

**Safe Food Fair Food:**  
from capacity building to Implementation  
Risk-based approaches to improving food safety  
and market access in smallholder meat, milk and  
fish value chains in four African countries

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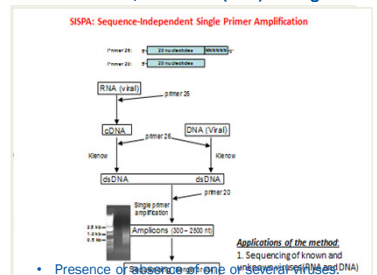
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### Multi-pathogen detection

Genomics and metagenomics based investigation of microbial communities in meat, milk and fish (MMF) focusing on:

**SISPA: Sequence-Independent Single Primer Amplification**



Applications of the method:

- Sequencing of known and unknown DNA
- Processing of as-isolates and viruses

- Presence of absence of one or several viruses
- Highly representatives – Molecular Diagnostics

Dijkeng & Stomeo 2009

### BecA Genomics Platform

Opportunities for genomics and metagenomics research

Capillary sequencing

ABI 3130-xl    ABI 3730-xl    ABI 3500-xl

Next generation sequencing

1 sample = 1 library  
= 1 plate  
500 mb/run  
1/2 cassava genome  
1/8 human genome

454 GS pyrosequencer

- Genomics
- Viral genomics
- Functional Genomics
- Metagenomics

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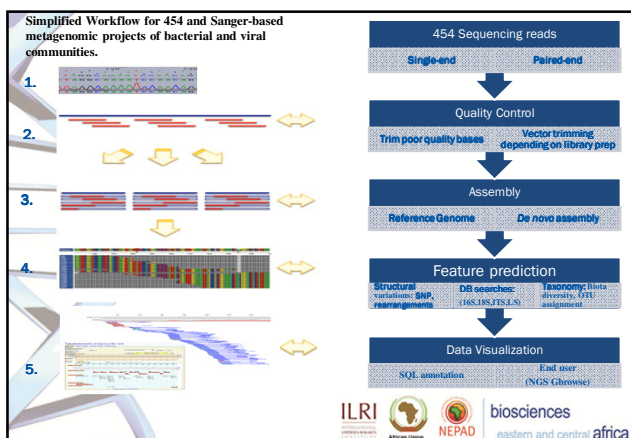
### The Bioinformatics Platform

- High-performance computing server:**
  - 32 total processing cores
  - 128GB of memory (RAM)
  - 8TB of disk space
  - 25TB LTO4 tape backup library
- Linux cluster**
  - 32 CPUs (AMD 64-bit)
  - 128 Gigabyte RAM
- >10 terabytes disk storage**
- Grid computing**
- Parallel applications:**
  - > Genome assembly (Newbler, MIRA, Celera, velvet, CAP3, ...)
  - > Genome annotation (glimmer, ...)
  - > Phylogenetic analysis (Beast, Mr Bayes)
  - > Other sequence analysis tools (BLAST, clustalw, HMMER, R)

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### Simplified Workflow for 454 and Sanger-based metagenomic projects of bacterial and viral communities.



- 454 Sequencing reads
- Quality Control
- Assembly
- Feature prediction
- Data Visualization

Single-end    Paired-end

Trim poor quality bases    Vector trimming depending on library prep

Reference Genome    De novo assembly

Structural variations, SNPs, rearrangements    DB searches: (NCBI, JGI, etc.)    Taxonomy: (NCBI, JGI, etc.)

SQL annotation    End user (NGS Genomics)

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### Bioinformatics Core Activities

- Statistical support**
  - Experimental design
- Primary data analysis**
  - NGS QC, spatial defect removal
  - 454 GA pipeline
- Secondary/downstream analysis**
  - Differential expression
  - ChIP-seq peak calling
  - Structural variation, genomic rearrangements
  - SNP and CN analysis
  - microRNA profiling
  - GO enrichment
- Training/Capacity Building**
  - motif finding
  - functional/network analysis
  - microarray analysis
- Data management**
  - NGS data storage and manipulation
  - Data warehouse facilities : databases
- Software development**
  - Bioconductor packages: NGS annotation packages
  - Automated NGS analysis packages
- Bioinformatics tools**
  - Ensembl, Galaxy, Cytoscape

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