



High-throughput strain identification and production of fungal enzymatic cocktails for the valorisation of lignocellulosic biomass

Quentin Haguet & Egon Heuson

quentin.haguet@univ-lille.fr / egon.heuson@centralelille.fr



The **perfect** enzyme **cocktail**
for **biomass degradation**

Virtual lab tour:

<https://www.vip-studio360.fr/galerie360/visites/vv-centrale-lille/vv-realcat-c.html>

The REALCAT platform

REALCAT

- Advanced High-Throughput Technologies Platform for all types of experiments in Chemistry and Biology, dedicated to biomass valorization.

3 main areas of expertise

➤ Catalysis

- **Chemical catalysis:** homogeneous and heterogeneous
- **Biocatalysis:** enzyme and fermentation

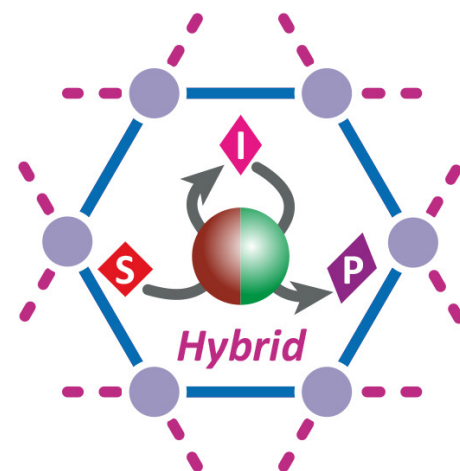
- **Structural and compositional characterisation** of chemical and biological materials used/generated (catalysts, metabolites, polymers, enzymes, etc.)

➤ Side activities in biology

- Proteomics, NRPomics
- Search for new antimicrobial molecules
- Production of secondary metabolites



*Combination of
chemo & Bio*



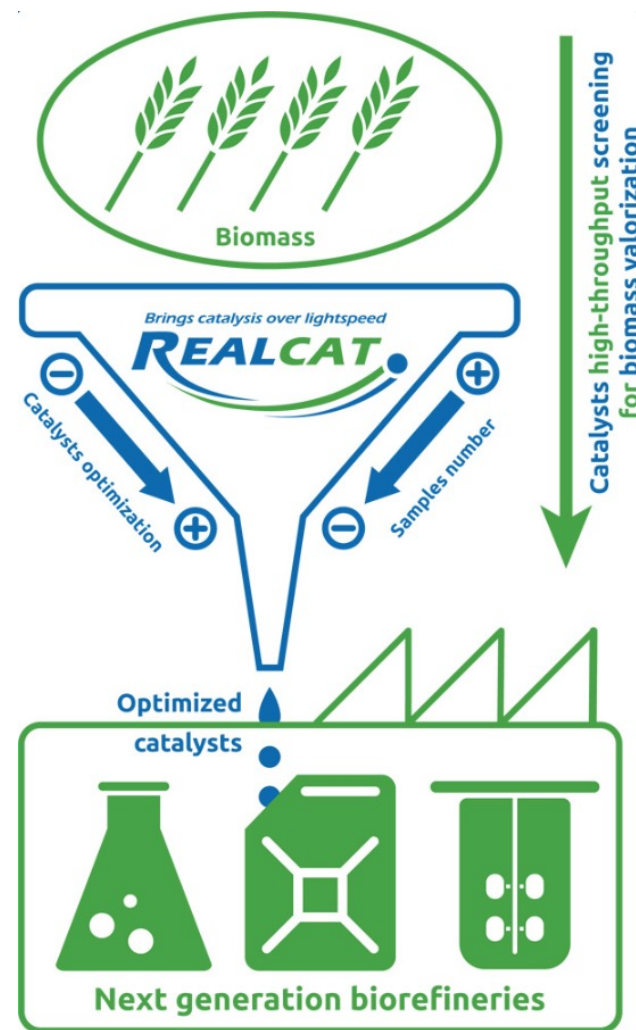
The REALCAT platform

3 main types of equipment dedicated to :

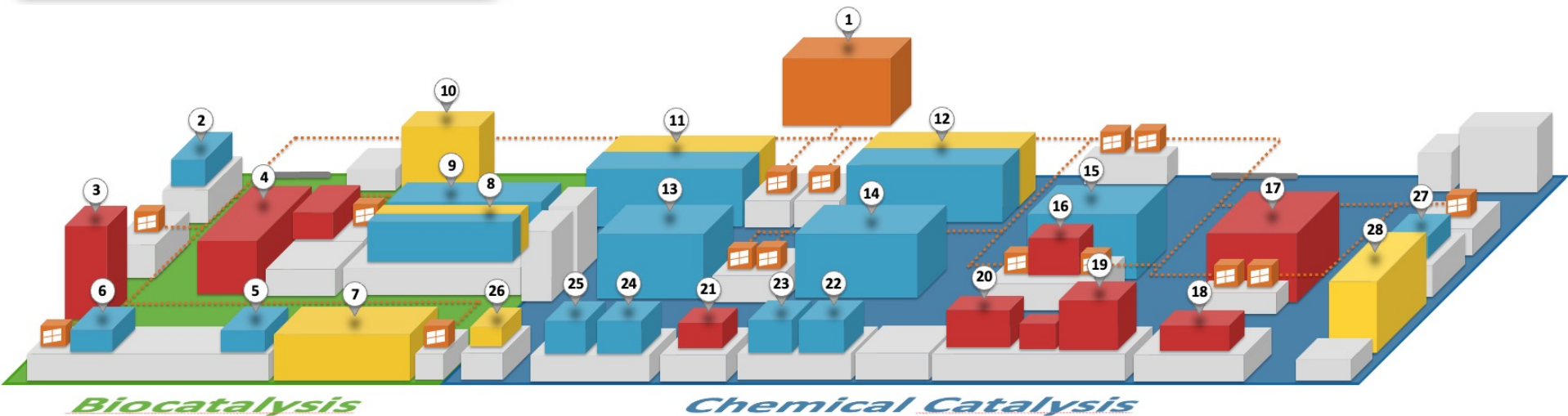
- **Synthesis** of chemical and biological materials (catalysts, strains, enzymes, metabolites, etc.)
- **Testing** of catalytic properties (catalytic, nutritional, antimicrobial, etc.)
- **Characterization** (structure, composition, physico-chemical properties, etc.)

Our final objectives :

- **Accelerate each step of the experimental phase** of a chemistry and biotechnology research project to significantly reduce the consumption of money and time
- Define new ways to **valorise biomass**



REALCAT floorplan



More than 30 automated devices

- All fully dedicated to **high-throughput experiments**
- **Very high modularity** allowing a large variety of subjects
- **Fully integrated** to allow synergy between machines

+ some other robots, technical rooms and offices.

