

# **Genefish : an alternate metagenomic approach for capturing** targeted bacterial diversity in an engineered recipient E. coli strain

N.Lombard<sup>1</sup>, A.Faugier<sup>1</sup>, C.Lavire<sup>1</sup>, S.Jacquiod<sup>1</sup>, L.Philippot<sup>2</sup>, X.Zhang<sup>1</sup>, J.C.Lazzaroni<sup>3</sup>, P.Simonet<sup>1</sup> and L.Franqueville<sup>1</sup>

Environmental Microbial Genomics Group, Laboratoire AMPERE, UMR CNRS 5005, Ecole Centrale de Lyon, 36 avenue Guy de Collongue, 69134 Ecully cedex, France <sup>2</sup>Soil and Environmental Microbiology, UMR1229, CMSE INRA, 21065 Dijon cedex, France

<sup>3</sup> Unité de Microbiologie, Adaptatation et Pathogénie, UMR5240, Université de Lyon, 69622 Villeurbanne cedex, France

## **1-Introduction**

Bacterial diversity in soil environment is so high that recovery of specific genes in soil extracted DNA requires construction and screening of metagenomic DNA libraries of several hundreds thousands of clones. The gene fishing approach we describe here can be considered as a simpler alternative to the traditional metagenomic technique to recover specific genes or DNA fragments in a metagenome.

## 2-Genefish concept



## **3-Host strain construction**

**Construction of an efficient** inducible counter selection system

Efficiency is estimated by the host strain survival after induction by calculating an escaping rate (Tx E)





Legend: Blue line : metagenomic DNA Blue box : recombination site Red line : counter selection cassette

- (A) **Transformation** of the host strain with fragmented metagenomic DNA
- (B) **Insertion of metagenomic DNA** in the recipient genome by double CO targeted on specific recombination cloned site
- (C) **Positive selection** of recombinant clones after inducible death of non transformed and unrecombined cells
- Tx E (toxic gene 1) =  $10^{-5}$ Tx E (toxic gene 2) =  $10^{-6}$ Tx E (two toxic gene 1) =  $10^{-6}$  to  $10^{-7}$ Tx E (toxic gene 1 & 2) <10<sup>-9</sup>

#### **Recombination site modification**

The counter selection cassette is flanked by 2 MCS and cloned in a medium copy number plasmid

✓ Easy extraction for modification ✓ Modification ability with MCS Orientation of recombination site

#### Legend:

Shaded red genes : counter selection cassette part Blue triangles: MCS for recombination site insertion Purple circle: element for high recombination efficiency

**Increased efficiency of transformation** and recombination in the host strain

✓ Host strain : Genetically engineered E. coli including the lamda red gam system ✓ DNA acquisition way : Electroporation

## 4-Lambda Red gam system evaluation for recombination



### 5-Genefish applications

Targeted gene for Genefish concept validation: *narG*, a widespread gene in bacteria encoding a respiratory nitrate-reductase

**5a**- Gene alignment for *nar* operon on several bacteria [6]

5c- Cloning of G1 / G2 PCR products into toxic plasmid

5d- recombination experiment in the engineered host strain

**Important Parameters** 

✓ Size of recombined DNA fragments



#### ✓Optimal size for cloned homeologous recombination sequences ✓ Homology between cloned domains and target DNA ✓ Detection limit

✓ Toxicity escaping rate

#### **References:**

[1] Yu, D., Ellis, H.M., Lee, E.C., Jenkins, N.A., Copeland, N.G. &Court, D.L. (2000). PNAS 97, 5979-5983

[2] Murphy, K. C. (1998). J Bacteriol 180, 2063-2071.

[3] Datta, S., Costantino, N. & Court, D.L. (2006). Gene 379, 109-115.

[4] Martinsohn, J.T., Radman, M. & Petit, M.A. (2008). Plos genetics 4, 1-12.

[5] Datsenko, K.A. & Wanner, B.L. (2000). PNAS 97, 6640-6645.

[o] Philippot, L. (2002) Biochimica et Biophysica Acta 1577, 335-376.



#### 6-Perspectives

Genefish efficiency evaluation with a wide range of DNA including PCR products, plasmid isolates, genomic DNA and soil metagenome

**INSA** 



Contact: <u>nathalie.lombard@ec-lyon.fr</u> http://www.genomenviron.org