



# BREAKTHROUGH IN MICROBIAL GENOME SEQUENCING

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MWG



## An international company

MWG Biotech AG, Ebersberg, Germany  
MWG Biotech PVT Ltd, Bangalore, India  
MWG Biotech Inc., Greensboro, NC, USA

## MWG Portfolio

- ➔ oligonucleotides
- ➔ SiRNA
- ➔ Sequencing



### **MWG Biotech AG Ebersberg, Germany**

Established 1990

Employees: 95

Technologies:

- Sequencing Services
- Oligonucleotides
- siRNA

Capacity:

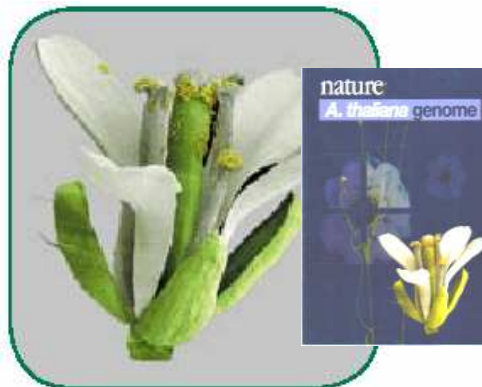
GS: 50 mio bases p.y.

GI: 1.5 to 2.0 mio reads p.y.

# MWGs Genome Sequencing

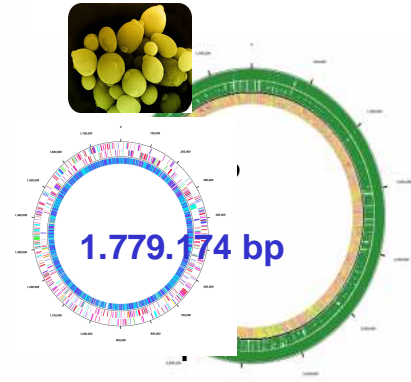


Participant of the rat sequencing consortium

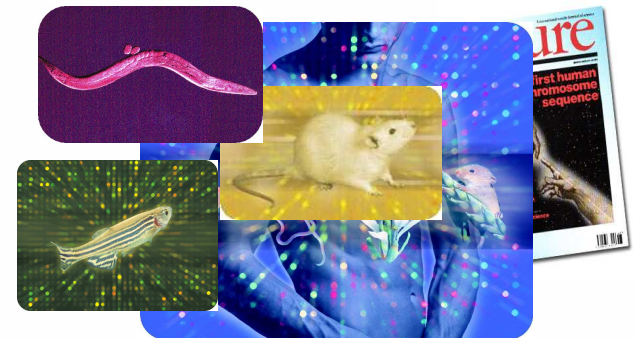


Participant of the Arabidopsis sequencing effort

- Helicobacter hepaticus
- Escherichia coli
- Lactobacillus helveticus
- Neisseria meningitis
- Protoclamydia amoebophila
- Mycobacterium (*strain is confidential*)
- Sacharopolyspora erythraea
- Azoarcus anaerobius
- Xanthomanas campestris
- Enterococcus (*strain is confidential*)
- Neurospora crassa
- Rat
- Mouse
- Arabidopsis
- Yeast
- Sheep
- Bovine
- Honeybee
- Apricot
- Coffee