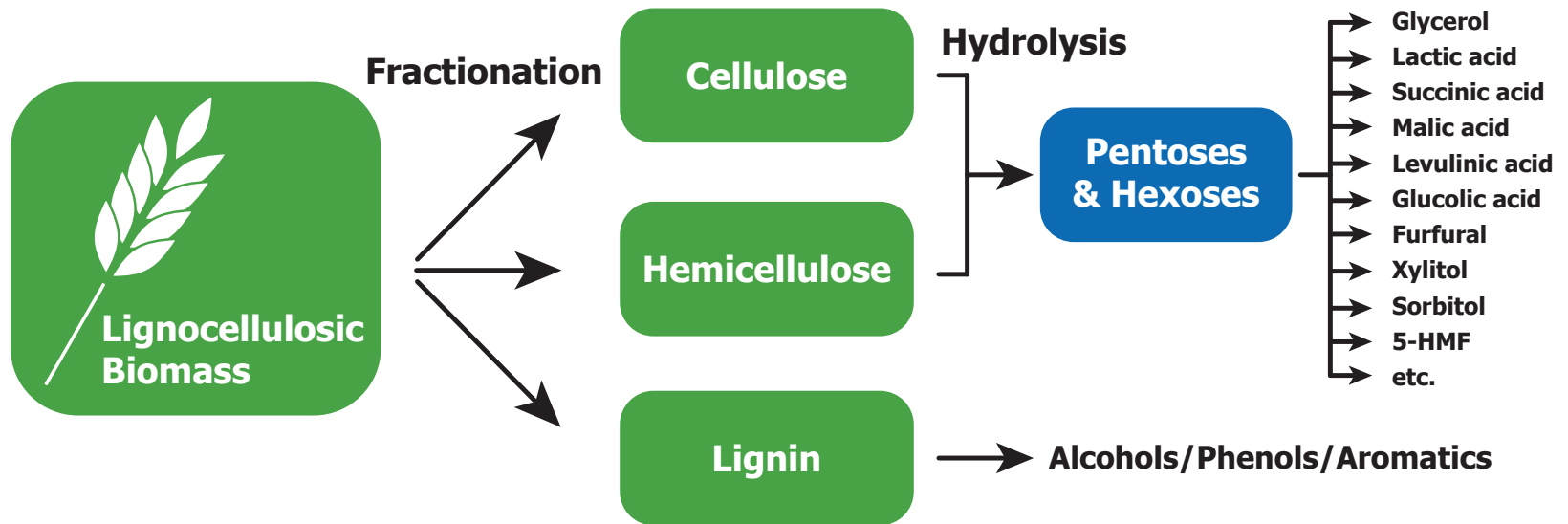
1	Central server - DELL	15	Flowrence - Avantium
2	Biomek NXp + BioLector Pro - Beckman Coulter/M2PLabs	16	M4 Tornado - Bruker
3	Autoflex Speed - Bruker	17	D8 Discover - Bruker
4	Acquity UPLC Synapt G2-Si HDMS - Waters	18	Tensor 37-HTS-XT - Bruker
5	Cary 3500 - Agilent	19	ICP-OES - Agilent
6	BioLector - M2pLabs	20	Vulcan 42S - Questron Technologies/Horiba
7	QPix 460 - Molecular Devices	21	XploRa - Horiba Jobin Yvon
8	Biomek FXp - Beckman Coulter	22	GC-FID-2010 Plus AF - Shimadzu
9	Biomek FXp - Beckman Coulter	23	GC-FID-MS-QP2010 Ultra EI - Shimadzu
10	Laminar flow hood - Aquaria	24	HPLC-UV-IR - Shimadzu
11	Catimpreg - Chemspeed	25	HPLC-DAD-MS - Shimadzu
12	Autoplant - Chemspeed	26	Calcination oven - Dislab
13	Flowrence - Avantium	27	Screening Pressure Reactor (SPR) - Freeslate
14	Flowrence - Avantium	28	Fume hood - Asem



Valorization of lignocellulosic biomass

Target: Biomass decomposition into biofuels, building blocks for fine chemistry and polymers:

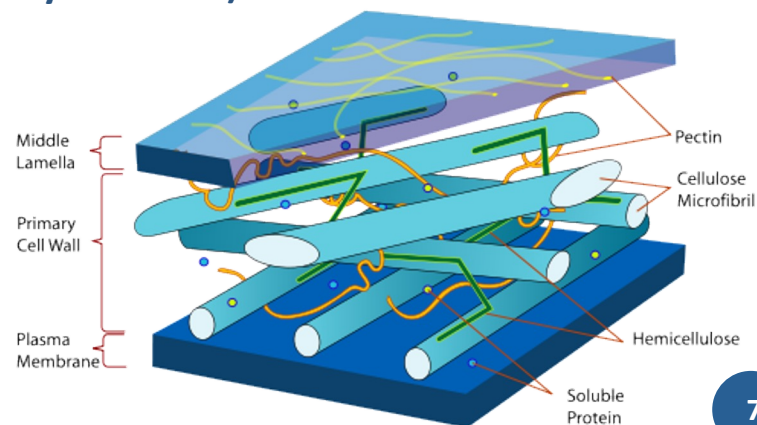
- Production of bioethanol from the fermentation of extracted sugars
- Production of 20 platform molecules from C5 and C6 sugars



- + alcohols/phenols/aromatics from lignin: methanol, benzoic acid, catechol, cinnamic acid, etc.

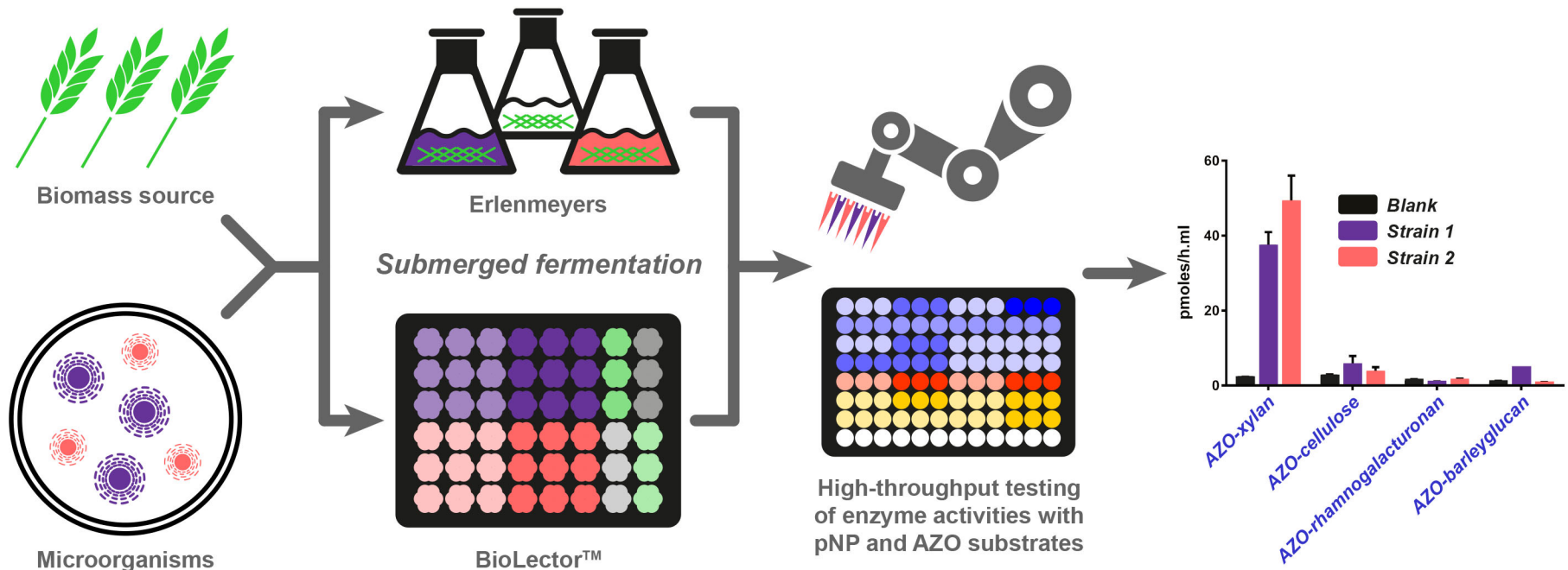
The challenge: designing the perfect enzyme cocktail for lignocellulose degradation

