Genetic diversity among oil palm (*Elaeis guineensis* Jacq) progenies used in a field trial in Solomon Islands.

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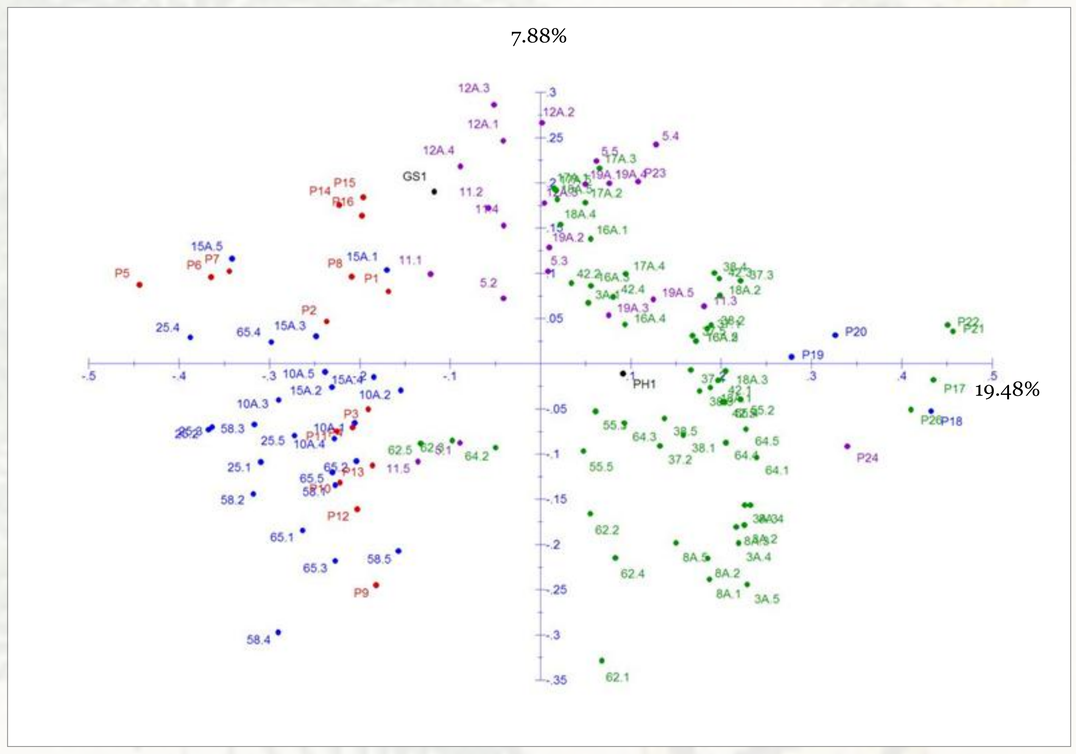
Oil palm is a long term perennial crop of great economic importance to many countries in tropical Asia/Oceania, providing export revenue. Basal stem rot (BSR), caused by the white rot fungus *Ganoderma boninense*, poses a major threat to the oil palm industry. The only long-term control for this disease is through implementation of improved cultural practices and the use of more resistant planting material.

