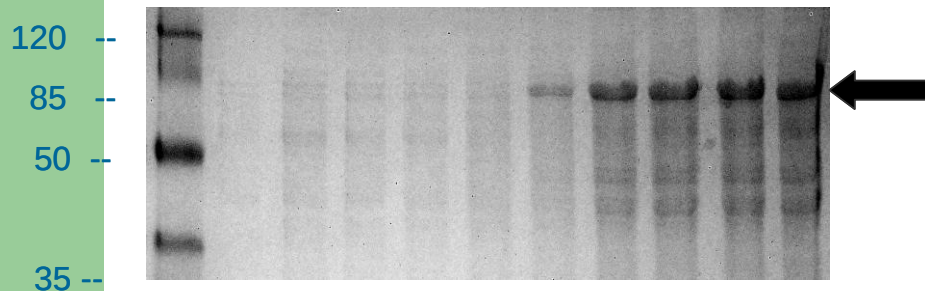
P. pastoris/pPICZ α

(control)

0 → 96 h



P. pastoris/pPICZ α -eng5

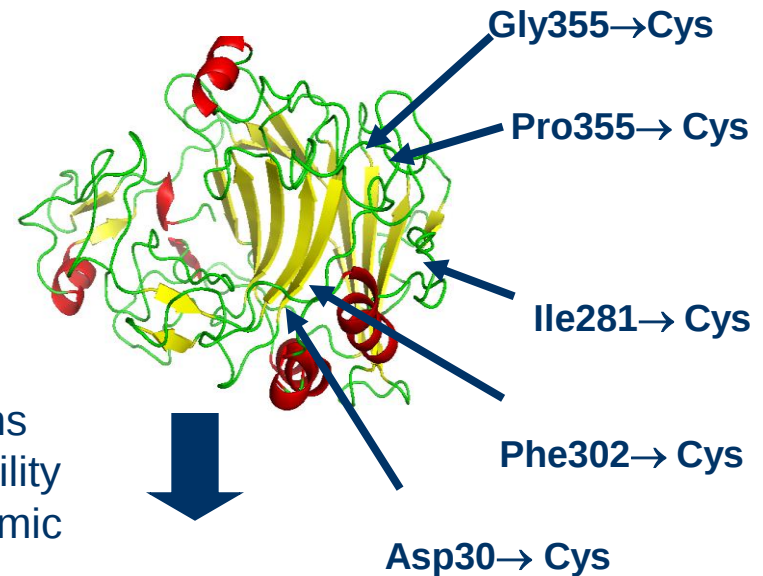


T. versicolor Eng5 is expressed as a functional cellulase in *Pichia pastoris*

Ahu85	SGTVCLSLILNEDGYWRPAITVVKILVLGGDILLDLPNPAIDPATDGVHLHCPDPVEYKRRVKLSKQYPAVL	160
OsUbc9	SGTVCLSLILNEDSGWRPAITVVKILVLGGDILLDLPNPAIDPATDGVHILPDKPVEYKRRVRQAKQYPAVL	160
PtUbc9	SGTVCLSLILNEDSGWRPAITVVKILVLGGDILLDLPNPAIDPATGAYOLPDPVEYKRRVRQAKQYPPPI	160
DdUbc9	SGTVCLSLILNEADGKPSVITKIVLLGGDILLDLPNPKSPQAQILHLPLTKKEEDKKVKVAKAKYPPSP	159
DdUbc9	SGTVCLSLILEDDGKPSVITKIVLLGGDILLDLPNPKSPQAQILHLPLTKKEEDKKVKVAKAKYPPSP	159
DdUbc9	SGTVCLSLILEDDGKWRPAITIKILLGLDILLDLPNPKSPQAQILHLPLTKKEEDKKVKVAKAKYPPSP	159
DmUbc9	SGTVCLSLILEDDGKWRPAITIKILLGLDILLDLPNPKSPQAQILHLPLTKKEEDKKVKVAKAKYPPSP	159
SpHus85	SGTVCLSLILEDDGKPAITIKILLGLDILLDLPNPKSPQAQILHLPLTKKEEDKKVKVAKAKYPPSP	157
ScUbc9	SGTVCLSLILEDDWRPAITIKILLGVDDILLDLPNPKSPQAQILHLPLTKKEEDKKVKVAKAKYPPSK	159
PtUbc9	SGTVCLSLILEDDGKPSITIKILLGLDILLDLPNPKSPQAQILHLPLTKKEEDKKVKVAKAKYPPSK	159