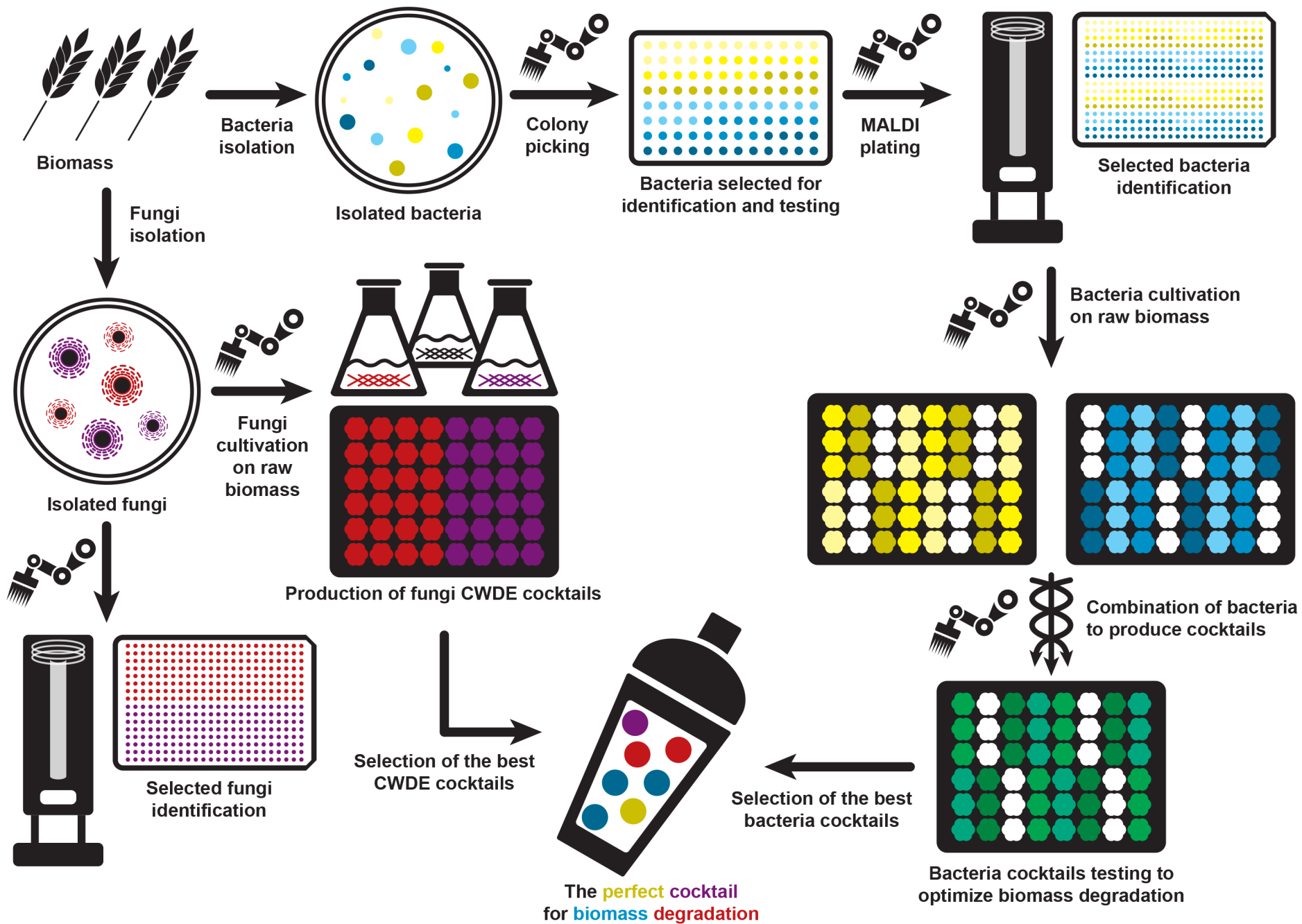
- Ideal case: no pre-treatment (mimic nature)
- No “universal” bacterial/fungal strain efficient on cellulose, hemicellulose AND lignin => Find the perfect enzyme combination
- Many available approaches: metagenomics, low throughput fermentation screenings, *de novo* design, commercial blends...
- Numerous drawbacks:
 - Very time and money consuming
 - High systems complexity (specially in biodiversity mixtures)
 - Model substrates are not representative
 - Lack of synergy and thermodynamic equilibriums issues

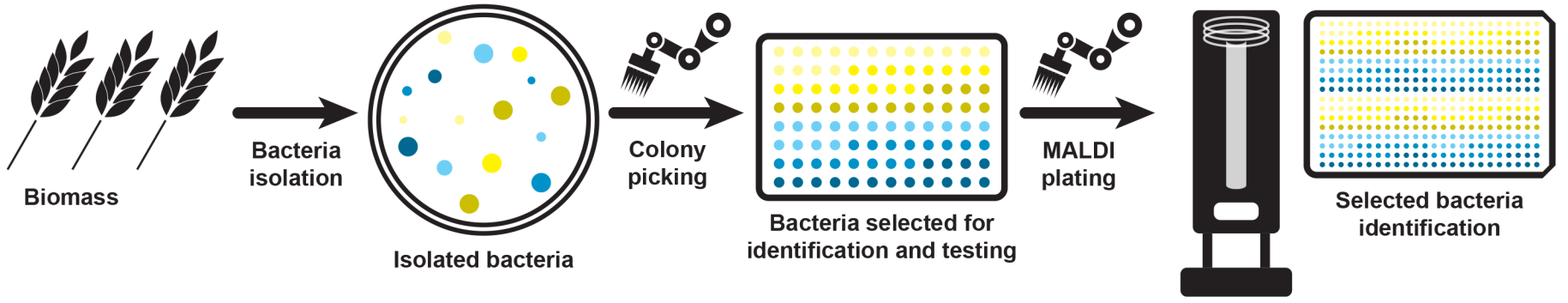


Harvesting enzyme from microorganisms living on target substrate

- Premise 1: Organisms that develop on biomass are the best equipped to degrade it
- Premise 2: No single organism can proceed to a complete degradation
- ⇒ Need for harvesting and combining numerous strains
- First semi-automated method presented in 2018



