

XVI ECIB 2012  
 XVI Encontro Científico do Instituto Biológico  
 V Jornada Científica de Bacteriologia  
 IV Workshop de Microbiologia Aplicada

BR - "CONTRIBUIÇÃO DA BIOLÓGIA MOLECULAR NO ESTUDO DA EPIDEMIOLOGIA, RELAÇÃO PATÓGENO-HOSPEDEIRO E TERAPÊUTICA DE DOENÇAS INFECCIOSAS?"

## Caracterização molecular de bactérias: ontem, hoje ... Amanhã

Aloysio de Mello F. Cerqueira  
 Professor Associado  
 MIP  
 19/10/2012

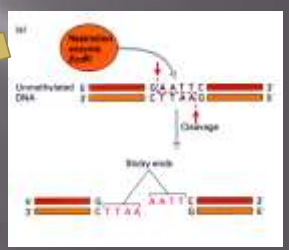


## Bactérias e biologia molecular

- Enzimas de restrição
- Plasmídios
- Clonagem

**1970**

*Escherichia coli*



A. B. J. van der Vliet, 2008

A. B. J. van der Vliet, 2008

I. Paulsson and Olofsson, 2008

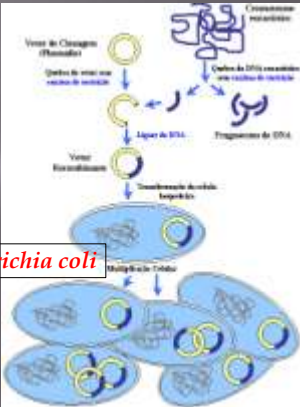
Department of Microbiology  
 Johns Hopkins University, School of Medicine  
 Baltimore, MD 21205, U.S.A.  
 Received 10 November 2008

## Bactérias e biologia molecular

- Enzimas de restrição
- Plasmídios
- Clonagem

Engenharia Genética

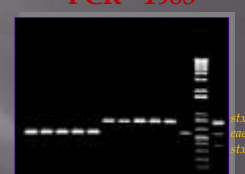

*Escherichia coli*



## Relação bactéria- hospedeiro

- Ensaio fenotípicos
- Ensaio genotípicos
- Diagnóstico
  - Crescimento lento
  - Ausência de crescimento
  - Confirmação de virulência
- Genética da resistência antimicrobiana

**PCR - 1983**

*Escherichia coli*

## Métodos Moleculares de Estudo Epidemiológico de Bactérias

- Genótipicos
  - Análise plasmidial
  - Polimorfismo de fragmentos de restrição (RFLP)
  - "Southern Blot" RFLP (Ex. Ribotipagem)
  - Eletroforese em gel de campo pulsado (PFGE)
  - Técnicas baseadas em PCR
    - PCR-RFLP
    - REP-PCR / ERIC-PCR
    - PCR-RIBOTIPAGEM
    - PCR randômico (AP-PCR / RAPD)
  - Sequenciamento de DNA

## Métodos de genotipagem baseados no padrão de bandas

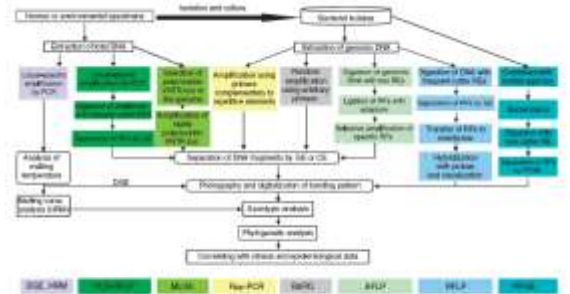
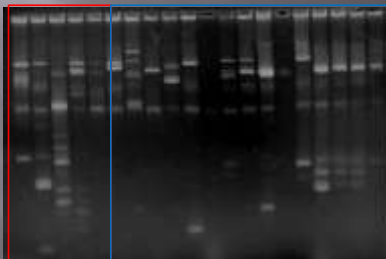


Fig. 1. Flow chart of DNA banding pattern-based genotyping methods for bacterial strains.  
© 2004 Federation of European Microbiological Societies. Reproduced by permission from John Wiley & Sons, Ltd.

