Genetic Improvement of Taro for taro leaf blight resistance in Hawai'i

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Abstract

Taro (*Colocasia esculenta*) is a clonally propagated root crop that is a staple of Pacific Islanders. Taro leaf blight (TLB) is the most devastating disease of taro in Hawai'i and the world. This disease is typically controlled by the use of fungicides, which are costly. Genetic resistance has been identified in taro populations from Palau, Papua New Guinea, and Indonesia. Here we explore the genetic architecture of TLB resistance in several breeding populations with resistant material being incorporated into the existing University of Hawaii taro breeding program. We have developed two mapping populations: 1) one F_2 population based on self-pollinating cultivar '230' (Hawaiian landrace Moi x TLB resistant Palauan landrace Dirratengadik); and 2) an F_1 mapping population based on crossing '230' with another breeding cultivar '255' [(Hawaiian landrace Red Moi x TLB resistant Papua New Guinean landrace PH15) x TLB resistant Indonesian landrace Sawahn Kurasae]. We have developed a linkage map based on these two populations using single nucleotide polymorphisms (SNP) markers to identify QTLs linked with TLB resistance, both in field trials and laboratory assays.

Breeding of Taro and Mapping Population

Taro flower

Pollen collection

Cross pollination

Taro Seeds

Fig 1: How breeding of taro occurs.
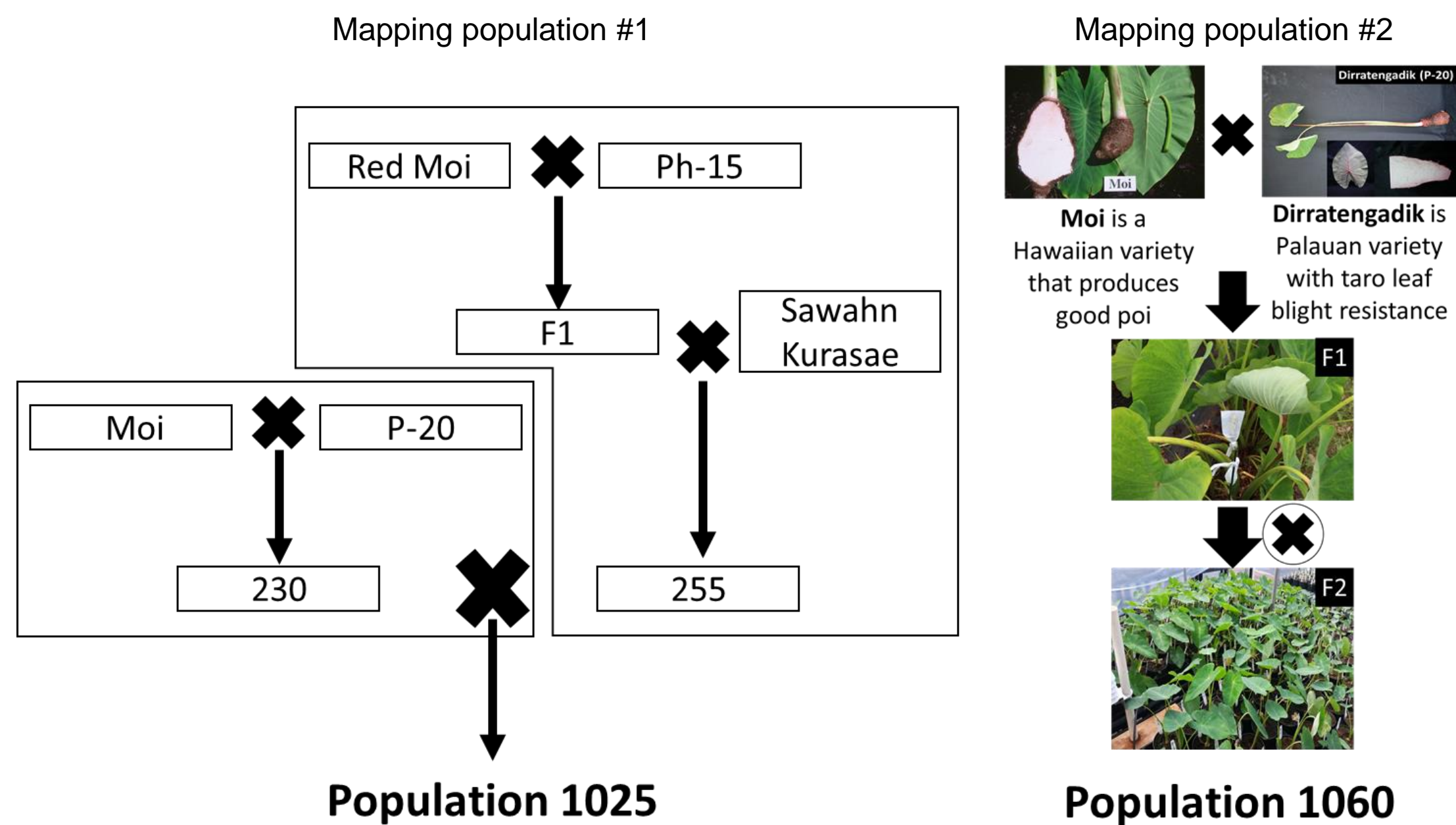

Fig 2: Mapping populations used to identify TLB resistance.

