Genome Lineup

Purpose

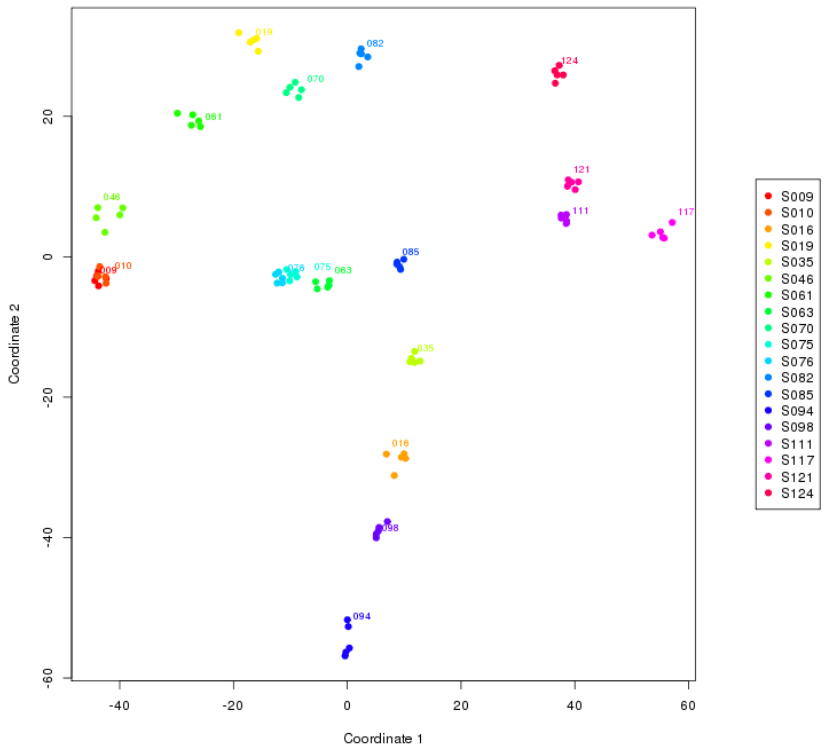
As plant-breeding is based on the redistribution of genetic information, knowledge of genomic variability of breeding material is pivotal. Although massive-parallel sequencing technologies have allowed for new opportunities to investigate the genomes of plants, the available genotyping-by-sequencing approaches often apply a genome-reductionist approach, thereby knowingly ignoring a large fraction of the interrogated genomes.

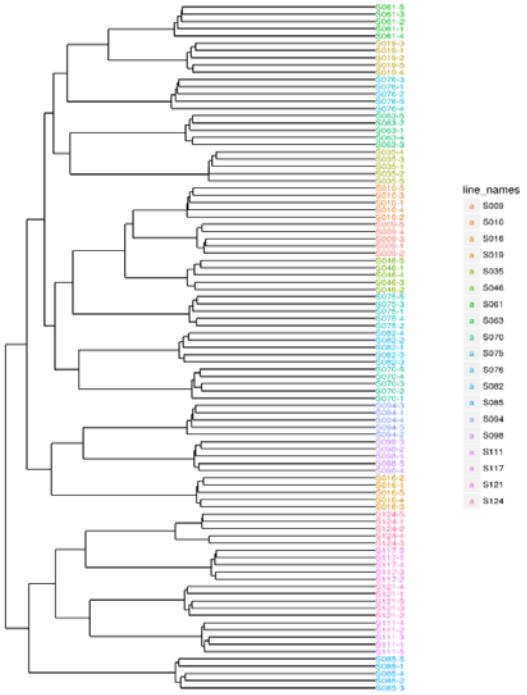
Skim- and Multi- sequencing

Skim- or shallow genome sequencing refers to a next-generation sequencing approach in which the average coverage of the genome by sequencing reads is less than ~2x. Multi(plex) sequencing refers to the next-generation sequencing approach in which DNA of many samples are barcoded and pooled before one library is made and sequenced. Both skim- and multi-sequencing approaches have a major impact on the cost of genotyping-by-sequencing.

Genome Lineup

The Genome Lineup method is based on massive parallel sequencing of complete genomes by employing a Multi-Skim approach. It encompasses two phases: In phase I, genomic differences in a substantial set of different accessions with replication (usually n=4x24) are determined and the genomic variability between the accessions is calculated and visualized, which will result in a “genomic landscape” of the analyzed species. This phase has to be done only once for a species of interest.





Visualizing the genomics landscape

All identified genomic differences between the analyzed accessions are used to plot the accessions in a dendrogram for example species X. The same colored dots are replicates of one accession.
NB: the distance in the lines of the replicates is non-informative.

In phase II, new accessions can be placed in this species-specific genomic landscape in singular. This can be of interest for many purposes in plant breeding. For instance, one can quickly see where own or competitors' new varieties are located in the genomics landscape. Once you have the Genome Lineup database of your species, you always have an overview on the total variability of your breeding material, which could be helpful in selecting the most promising crosses.

Application

Once you have the Genome Lineup database of your species, you have established an overview of the total variability of your breeding material. The information provided by the Genome Lineup data and visualizations can support, depending on the breeding strategy, your R&D process in many ways. The Genome Lineup approach is also well suited for (suspected) infringement of "het kwekersrecht", comparing two accession within the genomic landscape will (dis)prove infringement.

At the same time the Genome Lineup approach can give you a comprehensive overview of your competitors' accessions. An unprecedented insight and comparison of you breeding efforts compared to that of you competitors.

Due to the Multi-Skim sequencing approach, Genome Lineup analyses are quite affordable, but obviously depend on the genome size of the investigated species.

Samples

To obtain DNA for the Genome Lineup analysis, in principle any part of a plant could be used. However, experience has taught us that leaf material is best suited for this method. A small piece of a (seedling) leaf suffices, which allow genomics screening at an early life stage.

Information

Genome Lineup analysis is developed and executed by the MAD: Dutch Genome Service & Support Provider @ the University of Amsterdam (www.dutchgenomics.nl).
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