THE FAST TRACK FROM GENOMICS TO APPLICABLE BREEDING

NRGene

Dr. Gil Ronen, CEO NRGene

IT IS ALL ABOUT REVEALING GENOME COMPLEXITY & DIVERSITY

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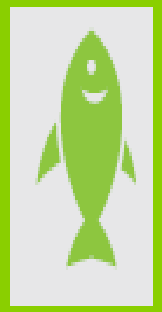
Our Mission:

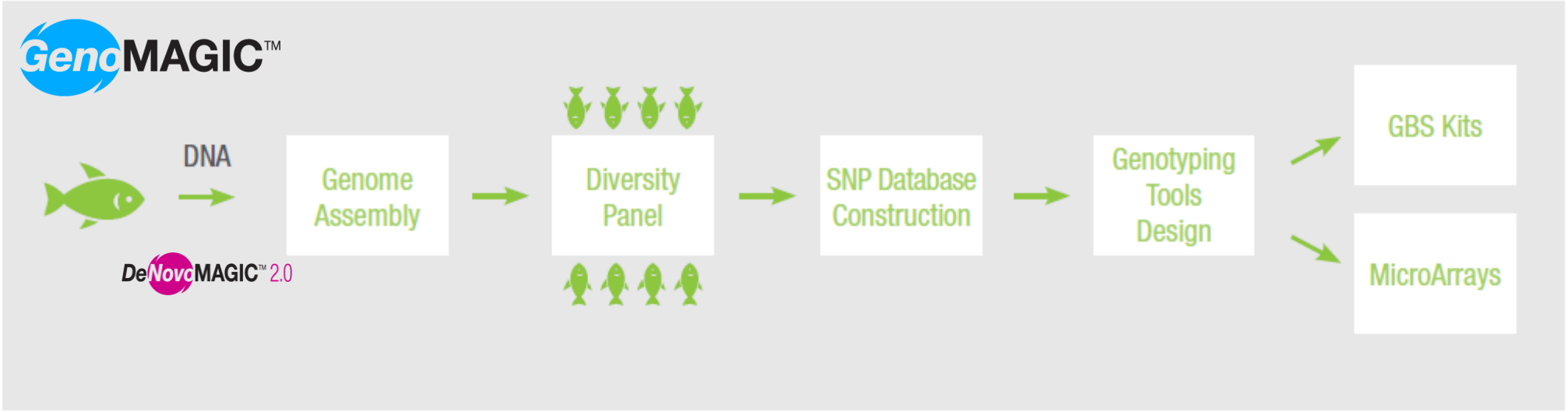


Translating genomic big data into most applicable tools boosting basic R&D and breeding of plants, livestock & aquaculture

- Established 2010
- 25 employees
- Located in Israel, subsidiaries in USA and India
- Develop and market genomic big data tools for agriculture
- Management team with extensive experience in the genomics market

AVAILABLE NOW -

NRGene's Comprehensive Aquaculture Genomic Solutions



NRGene's Cutting-edge Computational Tools Translate Genomic Big Data into Invaluable Breeding Support

GenoMAGIC™

Complete Solution to Analyze Genomics Big Data

Integrate all your genomic data to reach better breeding decisions. Analyze, synchronize and share genomic data between molecular breeders, bioinformaticians and the breeding team. ***Geno*MAGIC**™ includes a robust de novo assembler.