Segregating population for TLB resistance

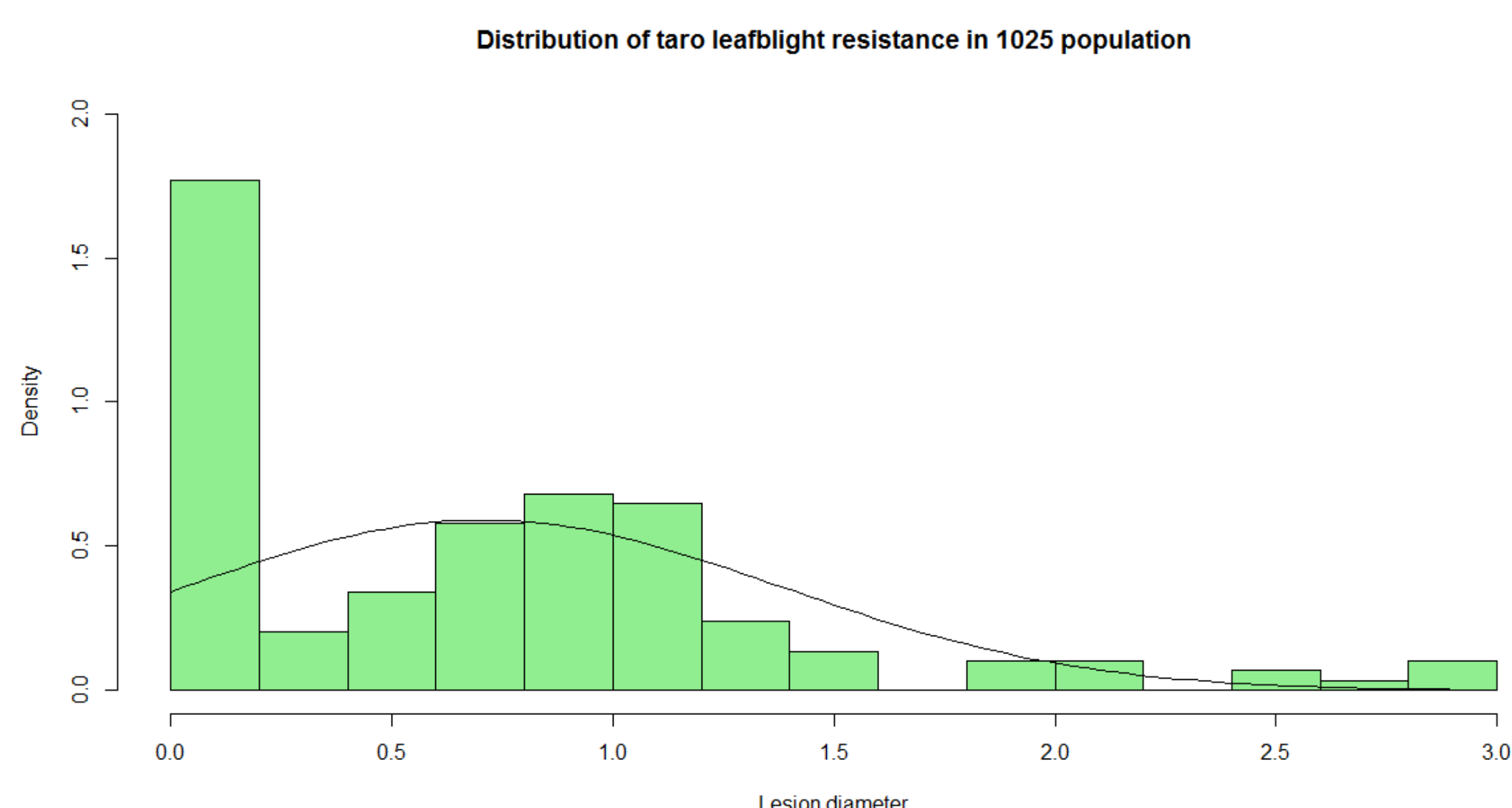Distribution of taro leafblight resistance in 1025 population

Fig 3: Frequency distribution of TLB resistance in an F_2 population (230× 255) of 148 individuals with Phytophthora colocasiae isolate. **The smaller the lesion diameter, the greater the disease resistance.**

Taro leaf blight

Fig 4: TLB affected plant at Pepeekeo, Hawaii.