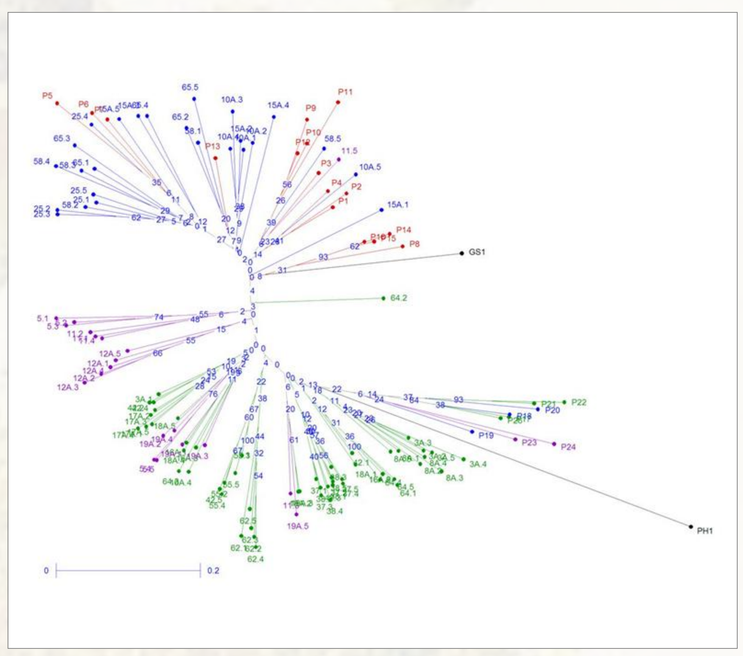
We aim to find markers closely associated with phenotypic traits such as resistance and/or susceptibility to BSR.

26 parental lines (of Deli, AVROS, AVROS-Ghana and Ghana germplasm) were used to produce progenies for a field trial in Solomon Islands. To ascertain the level of genetic diversity present in our palm populations we used simple sequence repeat (SSR) markers (Billotte *et al.*, 2005, TAG 110:754) on a collection of 100 progenies representing 20 families and their parental lines.

A total of 93 alleles were identified. A matrix of pairwise dissimilarities was calculated by simple matching with 1000 bootstraps. PCA (Principal coordinate analysis) and cluster analysis using the matrix revealed associations among progenies which were in close agreement with the pedigree data.



PCA calculated from the dissimilarity matrix showing Deli parents, AVROS, Ghana and A/G parents and progenies.



Unrooted unweighted Neighbor-Joining tree calculated from the dissimilarity matrix used in PCA. Deli parents, AVROS, Ghana and A/G parents and progenies.

18 SSR loci used in this study, sizes of alleles (bp), and PIC (polymorphism information content) values.

	Allele sizes	PIC
mEgCIR3546	305	0.22
mEgCIR3785	284	0.47
mEgCIR3543	209, 217, 222	0.59
mEgCIR1753	284, 317	0.32
mEgCIR3718	114, 118, 124, 131	0.41
mEgCIR0173	126, 130, 132	0.55
mEgCIR3275	126, 130, 139	0.63
mEgCIR0177	97, 102, 104, 106, 112, 120	0.66
mEgCIR3649	278, 283, 289, 294, 296	0.63
mEgCIR3292	171, 173, 177, 182, 184, 186	0.69
mEgCIR3363	180, 182, 189, 191	0.64
mEgCIR3574	173, 182, 191, 197, 201, 209, 217	0.76
mEgCIR3886	176, 180, 182, 190, 192	0.70
mEgCIR3389	82, 86, 88, 92	0.75
mEgCIR0353	86, 91, 94, 97, 98, 100	0.71
mEgCIR2414	338, 342, 350, 351, 353, 355	0.74
mEgCIR3282	222, 228, 230, 232, 236	0.73
mEgCIR3362	161, 162, 164, 171, 172, 176, 182, 190	0.77

% Polymorphism (%P), observed heterozygosity (Ho), expected heterozygocity (He) and the F statistic for the 3 populations of progenies.

	DxG	DxA	DxA/G
%P	83.33%	88.89%	88.89%
Ho (SD)	0.59 (0.07)	0.68 (0.08)	0.63 (0.09)
He (SD)	0.48 (0.06)	0.53 (0.05)	0.54 (0.06)
F (SD)	-0.23 (0.03)	-0.24 (0.06)	-0.12 (0.09)

Despite a narrow genetic origin of the Deli line, SSR markers revealed genetic diversity in the Deli parents, as well as genetic diversity within and between families. Deli x AVROS progenies had the highest level of genetic diversity, increasing chances of finding markers linked to BSR resistance &/or susceptibility.

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