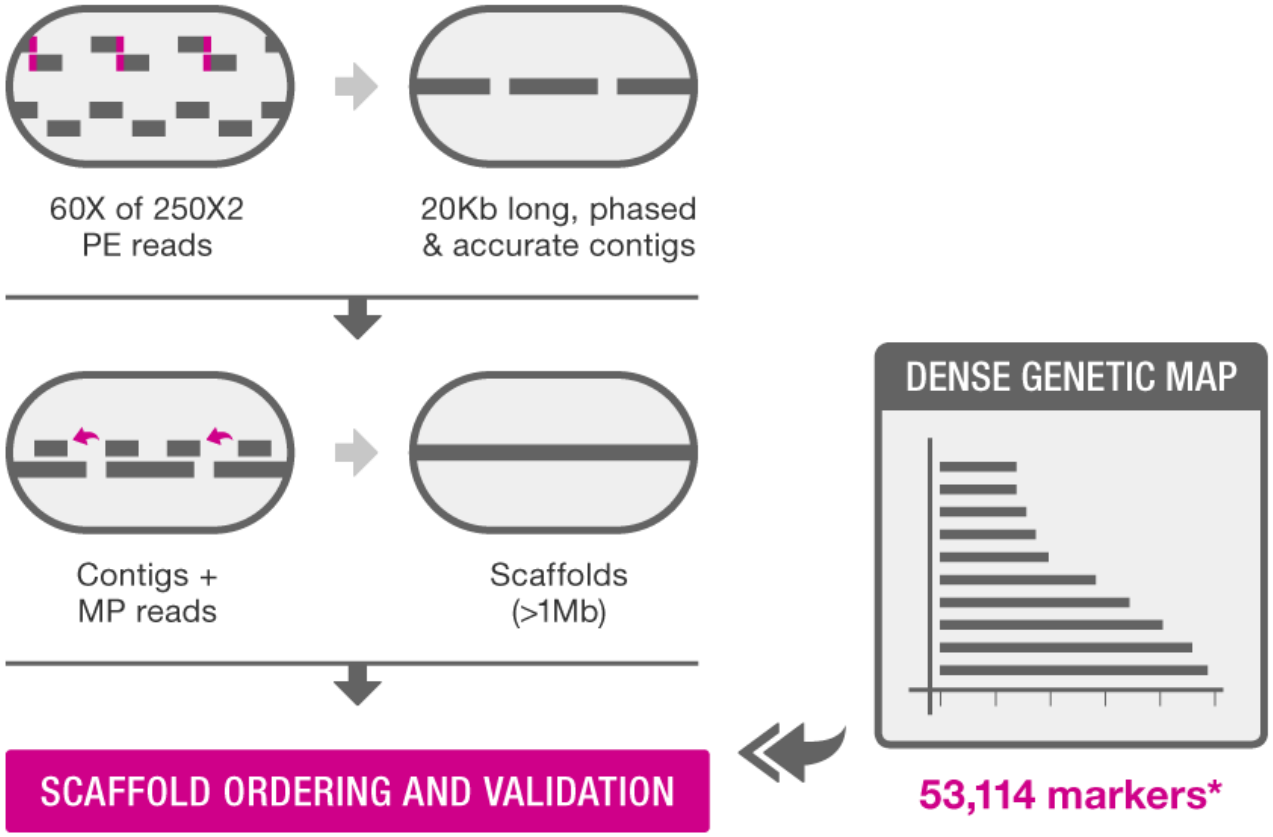
DeNovoMAGIC™

The Ultimate Genome Assembler

Quick, accurate and cost-effective construction of a reference genome. ***DeNovo*MAGIC**™ has the unique ability to assemble genomes for the most complex, heterozygote and polyploid organisms. Short term income are mainly generated by ***DeNovo*MAGIC**™.

DeNovoMAGIC™ 2.0

The DeNovo Assembly Process & QA



Two markers map to a single contig/scaffold were used for QA:

0 error rate for long contigs (0/8,505)

0.0027 error rate for scaffolds (12/4,461)

* Raw data from *"Genotyping-by-sequencing of maize NAM population"*, 2011, Buckler's Lab

DeNovoMAGIC™ 2.0

Assembly Results:

(2-14 days on a 50 CPU, 512 GB Linux Machine)

Parameter	Maize W22	Heterozygote Diploid	Tetraploid rainbow trout fish	Wild emmer wheat (Zavitan)
Fold coverage of short reads (PE & MP)	180X	173X	230X	60X (PE only)
Illumina chemistry	hiSeq rapid V2/V4	hiSeq rapid V2/V4	hiSeq rapid V2/V4	hiSeq rapid V2
Contig N50 (bp)	32,000	18,686	13,928	21,087
Contig assembly size	2,020M	867M	1,919M	9,927M
Scaffold assembly N50 bp (#)	**8.2M (79)**	**1.88M (157)**	**1.72 (252)**	
Scaffold assembly N90 bp (#)	595K (366)	21K (1381)	45K (4266)	
Total assembly size	2,395M	994M	2,178M	
% unfilled gaps (=n)	**4.5**	**4.8**	**11.5**	