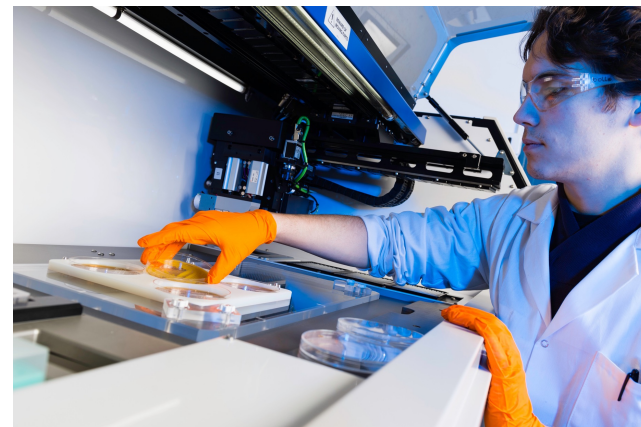
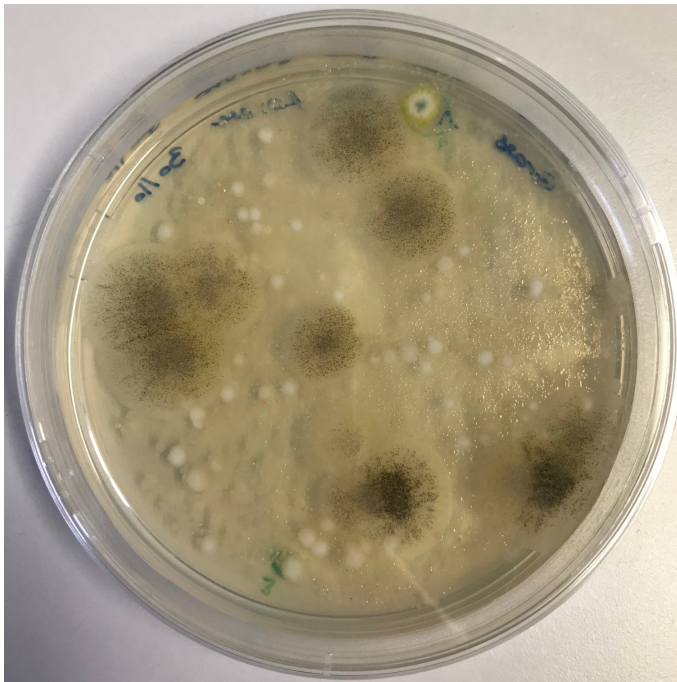




Step 1 – Colony picking

Manual and automated colony recovery: using the QPix 460 :

- 96-needle head (approx. 2000 colonies/hour)
- Up to 10 Petri (or 2 Q-Trays) dishes and 40 destination plates per batch
- “Intelligent” optical recognition software



Qpix 460 – Molecular devices

Step 1 – Colony picking

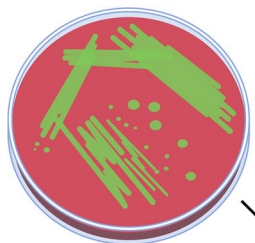
Automated colony picking



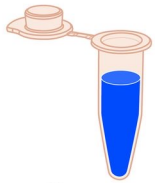
Step 2 – MALDI BioTyper

⇒ First **rapid identification** using a **MALDI-TOF** mass spectrometer

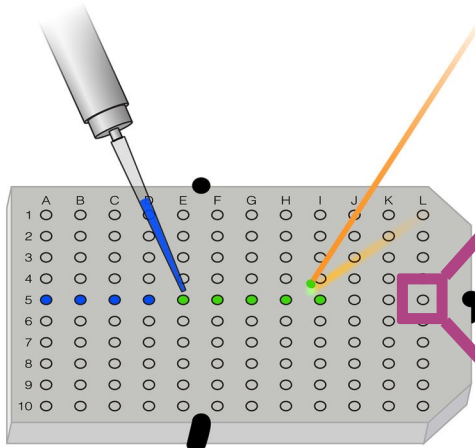
⇒ Confirmation by 16s / ITS RNA sequencing or API galleries if required



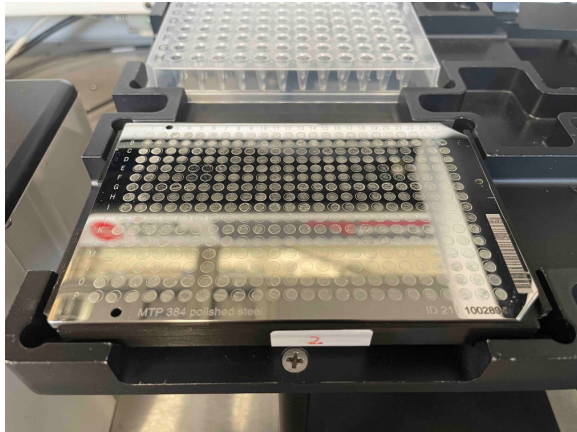
① Sample culture



② Matrix



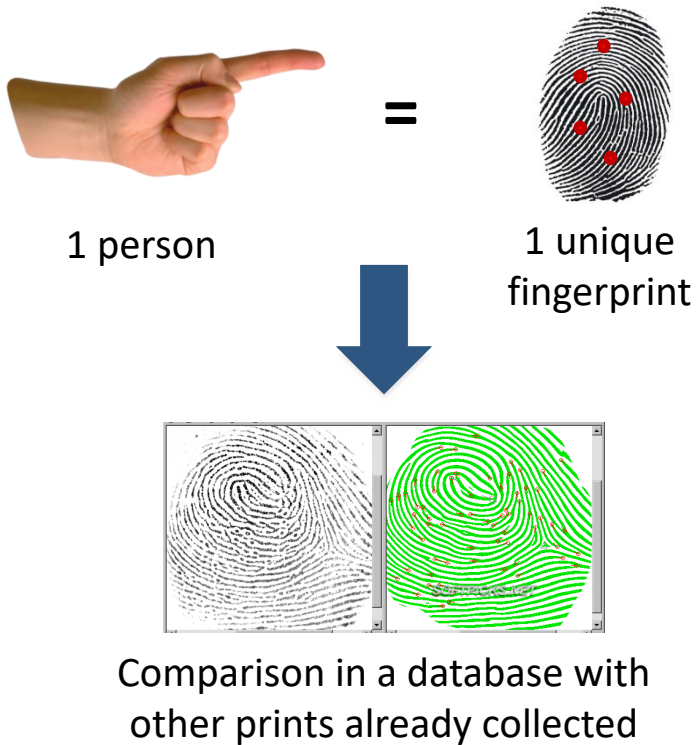
③ MALDI-TOF/MS sample plate



Autoflex Speed – Bruker

Step 2 – MALDI BioTyper

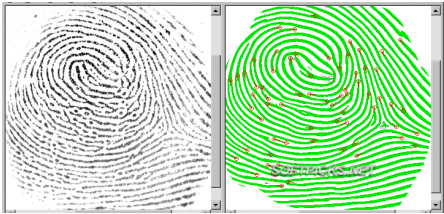
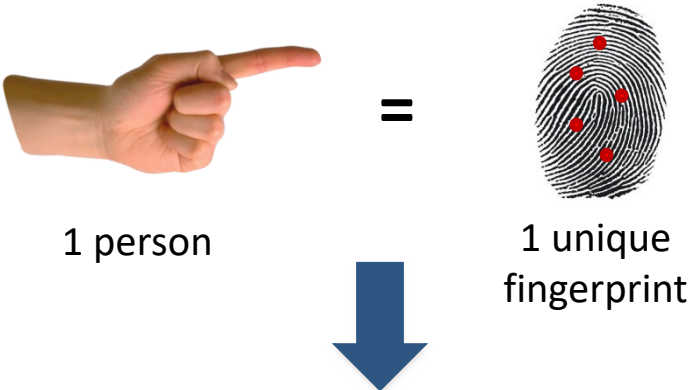
Principle of MBT identification: Digital fingerprinting technique based on the membrane proteins of microorganisms



