Deliverables

- Living BAC clones in 384-well format

- Sequence-based physical map - ready to be added to existing genome sequences

- BAC contigs and sequence tags

- Data carrier with all WGP data and customized physical mapping software to access, visualize, edit and export the WGP marker/sequence data

WGP project examples

- Arabidopsis genome - 135 Mb
  - Pilot project for proof of principle

- Melon genome - 450 Mb
  - Only 550 contigs on first assembly
  - Successfully linked to existing Whole Genome Sequence data set

- Potato genome - 840 Mb

- Tomato genome - 950 Mb

- Several other large genomes (e.g. 2,600 and 4,500 Mb)

Contact

KeyGene

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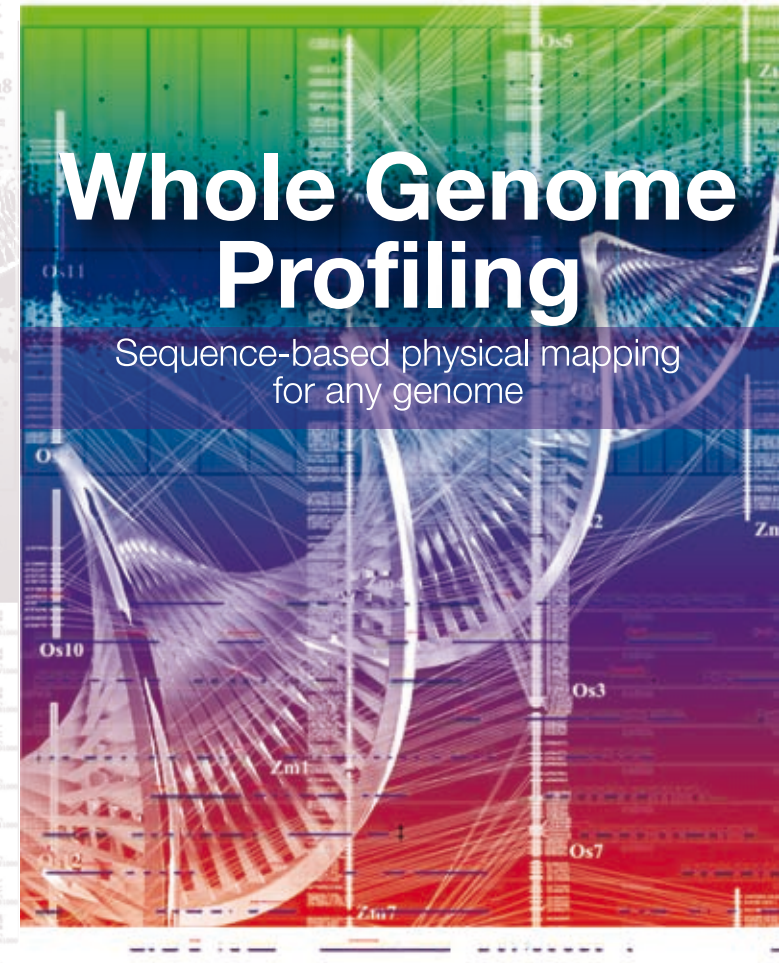The Netherlands
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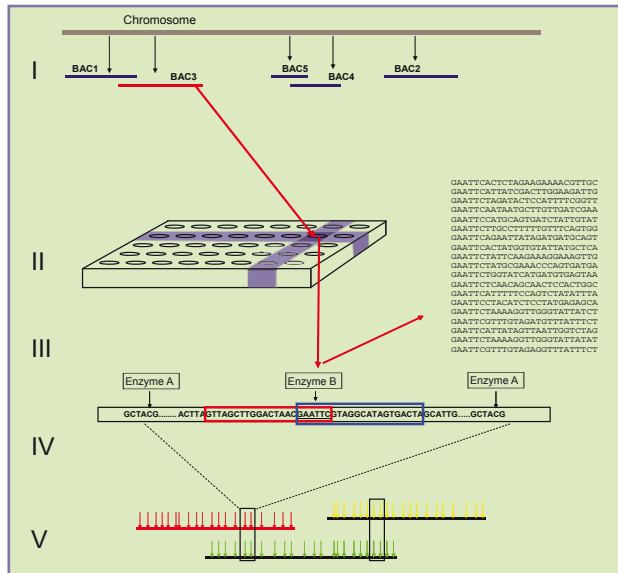Phone: +1 240 205 7083

Whole Genome Profiling

Sequence-based physical mapping
for any genome

AMPLICON express

KeyGene

You benefit from our combined expertise

A powerful method for Whole Genome Physical map construction

I   BAC library construction (125 to 175 kb inserts)

II   BAC clones are cleverly pooled

III Pooled BAC DNA is sequenced with Illumina GA II

IV   BAC specific sequence tags, spaced every 2-6 Kb are generated (knowledge of entire BAC, not just end sequence)

V   BAC clones are ordered into contigs, using sequence-based anchor points

Sequence-based genome physical map is completed and ready for client analysis.

The power of sequence tags for Whole Genome assembly

Superior high resolution whole genome assembly

- High level of confidence
- Limited number of gaps
- Large contigs of BAC clones
- Capable of resolving repeat regions and polyploidy levels
- Sequence tags spaced every 2-6 Kb across the BAC clones

WGP saves costs in Whole Genome Sequencing

- WGP physical map serves as an ideal framework for the assembly of Whole Genome shotgun sequence reads on gDNA
- Superior assembly metrics
- No Sanger sequencing required
- No BAC-end sequencing required for excellent assembly

A WGP map provides direct access to underlying gene sequences

- BAC clone plate and well positions are known
- Phenotypic information is directly linked to BAC sequences - giving immediate access to candidate genes
- Possibility to "zoom in" on region of interest for gene cloning, re-sequencing and other experiments

WGP is a competitive technology

- Full service - including BAC library construction, BAC library pooling, Whole Genome Profiling, contig assembly and customer support
- Sufficient computer power for Gb genome sizes
- Fast delivery - from starting tissue to physical maps can be completed in only a few months
- Pricing - comparable or more cost effective than BAC-end sequencing or SnapShot technology and other fragment based technologies.