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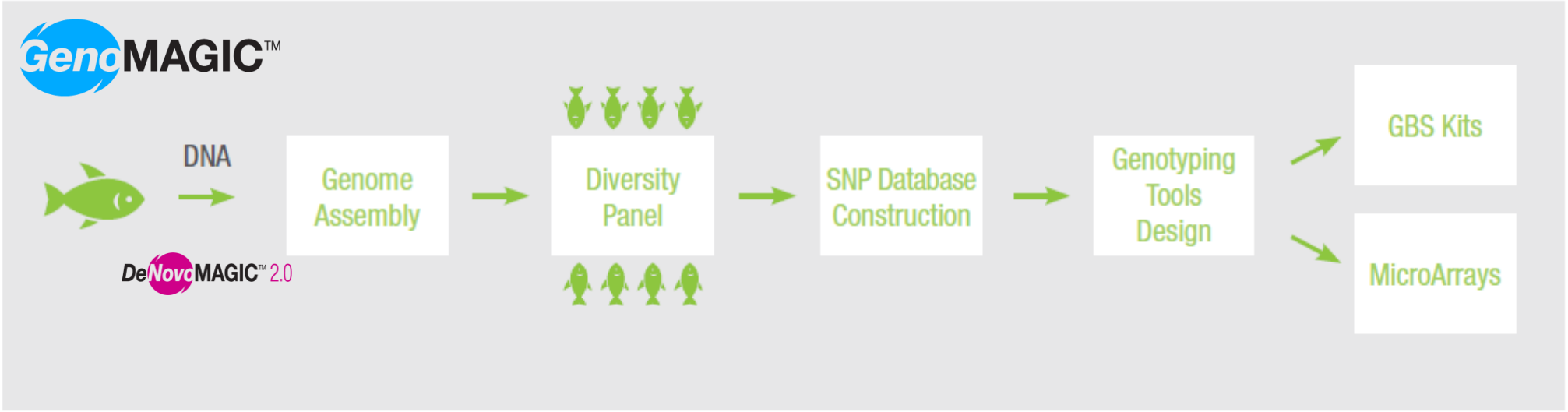
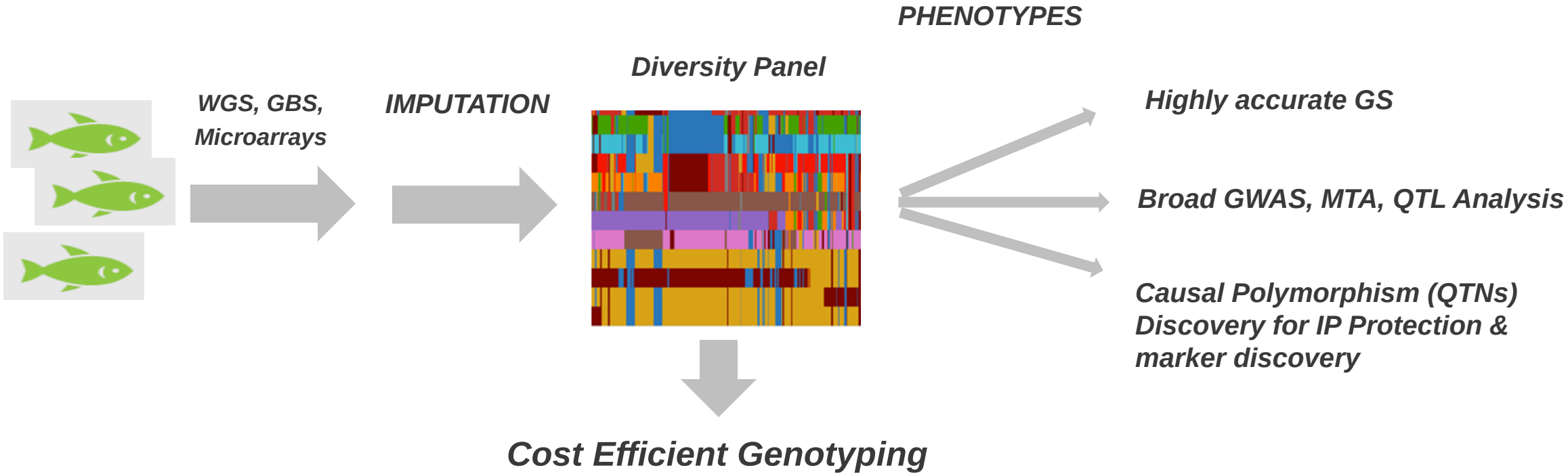


Diversity panel produced following all to all genome comparison and includes all types of polymorphisms (e.g. SNPs, INDELs, SV, gene content)

STEP 2 : Using Haplotypes for Cost Effective Breeding



Solving the Classical Big Data Challenge

GenoMAGIC™

Synchronizing Genetic Data on a Single Viewer

- Ref. Genome
- Rec. Rate
- 44K SNP Chip
- Total SNP DB
- Haplotypes
- Repeats
- Genes
- SNPs in Genes
- Indels
- Pheno/Geno R^2
- GBS
- Phenotypes