Human fingerprinting

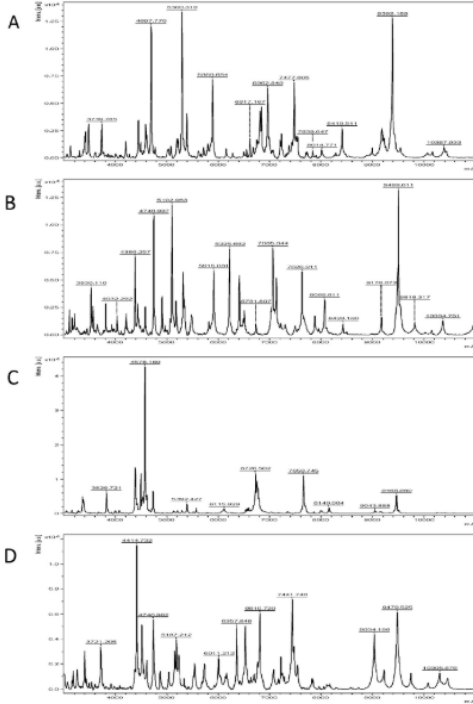
Step 2 – MALDI BioTyper

Principle of MBT identification: Digital fingerprinting technique based on the membrane proteins of microorganisms

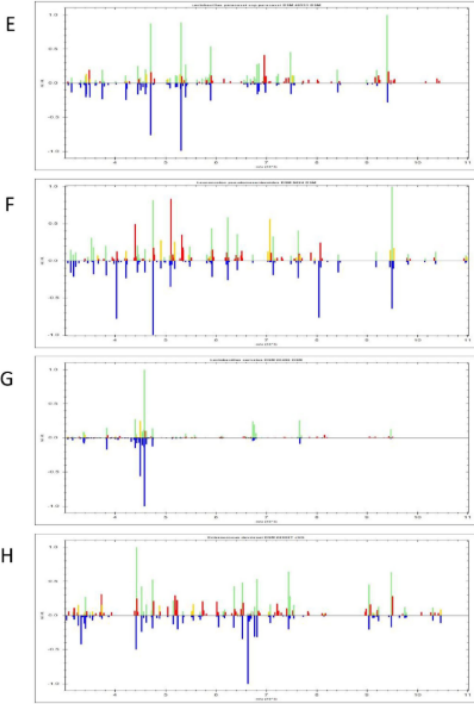


Comparison in a database with other prints already collected

Human fingerprinting



Mass spectra



Comparison with our in-house + Bruker databases (> 10000 strains)

Molecular fingerprinting

Step 2 – MALDI BioTyper

Principle of MBT identification: Digital fingerprinting technique based on the membrane proteins of microorganisms

Sample Name	Sample ID	Organism (best match)	Score Value	Organism (second-best match)	Score Value
<u>N9</u> (+++)(C)	8 (standard)	Lactobacillus plantarum	<u>2.40</u>	Lactobacillus plantarum	<u>2.39</u>
<u>N10</u> (+++)(C)	9 (standard)	Lactobacillus pentosus	<u>2.37</u>	Lactobacillus pentosus	<u>2.29</u>
<u>N11</u> (+++)(C)	10 (standard)	Lactobacillus plantarum	<u>2.24</u>	Lactobacillus plantarum	<u>2.24</u>
<u>N12</u> (+++)(C)	11 (standard)	Lactobacillus pentosus	<u>2.07</u>	Lactobacillus pentosus	<u>2.03</u>
<u>N13</u> (+++)(C)	12 (standard)	Lactobacillus plantarum	<u>2.47</u>	Lactobacillus plantarum	<u>2.45</u>
<u>N14</u> (+++)(C)	13 (standard)	Lactobacillus brevis	<u>2.13</u>	Lactobacillus brevis	<u>2.13</u>

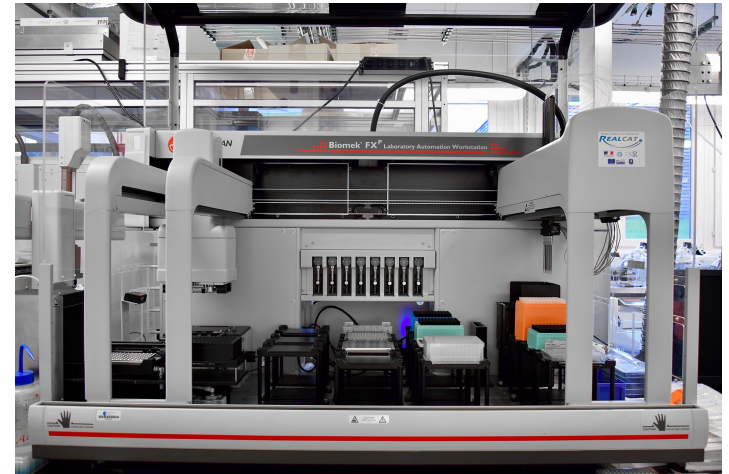
Meaning of Score Values

Range	Description	Symbols	Color
2.300 ... 3.000	highly probable species identification	(+++)	green
2.000 ... 2.299	secure genus identification, probable species identification	(++)	green
1.700 ... 1.999	probable genus identification	(+)	yellow
0.000 ... 1.699	not reliable identification	(-)	red

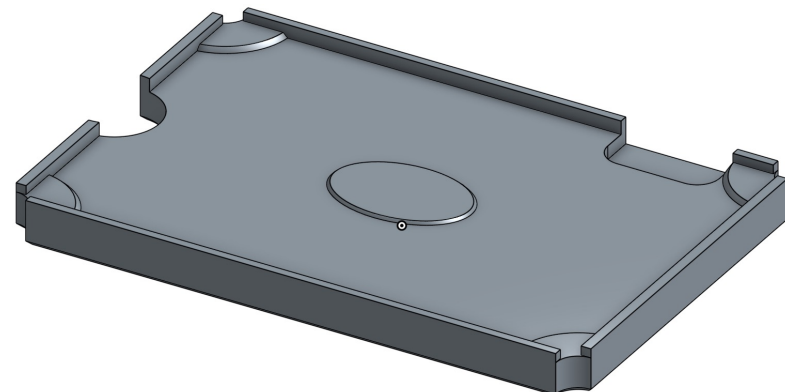
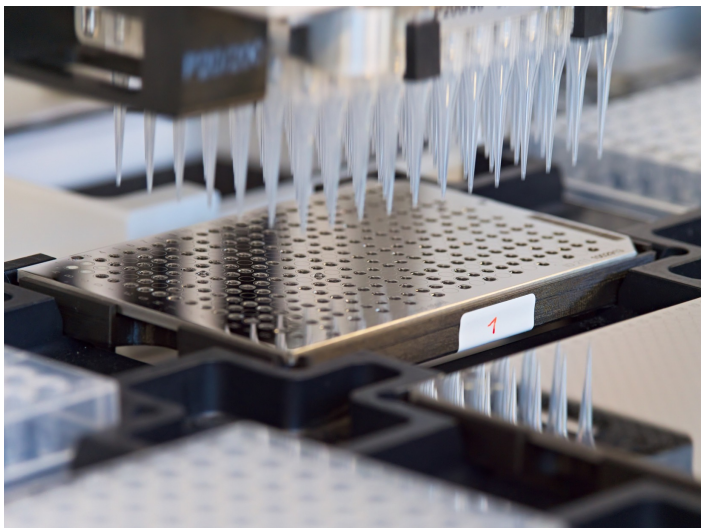
Step 2 – MALDI BioTyper

