

Characterization of the genetic diversity of tetraploid potato using genome-wide high-density SNP genotyping

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Introduction

The recent sequencing of the potato genome offers an opportunity to provide a 'step change' in the way that potato genetics and breeding are performed. Due to the genetic complexities posed by tetrasomic inheritance, most potato genetic studies are carried out at the diploid level using biparental populations. This causes some difficulties in translating and applying the derived results at the tetraploid level. For practical reasons, the molecular dissection of traits at the tetraploid level and across a wider germplasm using high-throughput molecular marker platforms is highly desirable. Genome-wide association studies (GWAS) are gaining importance for studying the genetics of natural variation and traits of agricultural importance and offers significant advantages such as enhanced mapping resolution, a greater number of segregating traits, and higher allelic diversity. Single nucleotide polymorphisms (SNPs) represent the most abundant type of genetic polymorphism in plant genomes and are preferred molecular markers for population genetic studies and association mapping efforts. We are analysing the potential of genome-wide association mapping in tetraploid potato using high-density genotyping to assess marker-trait associations.

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References

* Voorrips *et al.* BMC Bioinformatics 2011, 12:172

Genotypic analysis

Genomic DNA samples from a panel of 350 diverse tetraploid potato clones were genotyped using the Illumina Potato 8303 Infinium SNP array. Genotypes were called using an R package fitTetra*. Results for the different genetic aspects of potato such as genetic diversity, population structure, linkage disequilibrium (LD) are presented.

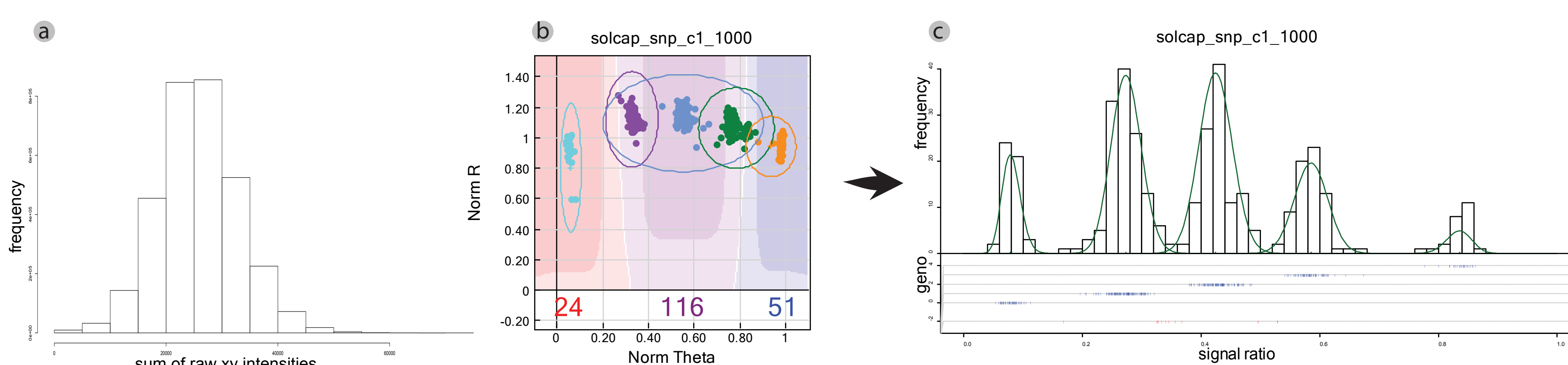


Figure 1: Illumina 8303 Infinium SNP array analysis (a) plot of sum of raw xy intensities, (b) example of manual genotype calling using Illumina Genome Studio software and (c) automated genotype calling using an R package fitTetra.