## Epidemiologia molecular

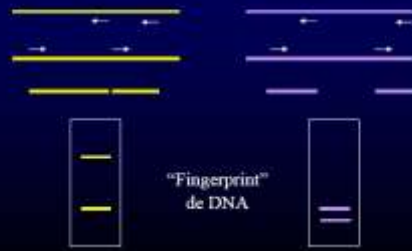
- Perfil plasmidial aEPEC humanos e caninos



Araes, 2010

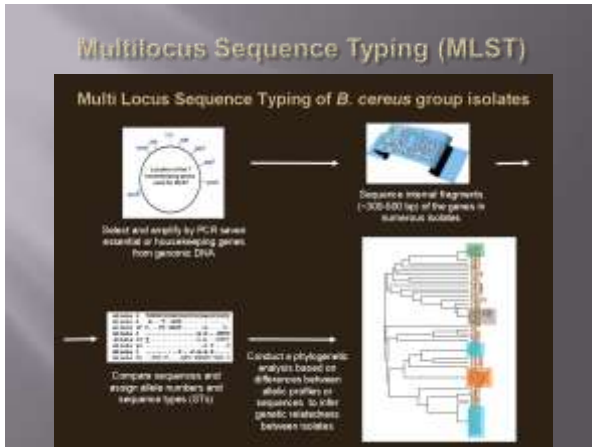
## Randomly Amplified Polymorphic DNA - RAPD

Pequenas quantidades de DNA, dispensa conhecimento prévio de seqüências alvo, único iniciador pequeno (~10 bases) de seqüência inespecífica, baixa stringência.









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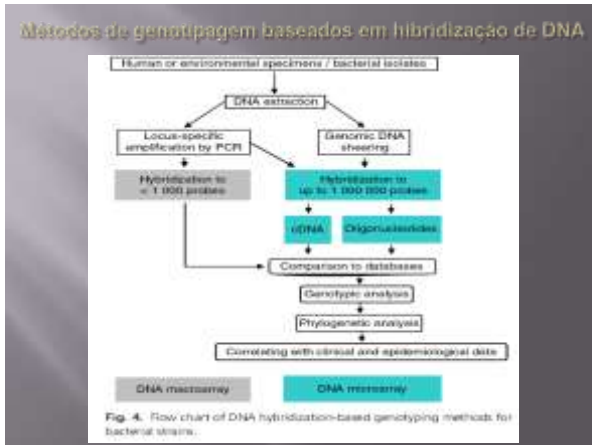
**Primers used for MLST of *Escherichia coli***

Genes

The *Escherichia coli* MLST scheme uses internal fragments of the following eight housekeeping genes:

- *adhE* (DNA polymerase)
- *uidA* (uracil-DNA glycosylase)
- *proA* (proton-activated phosphatase)
- *gltB* (glutamate synthase)
- *gltD* (glutamate synthase)
- *trpE* (tryptophan synthase)
- *trpB* (tryptophan synthase)
- *trpA* (tryptophan synthase)

[http://www.pasteur.fr/recherche/genopole/PFS/mlst/primers\\_Ecoli.html](http://www.pasteur.fr/recherche/genopole/PFS/mlst/primers_Ecoli.html)