Use of a liquid handling robot : Automated protein extraction and MALDI target preparation

- 3 main steps:
 - ⇒ Cryo-stocks preparation in 30% glycerol solution for bank conservation
 - ⇒ Cells washing and protein extraction
 - ⇒ Mixing the protein extracts with the matrix and depositing on the target



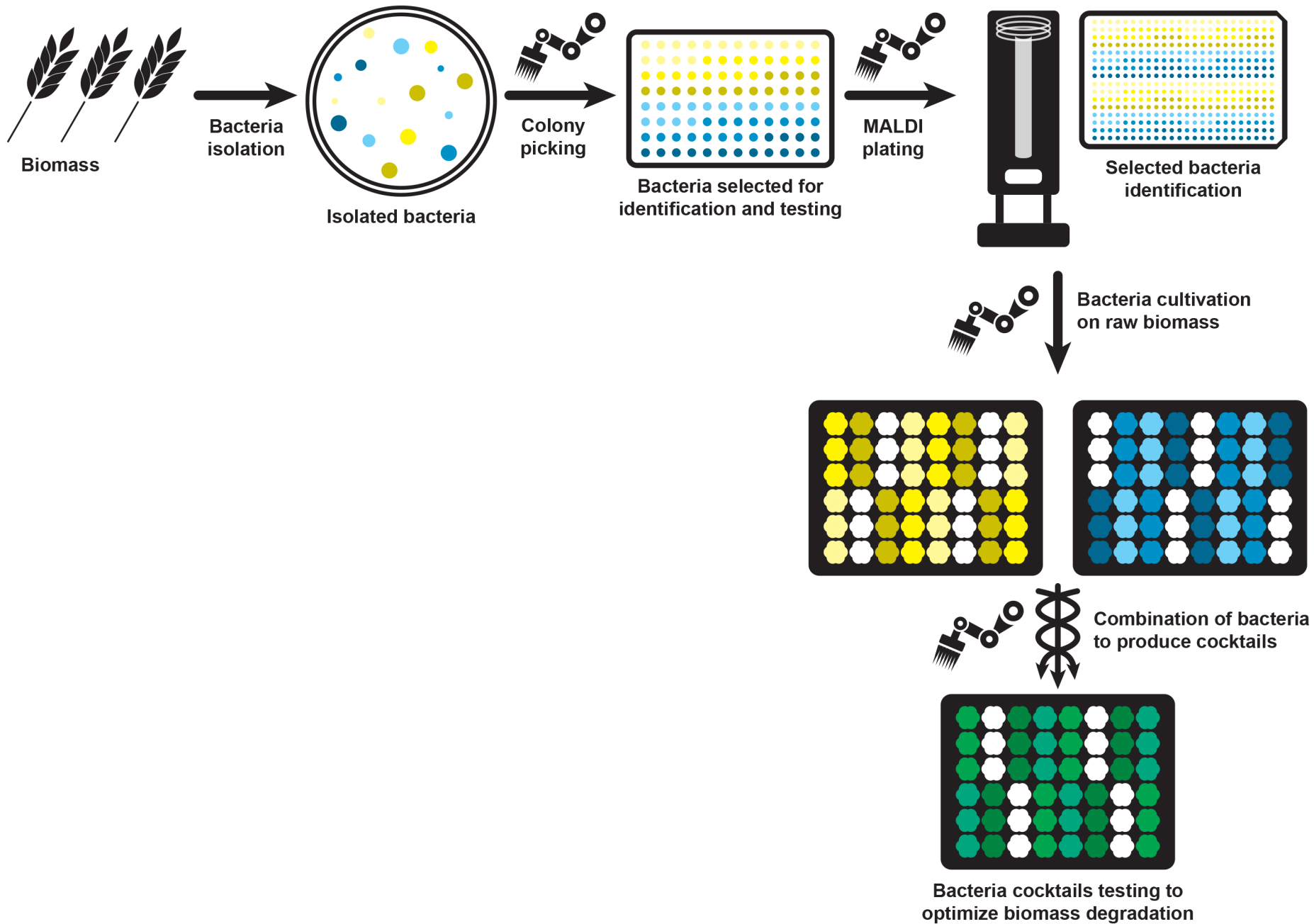
Biomek FXp – Beckman Coulter



Step 2 – MALDI BioTyper

Deposition of the sample/matrix mixture





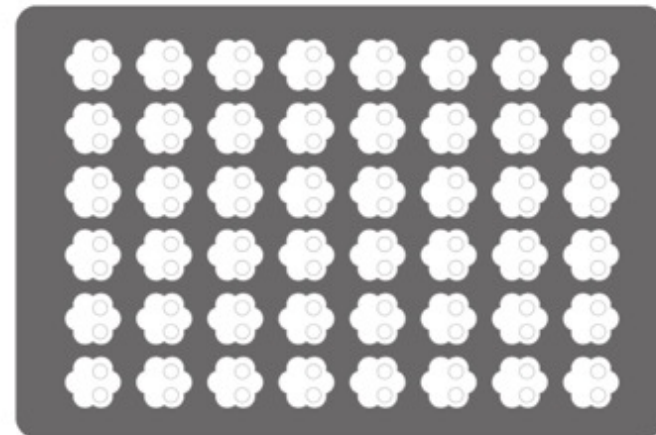
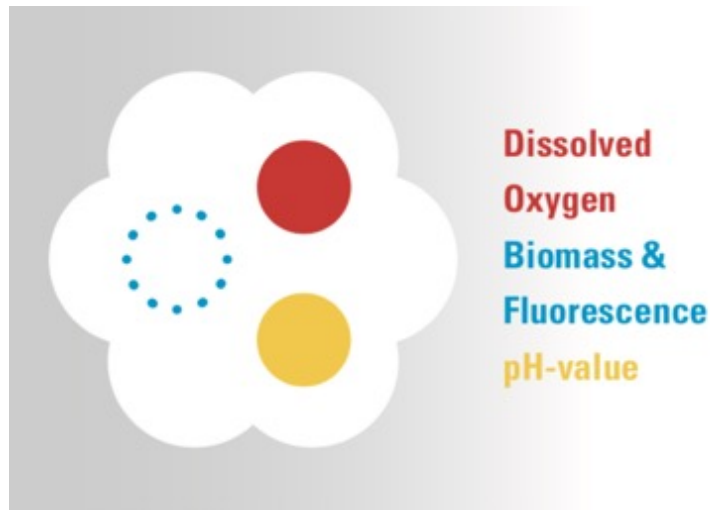
Step 1 – Cultivation and CWDE induction

Use of a high throughput culture device: *The BioLector*

- ⇒ 48 x 1mL parallel fermentations
- ⇒ On-line monitoring and control of pH, pO₂ and biomass
- ⇒ Temperature, humidity and atmosphere control (aerobic and anaerobic fermentation)