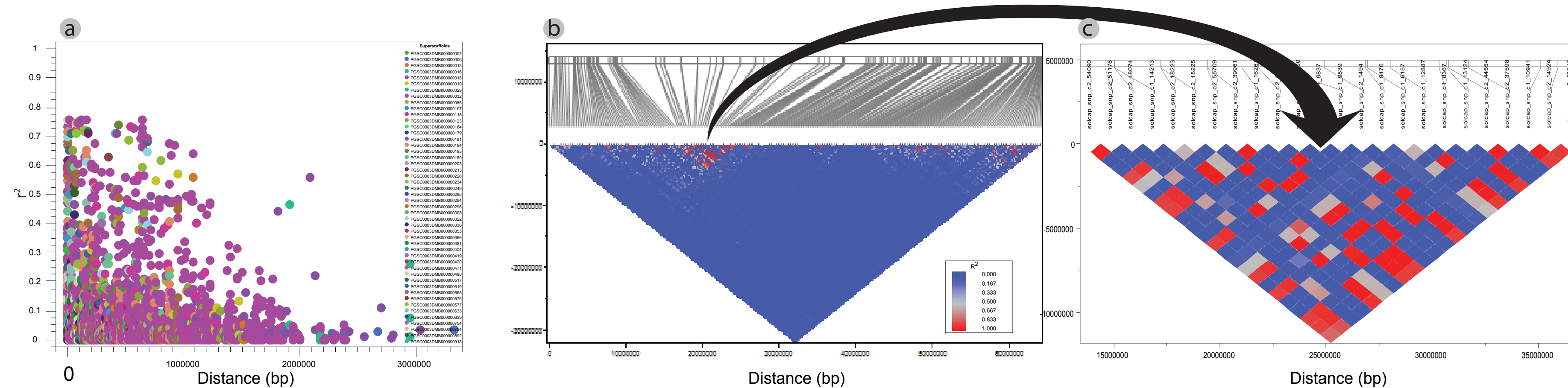


Figure 2: Representations from chromosome IV. (a) LD decay plot. LD measure r^2 plotted versus the physical map distance between all pairs of SNP markers (calculated for markers that are no more than 50 markers apart) and for all the superscaffolds anchored to chromosome IV, (b) LD plot on a chromosome scale level, and (c) selected block showing region with higher LD.

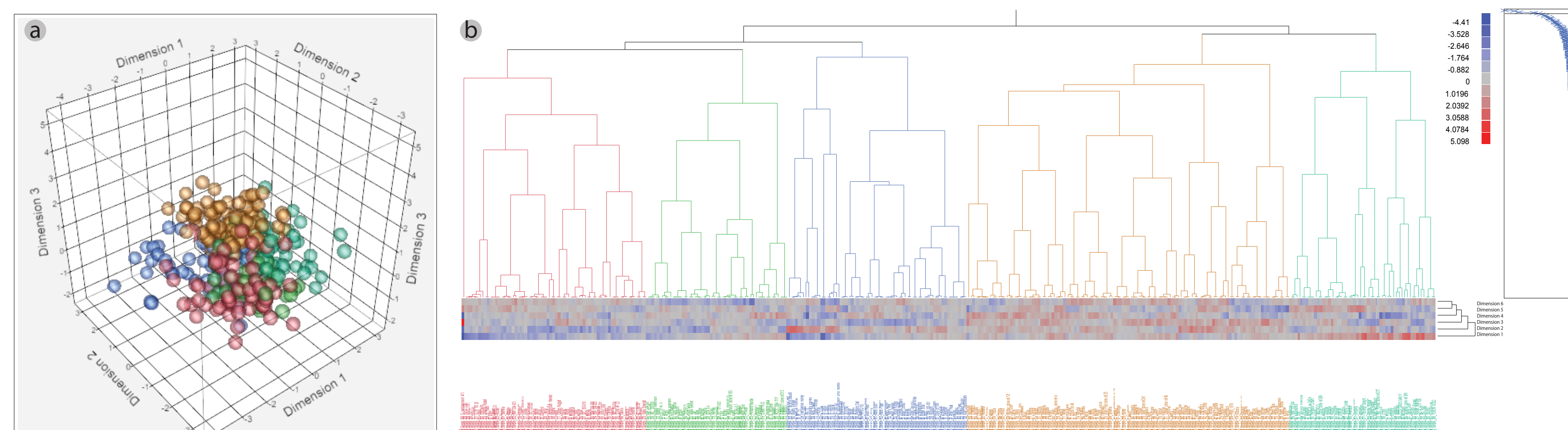


Figure 3: (a) Scatter plot and (b) clustered heat map showing estimated population structure in the studied potato collection as revealed from Multidimensional Scaling (MDS) analysis.

Phenotypic analysis

Phenotyping for a range of agronomically and economically important traits is in progress at two different locations.



Figure 4: (a) a subset of association panel and (b, c) replicated field trials at two different sites.

Ongoing and future work

- Genotype association panel using 'Genotyping by Sequencing' (GBS) approach.
- Phenotype association panel for targeted traits for two years (2012, 2013).
- Estimate population structure and kinship, perform GWAS using SNP and GS data.
- Identify genomic regions associated with target traits.