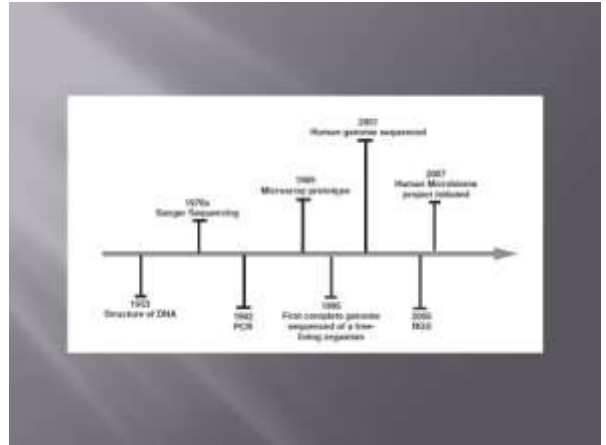
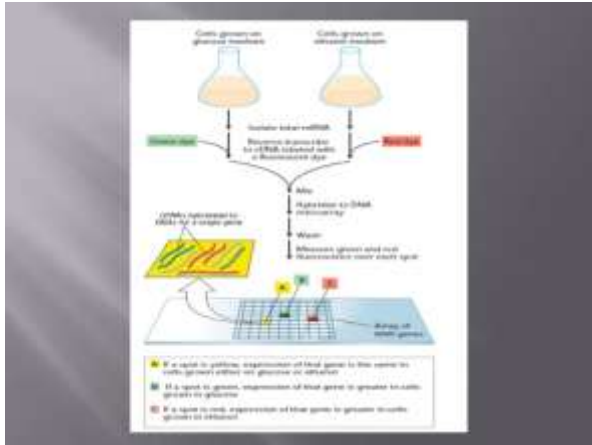


### Microarray

Preparation of probes

Preparation of target

Fig. 1. An illustration of the processes involved in making and using an array. At the top is depicted the cycle from the clone of interest in the genomic library (sequencing and sequence analysis) are shown. At the bottom, DNA or RNA is extracted from samples, amplified and labeled with either Cy3-ATP (green) or Cy5-ATP (red). When applied to the array bearing the immobilized probes, the target binds to complementary sequences. An example of an array result is shown on the right: the green spots represent hybridizations of the probe sets with target sequences labeled with Cy3-ATP; the red spots represent hybridizations of the probe sets with target sequences labeled with Cy5-ATP; the yellow spots represent hybridizations with both target sequences.



**Table 1. Comparison of high-throughput sequencing technologies available**

Technology	Throughput	Length	Quality	Cost	Applications	Main sources of error
Sanger	~100 Mb/day	~1000 bp	~99.99%	~\$1000/100,000 reads	Small-scale clone genome analysis, Sanger sequencing, long reads, de novo sequencing, etc.	Polymorphism, indels, GC bias, sequencing errors, etc.
454/Flux	~100 Mb/day	~100 bp	~99.9%	~\$1000/100,000 reads	Genome-wide, metagenomic, transcriptomic, etc.	Indels, GC bias, sequencing errors, etc.
Solexa	~100 Mb/day	~100 bp	~99.9%	~\$1000/100,000 reads	Genome-wide, metagenomic, transcriptomic, etc.	Indels, GC bias, sequencing errors, etc.
Roche	~100 Mb/day	~100 bp	~99.9%	~\$1000/100,000 reads	Genome-wide, metagenomic, transcriptomic, etc.	Indels, GC bias, sequencing errors, etc.

**Notes:**

- The table summarizes throughput, length, quality, and cost for the current versions of the mentioned technologies. These approximate numbers are constantly improving and based on figures available in January 2010. Costs do not include instrument acquisition and maintenance. Further data may be affected by absolute and relative effects for multiple instruments. Where numbers are not similar across sequencing and low performance means good performance indicates a general trend in the last 12 months, except for applications using the throughput and error profiles of each of the platforms are given. Typically, this does not mean that the technology is suited to these applications, but that it is currently being applied to such applications.
- \* High sequencing throughput of type applied.

**Mark Kitcher and David Ralston**  
 Reviews in Cell and Tissue Research

**Journal Article Cover:**

**Infection, Genetics and Evolution**

**ARTICLE**

**Structure, function and diversity of the healthy human microbiome**

The Human Microbiome Project Consortium\*



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