BioLector – M2PLabs



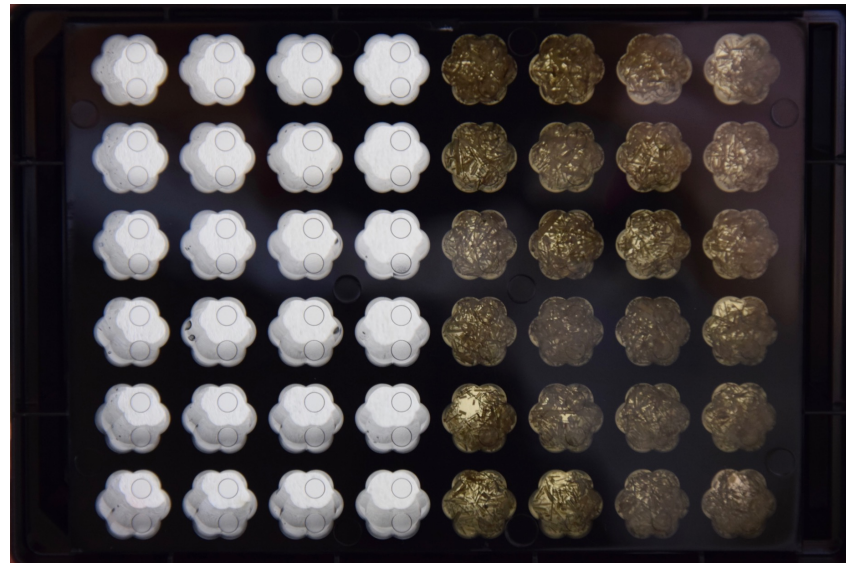
Step 1 – Cultivation and CWDE induction

*Use of a high throughput culture device: **The BioLector***

- ⇒ 48 x 1mL parallel fermentations
- ⇒ On-line monitoring and control of pH, pO₂ and biomass
- ⇒ Temperature, humidity and atmosphere control (aerobic and anaerobic fermentation)
- ⇒ Adaptation to offer the possibility to use raw materials directly (straw, stover, etc.)



BioLector – M2PLabs

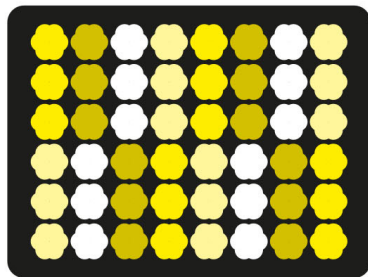
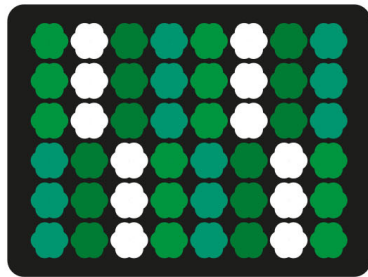


Step 2 – Secreted CWDE mixing

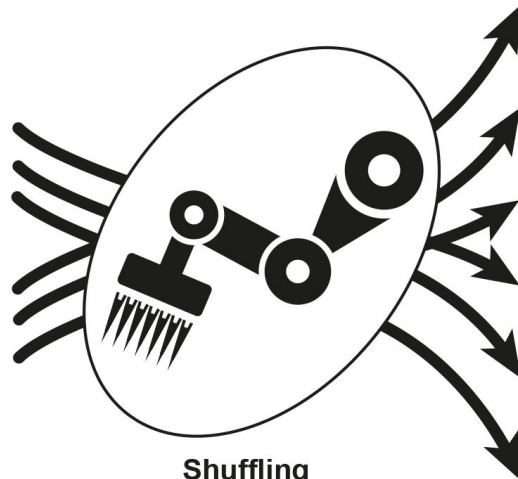
Rational mixing using fully automated workflow using Biomek FXP

⇒ **384 cocktails** combinations created from each batch of **3 strains** / **1 inducing biomass** / **2 tested substrates**

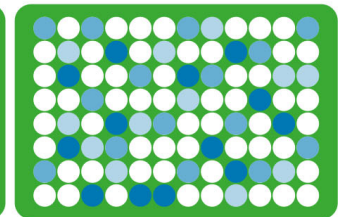
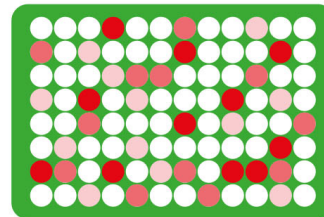
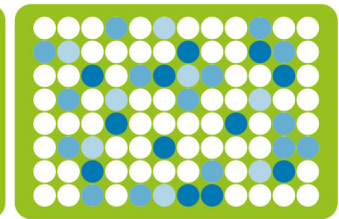
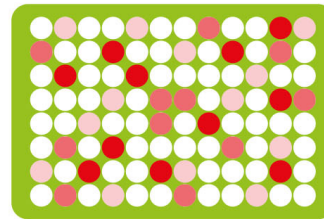
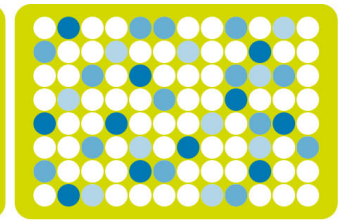
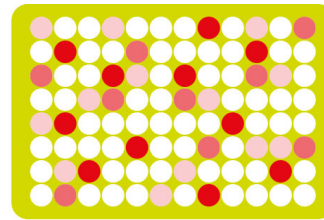
⇒ **New automation compatible DOE program developed**



Submerged fermentation with selected strains (BioLector®)



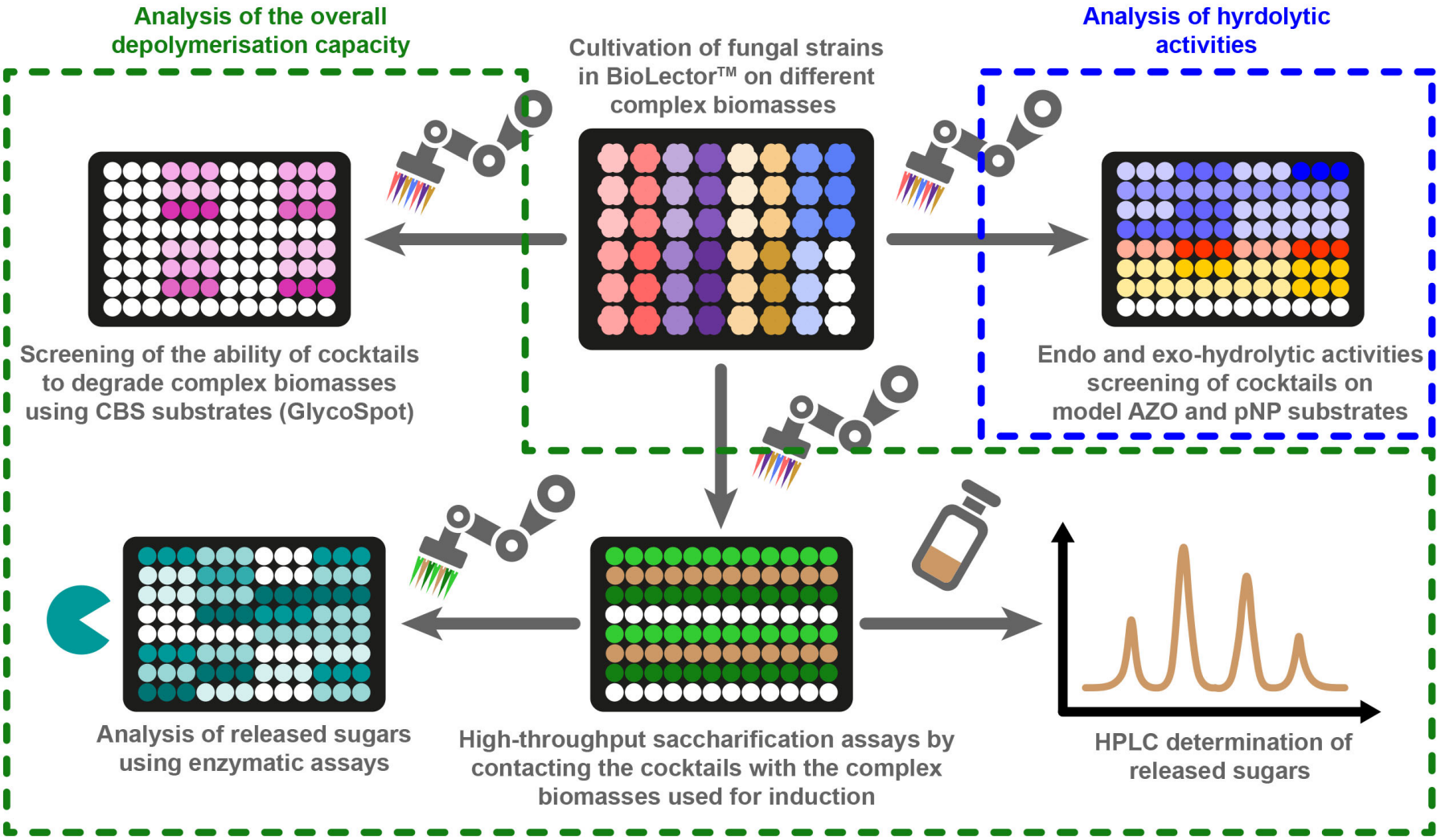
Shuffling (Biomek FXP)