Model of the three-dimensional structure



Experimental validation

Concluding Remarks

- White rot fungi *Trametes versicolor* and *Agrocyte aegerite* produce cellulase activities able of degrading *Nothofagus pumilio* wood chips and soluble cellulose (CMC).
- Under our experimental conditions, values of cellulose to glucose conversion were similar to those exhibited by Celluclast 1.5L, a commercial preparation.
- Sequences encoding for one endoglucanase and one cellobiohydrolase were cloned from *T. versicolor* and *A. aegerita*, respectively. The new cellulase genes share variable sequence identity (55 – 90 %) to cellulases described in literature. To our knowledge these genes have not been previously described in the mentioned fungi or any other fungus
- Sequence alignment showed that the these sequences encode for glycosyl hydrolases belonging to families 5 and 7. One Family 1 carbohydrate binding module was identified in the amino end of Eng5 and the carboxy end of Cel7.
- Eng5 was cloned into the vector pPICZ α and transformed into *P. pastoris* GS115, resulting in functional expression of the endoglucanase to the extracellular space.
- **White rot fungi are a promising source of cellulases, con high potential to be used in the bioethanol production process.**

Main Outcomes

Students formation

- 2 undergraduate and 5 postgrade students

International meetings:

- II Latin America Congress Biorefineries, May 2009. Concepción, Chile
- The 13 European Congress in Biotechnology, September 2009, Barcelona, Spain.
- 14th International Biotechnology Symposium and Exhibition. Biotechnology for the Sustainability of Human Society. September 2010 Rimini Italy.

Publications:

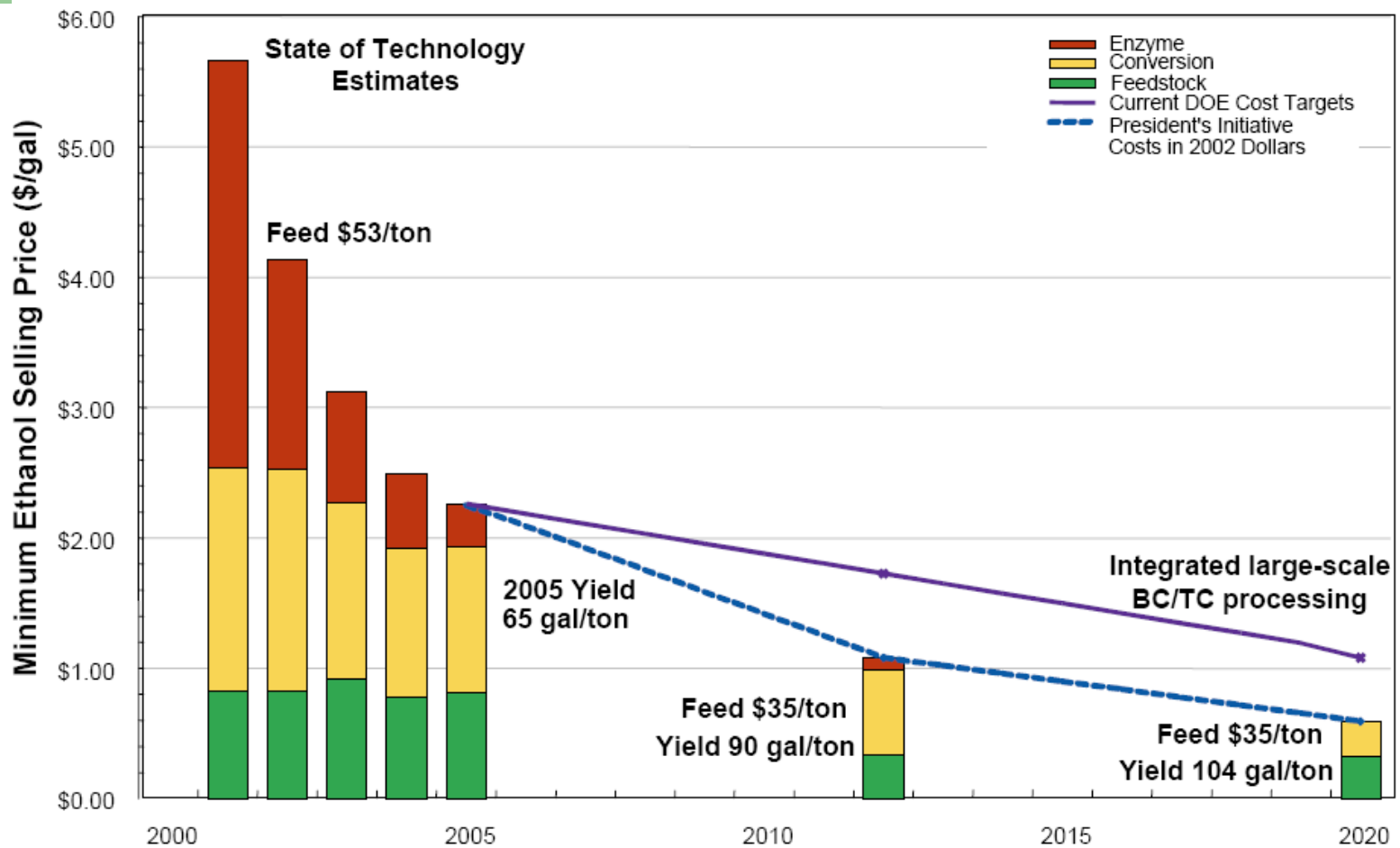
- Two manuscripts in redaction, containing results about cloning, recombinant expression and characterization of the two novel cellulases
- One manuscript including the thermostabilization of the cellulase cel7.