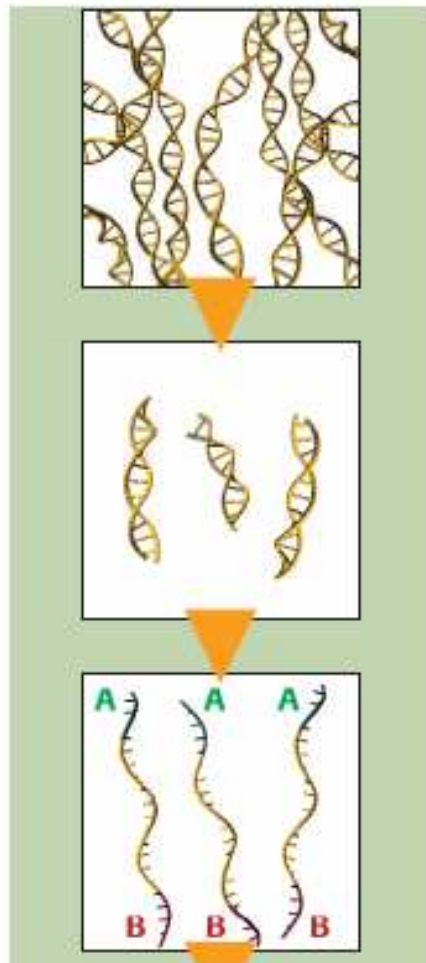
More than 25 microbial genomes



More than a 100 large EST projects

# Genome Sequencer Workflow

One fragment = One bead = One read



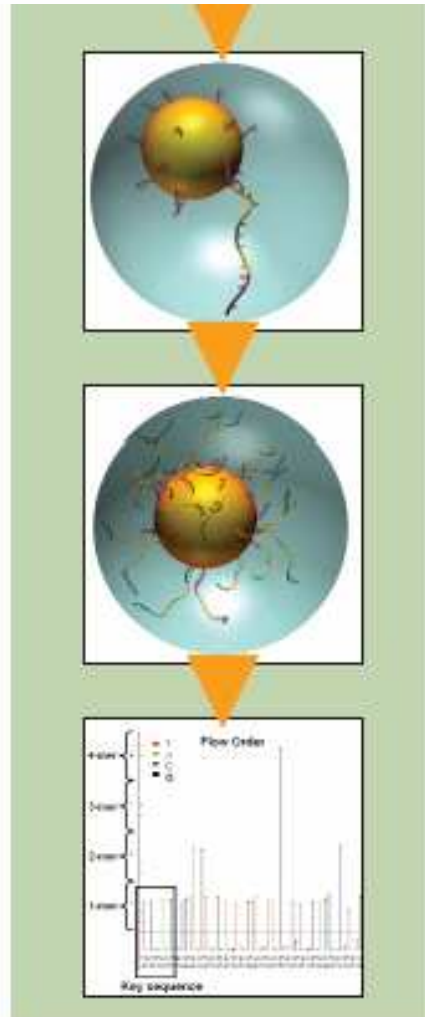
**1) Sample Input:** The Genome Sequencer FLX System supports the sequencing of samples from a variety of starting materials, including genomic DNA, PCR products, BACs, and cDNA.

**2) Sample Fragmentation:** Samples such as genomic DNA and BACs are fractionated into small 300 to 800 base-pair fragments. For some samples, such as small non-coding RNA, fragmentation is not required. Short PCR products can be amplified using Genome Sequencer fusion primers to go directly to Step 4, shown below.

**3) Adaptor Ligation:** Using a series of standard molecular biology techniques, short adaptors (A and B) – specific for both the 3' and 5' ends – are added to each fragment. The adaptors will also be used for purification, amplification, and sequencing steps. Single-stranded fragments, shown here, are used in subsequent steps in the workflow.

# Genome Sequencer Workflow

One fragment = One bead = One read



**4) One Fragment = One Bead:** The first step in emPCR (emulsion PCR) is shown. The adaptors enable hundreds of thousands of single-stranded fragments to bind to their own unique beads. The beads are then encapsulated into individual droplets formed by a water-in-oil emulsion, creating a microreactor containing one bead with one unique fragment. Each unique fragment is amplified without the introduction of competing or contaminating sequences. The entire fragment collection is amplified in parallel.

**5) One Bead = One Read:** The emPCR process amplifies each fragment to a copy number of several million per bead. Subsequently, the emulsion is broken while the fragments remain bound to their specific beads. After enrichment, the clonally amplified bead is ready to load onto the PicoTiterPlate device for sequencing.

**6) Sequence Generation and Data-Analysis Tools:** The Genome Sequencer FLX System produces over 400,000 reads per 7.5-hour instrument run. For sequencing-data analysis, three different bioinformatics tools are available for the following applications: resequencing up to 3 gigabases; amplicon variant detection by comparison with a known reference sequence; and *de novo* assembly up to 120 megabases.

## Two technologies for your ultimate service experience



### GS20/FLX SEQUENCING

- decipher more than 100 million bases in just 7,5 hours in one run
- easy sequencing of organisms with high GC content
- generate complete libraries with no cloning bias in AT rich regions
- very high accuracy of more than 99.99% at 20fold coverage
- No cloning is needed: no problems with pathogens or biohazard  
biosecurity and biosafety is guaranteed



*delivering coverage sequencing of genomes in week instead of months*



**Competitive price in comparison of Sanger technology**

### SANGER SEQUENCING

- system of choice for finishing projects
- read lengths up to 1100 bases

# Applications of the GS 20 Sequencer for whole genome sequencing



## Applications

De novo sequencing or resequencing of bacterial and fungal genomes, BACs and Cosmids/Fosmids

### **De novo sequence of bacterial and fungal genomes and BACs**

- ***Institutes for Microbiology and for Clinical Microbiology***
- ***Botanical and zoological Institutes***
- ***Plant and animal Breeders***
- ***Plant and Animal Health***
- ***White Biotechnology (Production of compounds in bacteria)***
- ***Dairy Industry (Probiotic products)***
- ***Pharmaceutical Companies with anti-infective and antibiotic research focus***

### **Comparative sequencing of bacterial genomes**

- ***White Biotechnology***  
***Comparison of production strain with wild type strain***  
***Metabolic Engineering, Strain optimisation***
- ***Medical Microbiology Institutes***  
***new pathogenic strains, new isolates drug resistant strains***

MWG is the first European service provider with this technology inhouse. In addition we can combine GS 20 / FLX technology with Sanger technology.

From the beginning of 2007, MWG sequenced

- \* 5 bacterial genomes (Most are confidential production strains. One is a de novo sequencing of an industrial important strain with assembly and bioinformatic analyse - strain comparison with proprietary tools )
- \* Plant BAC clones (8 Bacs per run)
- \* miRNA library

## More informations...



If you need informations about this technology and applications,  
please contact:

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Europe & USA => Georg Gradl [ggradl@mwgdna.com](mailto:ggradl@mwgdna.com)