High-Throughput assays on different substrates from different biomasses (Biomek FXP)

Step 3 – CWDE activity measurement

Extension of the activity measurement panel



Results for strain identification and enzymes production:

- ⇒ 55 Bacteria isolated / 22 identified - 23 Fungi isolated / 14 identified from 5 biomass sources
- ⇒ Screenings of 3 Fungi + 3 inducing biomass sources for CWDE production
- ⇒ Correlation of enzyme activities detected with complementary analytical methods
- ⇒ Strong correlation between biomass composition and CWDE composition
- ⇒ Successful use of CWDE cocktails to increase the production of short chain organic acids by bacterial dark fermentation, including the implementation of a Plug Flow Reactor (PASS-BIO)



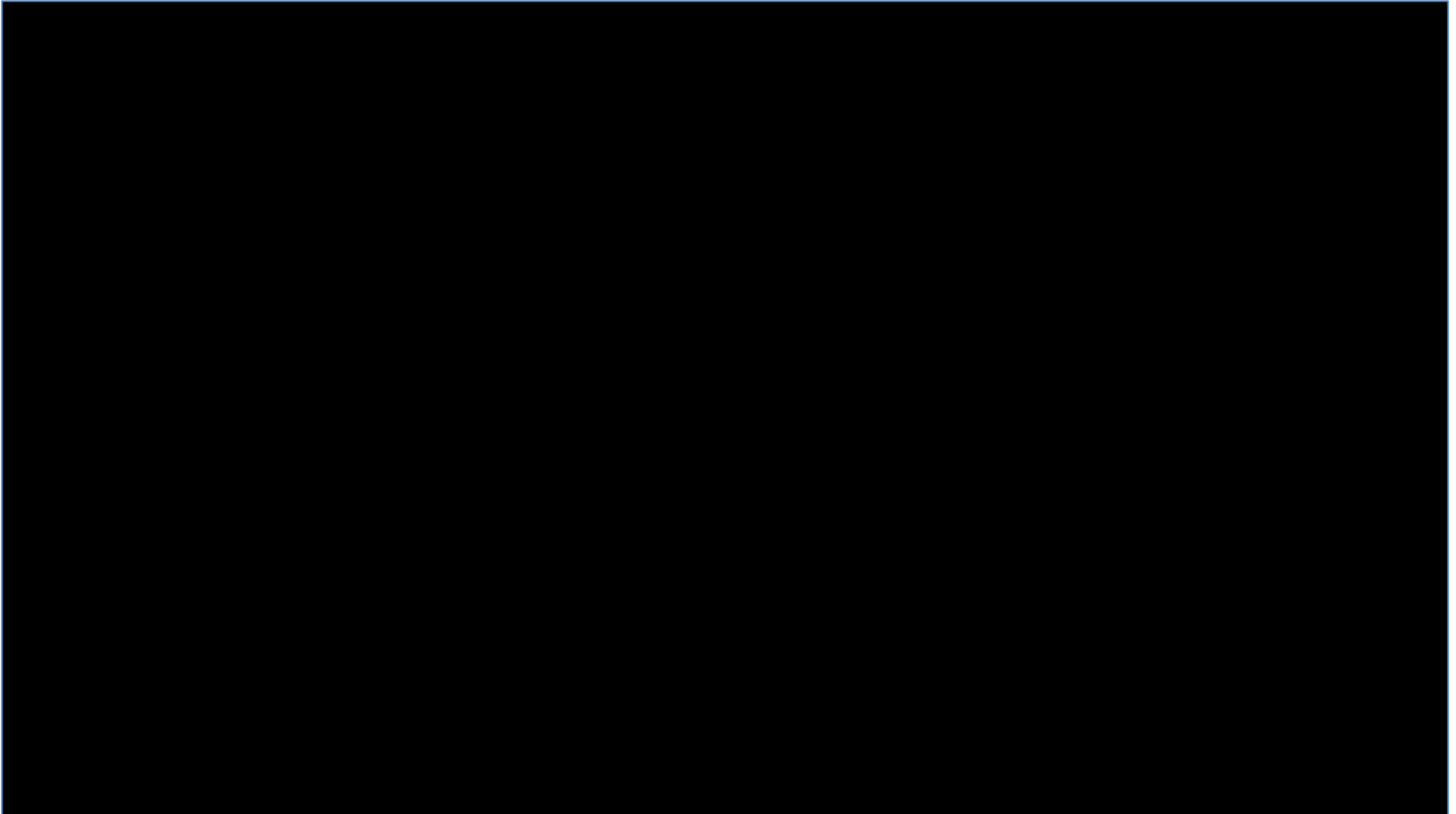
New developments in progress:

- ⇒ Analysis of the protein composition of cocktails (proteomics)
- ⇒ Attempt to correlate the enzyme composition of the cocktails with the screening parameters (biomass, conditions, strains, etc.) by machine learning.
- ⇒ Creation of artificial cocktails
- ⇒ Attempt at direct solid deposit of strains from agar plates for faster identification



Ongoing developments

Attempt to transfer strains directly from solid agar to MALDI target



Thank you for your attention!

Brings catalysis over lightspeed

REALCAT

The logo for REALCAT features the word "REALCAT" in a bold, sans-serif font. The letters "REAL" are blue, and "CAT" is green. Below the text is a large, stylized arc that starts blue on the left and transitions to green on the right, ending in a blue sphere. The arc has a slight shadow effect.

www.realcat.fr

... au Nord, c'étaient les Corons!