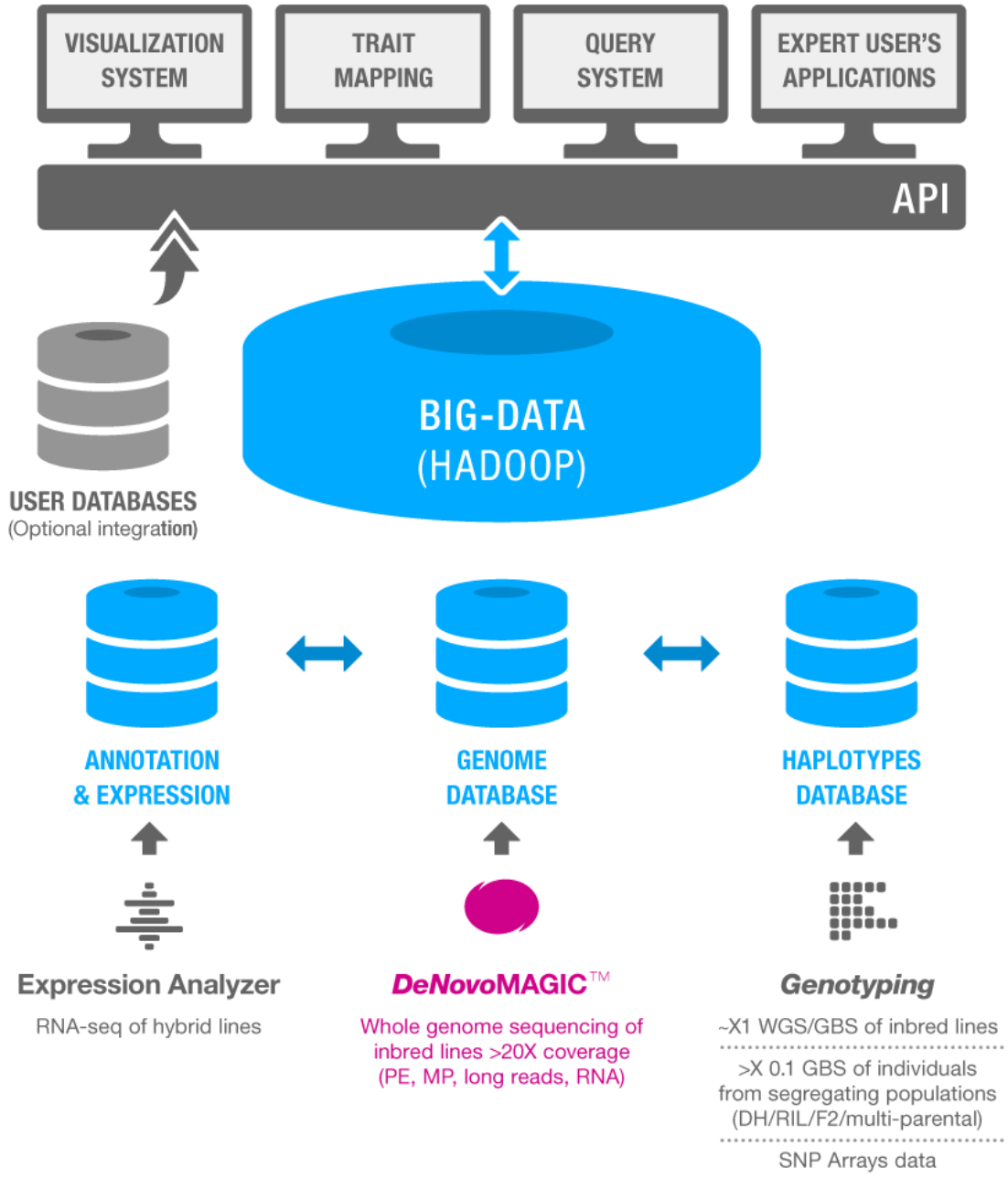
Haplotype Detection: GBS vs. Microarray

Summary

- Fast and accurate genome assembly is now available
- Re-Seq data analysis generates diversity panel (=haplotypes)
- Diversity panel is translated into most informative SNP DB
- GBS & Microarrays can be designed according to diversity level within the breeding population
- Genomic, genotypic, RNA, expression and phenotype data on millions of individuals is co-analyzed, stored and queried

GenoMAGIC™

- *Reconstructs and compares the full genome content of an unlimited number of individuals*
- *Associates genome variability with field performance data*
- *Cloud-based or locally installed system.*

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Thanks