

Business from technology

Enzymes and biotechnology: could we overcome modern challenges?

2nd International Conference on Genomics & Pharmacogenomics

Dr. Junio Cota VTT Brasil LTDA

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SUMMARY

- What is VTT?
- The OMICS Era
- New Enzyme Discovery
- Protein Engineering





VTT Group in brief

Turnover 292 M€ (2010) ■ Personnel 3,167 (1.1.2011)





Customer sectors

- Biotechnology, pharmaceutical and food industries
- Electronics
- Energy
- ICT
- Real estate and construction
- Machines and vehicles
- Services and logistics
- Forest industry
- Process industry and environment

Focus areas of research

- Applied materials
- Bio- and chemical processes
- Energy
- Information and communication technologies
- Industrial systems management
- Microtechnologies and electronics
- Services and the built environment
- Business research

VTT's operations

Research and Development Strategic Research Business Solutions IP Business Group Services

VTT's companies

VTT Expert Services Ltd (incl. Labtium Ltd, Enas Ltd) VTT Ventures Ltd VTT International Ltd VTT Memsfab Ltd



VTT Group on the map





BIOREFINERY

Brazilian biomass raw material







BRAZIL





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Human Genome Project



http://web.ornl.gov/sci/techresources/Human_Genome/project/whydoe.shtml

VTT BRASIL LTDA

07/10/2014



Evolution of Cost per Megabase



http://evomics.org/2014/01/sequencing-technology-wheres-my-minion/



Evolution of Whole-Genome Sequencing



Su, Andrew (2013): Cumulative sequenced genomes. figshare.





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Enzyme discovery in the OMICS Era

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Liebl, Wolfgang (2011): Metagenomics



New Enzymes for Biofuels: GH 10 Xylanase

OPEN a ACCESS Freely available online



Development and Biotechnological Application of a Novel Endoxylanase Family GH10 Identified from Sugarcane Soil Metagenome

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Enzymes for Biofuels: GH 10 Xylanase





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Proteomics: Secretome of *Penicillium equinulatum*

OPEN O ACCESS Freely available online

The *Penicillium echinulatum* Secretome on Sugar Cane Bagasse

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SCE

MCL

DNPC

BIX

SAT

Proteomics: Secretome of Penicillium equinulatum





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Proteomics: Secretome of Trichoderma harzianum

Bioresource Technology 131 (2013) 500-507



Understanding the cellulolytic system of *Trichoderma harzianum* P49P11 and enhancing saccharification of pretreated sugarcane bagasse by supplementation with pectinase and α -L-arabinofuranosidase



Priscila da Silva Delabona^{a,*}, Júnio Cota^a, Zaira Bruna Hoffmam^a, Douglas Antonio Alvaredo Paixão^a, Cristiane Sanchez Farinas^b, João Paulo Lourenço Franco Cairo^a, Deise Juliana Lima^a, Fábio Marcio Squina^a, Roberto Ruller^a, José Geraldo da Cruz Pradella^a

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Proteomics: Secretome of *Trichoderma harzianum*



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Protein Engineering is a tailor-made process

THE SCIENCE OF WHAT'S POSSIBLE.™





What's on your mind? What's your need?



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Protein Engineering: Rational or Non-rational Design?

Current Paradigms

X

Mechanism-based

(Rational)

Detailed structural analysis



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Building a Xylanase – Lichenase Chimera

Biochimica et Biophysica Acta 1834 (2013) 1492-1500



Assembling a xylanase–lichenase chimera through all-atom molecular dynamics simulations



Junio Cota ^{a, d, 1}, Leandro C. Oliveira ^{a, b, 1}, André R.L. Damásio ^a, Ana P. Citadini ^a, Zaira B. Hoffmam ^a, Thabata M. Alvarez ^a, Carla A. Codima ^a, Vitor B.P. Leite ^b, Glaucia Pastore ^c, Mario de Oliveira-Neto ^d, Mario T. Murakami ^e, Roberto Ruller ^a, Fabio M. Squina ^{a,*}

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Chimeras: Multidomain Proteins

- Multidomain/multifunctional proteins can reduce costs with enzyme load;
- End-to-end fusion between the N and C termini of the parental enzymes can result in nonfunctional chimeras.



S.Y. Hong et al., Biotechnology Letters, 29, 931-936 (2007)

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Chimeras: Multidomain Proteins

✓ The selection of the linker sequence is particularly important for the construction of functional fusion proteins



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Building Chimeras: Molecular Dinamics

- ✓ Energy Landscape Theory
- ✓ Structure Based Models
- The topology could drives the protein folding
- ✓ Save computational time



X. L. Ji, and S. Q. Liu. J. Biomol Struct Dyn 28, 621-623 (2011)

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Structure Based Models (SB)



The unique Free Energy basin suggests a group of structures candidates: simulations are mainly driven by the entropy of the system

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Building Chimera

Overlap PCR

SDS-PAGE



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SAXS experimental and theoretical curves





Optimal pH





Optimal Temperature





Substrate Specificity

	Specific activity (U/nmol)		
Substrate	Xylanase	Lichenase	XylLich
Birchwood Xylan	3.73 ± 0.29	ND	2.71 ± 0.13
Beechwood Xylan	3.17 ± 0.07	ND	2.87 ± 0.08
Rye Arabinoxylan	3.73 ± 0.14	ND	3.03 ± 0.15
Wheat Arabinoxylan	1.36 ± 0.12	ND	0.88 ± 0.07
Oat Spelt Xylan	3.28 ± 0.27	ND	2.15 ± 0.06
Lichenan	ND	3.65 ± 0.29	3.85 ± 0.16
β-Glucan	ND	5.03 ± 0.20	5.11 ± 0.07
Laminarin	ND	ND	ND
Xyloglucan	ND	ND	ND
Glucomannan (Konjac)	ND	ND	ND



Capillary Electrophoresis



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Capillary Electrophoresis

Xylohexaose + Lichenan









Conclusions

- This work presented a novelty way to predict the disposal of chimera domains in solution before experimental assays;
- A potential tool for screening and development of enzyme cocktails for second generation biofuels;
- The expansion of hydrolase activities in an unique protein could be a route for increase cost-effective of biomass saccharification;
- Enzyme production data suggests an advantage on producing the fused protein instead the wild type ones separated.

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Protein Engineering: Typical Challenges

- Design proteins with certain function;
- Design proteins which bind novel ligands;
- Alter binding affinity and specificity of proteins;
 - Increase activity of enzymes;
 - Change thermal tolerance, pH stability;
 - Alter allosteric regulation;
 - Decrease inhibition of enzymes;
 - Increase protease resistance;
 - Reactivity in nonaqueous solvents;
 - Eliminate cofactor requirement.



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Acknowledgements





Centro de Ciência e Tecnologia do Bioetanol





RCNPg **FAPESP**



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