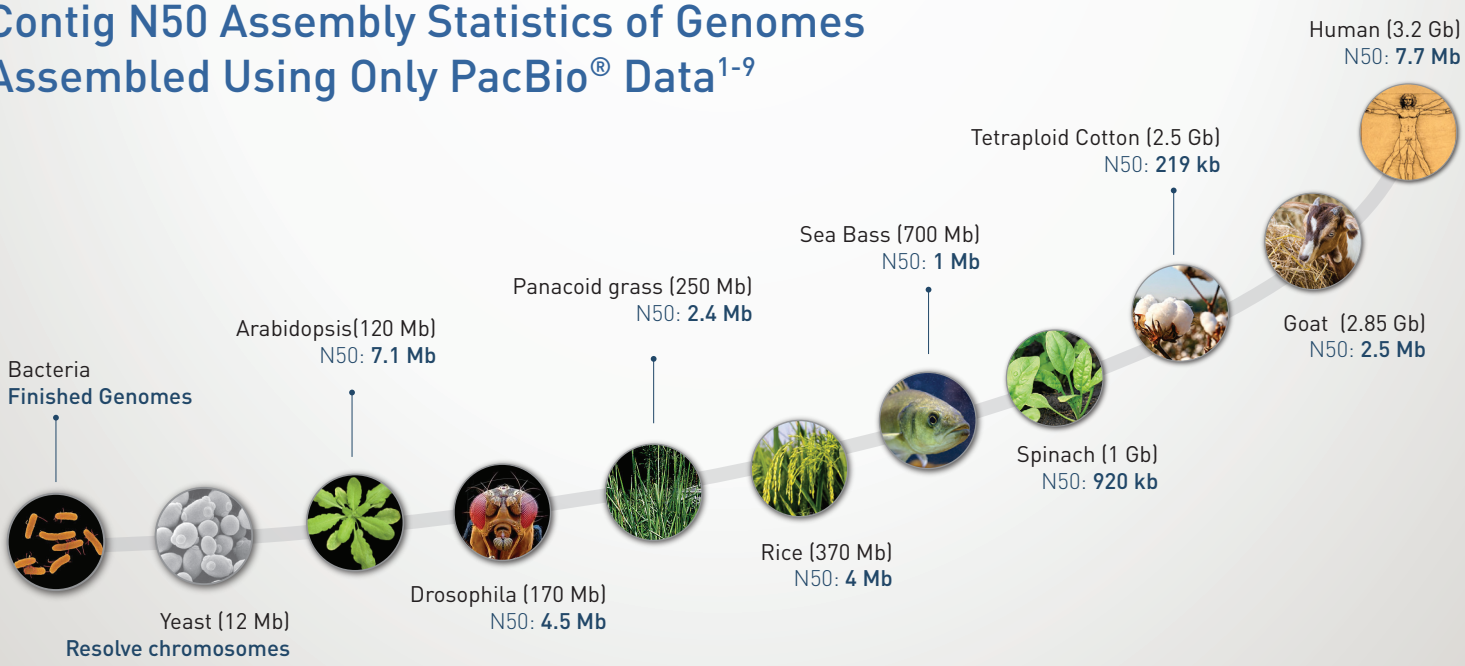
PACIFIC BIOSCIENCES®

Bringing the "W" Back to Whole Genome Sequencing

Single molecule, real-time (SMRT®) Sequencing delivers long read lengths with unbiased coverage in the most **comprehensive *de novo* genome assemblies** generated today. True whole genome sequencing provides **complete and accurate views of all types of genomic variation** revealing structural variants, mobile elements, haplotypes, epigenetics, and low complexity regions.

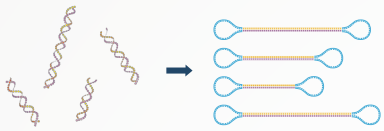
- Go beyond draft genomes, generate megabase-sized contigs, and finish assemblies
- Access genomic variations beyond SNPs
- Reveal genomic regions inaccessible to amplification-based sequence methods
- Annotate complete gene models with promoter regions
- Phase haplotypes with diploid assembly
- Capture epigenetic information

Contig N50 Assembly Statistics of Genomes Assembled Using Only PacBio® Data[1-9]



From DNA to Comprehensive Genome Assemblies

Long Insert Library Preparation



- Single library type required
- Size-selection options enrich for longest inserts
- Library input as low as 100 ng of gDNA
- Library automation supported

SMRT Sequencing on the PacBio® RS II

- Average read lengths 10-15 kb
- Scalable throughput:
  - Complete microbial genomes in 1 SMRT Cell
  - 5-10x coverage per genome recommended for gap filling
  - 25x coverage per genome for hybrid assembly
  - 50x coverage per genome recommended for de novo assembly
- Simultaneous capturing of epigenetic information using kinetics

De Novo Assembly & Structural Variation Detection

- Analysis tools available through SMRT Software Suite and community
- Megabase-sized contig N50s with demonstrated consensus accuracies >99.999%
- Diploid assemblies with haplotype information

References

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