Company Overview: NRGene is a computational Agri-tech company that provides premium genomic services to leading molecular breeding companies to reduce their breeding costs and time.

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Solution Overview

TraitMAGIC is an advanced analysis package for genotype-phenotype association research in a segregating population. NRGene has developed a unique "haplotype blocks" method that can efficiently and successfully analyse bi-parental populations, even of heterozygous parents, to yield a high-density markers map (genetic map) and identification of parental origin of every sequence in the progenies. The resulting markers map can then be added with phenotypic data to perform a high-resolution and robust quantitative trait locus (QTL) analysis for the identification of genomic regions that show high correlation with the desired traits.

Audience – Target Market/Customer

- **Academic or governmental institute** interested in high impact publications. the genetic map (markers map) can be used for pseudo-chromosomes alignment of a scaffolds-level assembly and to find unique traits affecting genes/loci.
- **Medium to large breeding entity** that can utilize the QTL analysis in order to identify multiple markers (for markers assisted breeding or genome editing) that have a high linkage with a desired trait.
- **Best/advantageous fit for:**
  - **Heterozygous (non-inbred) genomes (unique for NRGene)**
  - **Homozygous genomes with high complexity (size/ploidy)**
  - A breeding program that seeks new traits introduction to elite lines (also from wild varieties)
  - A pseudo-chromosomes alignment is required for a new reference genome (higher impact publications, larger academic value)

Customer Pain

- Self-incompatible species (non-inbred, heterozygous) do not have any available tool that can successfully differentiate between homologous (and/or homeologous) alleles- making it nearly impossible to perform QTL mapping and very difficult to identify genomic regions in linkage with the traits of interest.
- Low density and low applicability of markers: Most genetic maps are based on statistical calculations of recombination events and yield low density of markers, that are not necessarily strongly linked to the traits of interest.
- Development of applicative markers for Markers assisted selection is halted due to lack of full and accurate genomic context and thus predictive models' accuracy is limited.

Business Benefit

- Fully phased genetic maps with full genomic context (physical location mapping) are provided for heterozygous (non-inbred) species, allowing a full scope of allelic differentiation and origin identification.
- The analysis is based on illumina short reads technology with high quality sequencing data. The progenies are sequenced in low coverage (up to x3) that is enhanced and imputed by NRGene's novel algorithms.
- The analyses are fast and accurate and yield highly successful correlations analysis that may be used to build an accurate predictive model.
- High density of markers delivered- each haplotype block in the region of interest might contain tens to thousands of applicative markers. This allows both high applicability for MAS or genome editing purposes and also accurate pseudo-chromosomes alignment.

When to Engage / When Not to Engage

- Engage:
  - heterozygous genomes.
  - Budget allocation within 12 months.
  - Construction of a bi-parental segregating population is possible (parent plants are crossable and generation time is reasonable)
  - A reference genome is available, or the customer is willing to fund at least one of the parental lines DeNovoMAGIC assembly.
- Not-engage:
  - Budget allocation is too far- longer than 24 months.
  - No reference genome and no funds to have at least one parental genome assembled by DeNovoMAGIC.
  - Plants have a complex hereditary mechanism that might lead to non-homologous recombination (e.g. potato that have recombinations of homeologous chromosomes)

Key Features

- High density genetic map with full physical locations.
- Fully phased genetic maps to the different alleles.
- Heterozygous QTL mapping that is highly complex and inapplicable in other technologies.
- High density of markers in the region of interest (QTL) that can be used in the design of applicable genotyping predictive model.

Customization

TraitMAGIC is a complete solution that is a part of the **GenoMAGIC** platform all-inclusive holistic solution. With TraitMAGIC researchers may obtain high impact publications of important traits QTLs or reaching a pseudo-chromosomes level reference genome. In addition, multiple applicable markers in the QTLs yielded can be used for the design of genotyping arrays or other predictive models. The services might include a single segregating population analysis or multiple populations analyses to increase the number, predictability and relevance of the markers to multiple populations with larger diversity. TraitMAGIC might be purchased with or without the QTL analysis.

Differentiator

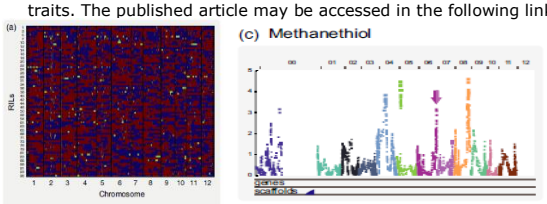
1. The sole solution for heterozygous phased QTL analysis- no other proprietary or open source tool can handle heterozygous species (non-inbreds).
2. Highly accurate and robust analysis that has been validated to produce prediction accuracy on the field (by using a prediction model) of up to 70%.
3. High density phased genetic map, with tens of thousands of markers and their genomic positions (on a given or constructed physical map). The map can be used to align genomic scaffolds to pseudo-chromosomes and to identify usable markers for genomic selection or genome editing.
4. Multiple traits analysis at a single run (subject to phenotypic data collection).

FAQs

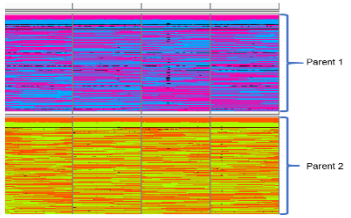
Question: What is the format of the phenotypic data required for the QTL analysis included in TraitMAGIC?
Answer: NRGene accepts most types of formats yet it is recommended to provide a simple table with the progenies and parental lines unique identification names/number as provided with their DNA samples and a grading scale of the phenotypes observed (for discrete phenotypes please attach a legend explanations) ns.
Question: Are markers included in the deliverables of TraitMAGIC? Will I get a markers' list per trait?
Answer: The deliverable file of the QTL analysis includes QTL physical locations and their P-value (each region's statistical correlation to the analysed trait's phenotype) in addition a high-density genetic map with thousands of markers (SNPs and others) is delivered with their physical positions. A simple downstream analysis (not provided) can be done to yield all markers in the QTLs and then a markers array may be designed based on technical requirements of each technology.
Question: Do the parental lines must be sequenced and assembled?
Answer: both parental lines must be analysed for haplotypes discovery (compared one to the other to detect the differences between them).
NRGene highly recommends to have at least one of the parental lines assembled to scaffolds level (that also might be aligned to pseudo-chromosomes according to the yielded genetic map), this will significantly improve the analysis accuracy and overall quality.

Customer / Case Study Reference

NRGene has validated the analyses through several POC projects testing the accuracy level, prediction accuracy and overall applicability.
A research in a Recombinant Inbred Lines (RIL) population of Melon has yielded approx. 58,000 markers and 241 QTLs for 129 fruit quality traits. The published article may be accessed in the following link:



Another POC done on a 200 individual F1 population of 2 heterozygous parental lines yielded 8 QTLs for a single trait of interest and tested through a prediction model utilizing selected markers linked to the QTLs to achieve 70% prediction accuracy level.



Haplotype blocks identification (genetic map) in a segregating population of 2 Heterozygous parental lines.

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Comparisons

Comparing PanMGIC to other pan-genomic comparison methods, shows that only PanMGAIC delivers the full and informative pan-genomic comparison set of analyses. PanMAGIC is the only solution to provide full genomic context allowing coordinate conversions and eliminating the single-reference bias. In addition PanMAGIC is the only solution that provides the full scale transcripts analysis including structural variations and copy number variations.

Additional Resources

Website (www.nrgene.com)

- **Publications** www.nrgene.com/publications/
- **Press-releases** www.nrgene.com/press-releases/
- **Videos and Presentations** https://www.nrgene.com/videos/