Acknowledgements

- Undergraduate students:
 - Alejandra Guerrero
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 - The Institute for Cell Dynamics and Biotechnology (ICDB).

Thanks !



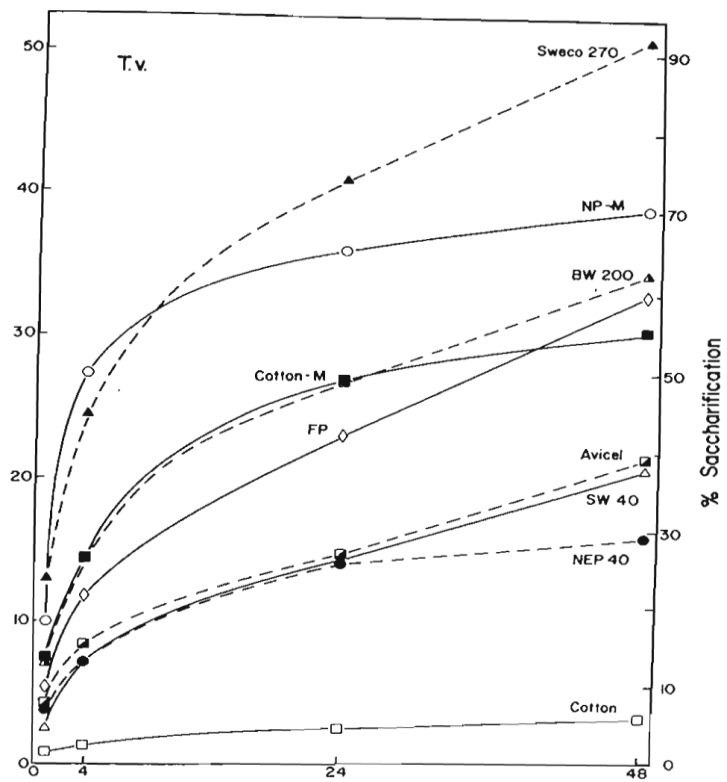


Cellulases are grouped in families, depending on their sequences

- Fungal Endoglucanases
 - Family GH5
 - Family GH7
 - Family GH61
- Fungal Exoglucanases
 - Family GH6
 - Family GH7
 - Family GH74

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Enzymes

- Functional proteins; catalyse biochemical reactions
- Primarily made up of chains of amino acid linked together by peptide bonds.
- Found in all living organisms
- Work under mild conditions
- Replace harsh chemicals such as strong acids
- Biological degradable
- A “clean” technology