• Caused by Oomycete *Phytophthora colocasiae*

• Introduced to Hawai'i around 1920 (CTAHR 2009)

• Can reduce corm yield by up to 50% and leaf yield by 95% in susceptible cultivars (Singh et al. 2012).

Phenotyping for leaf blight resistance

• Place a 10 microliter drop containing 10-20 zoospores per microliter on each leaf disk

• Incubate at about 27°C for 3 days. Photograph disk on days 2 and day 3
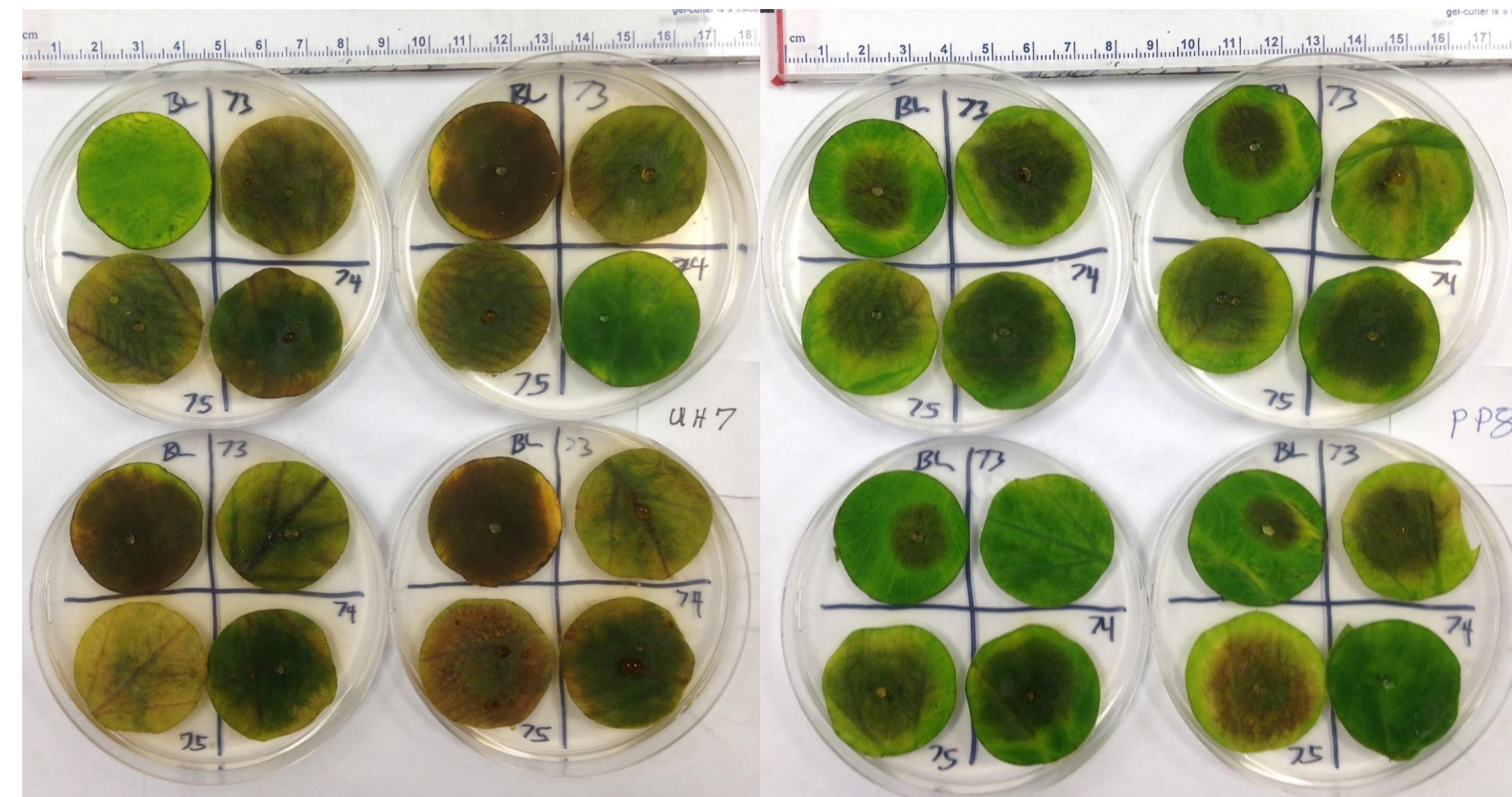
• Measure diameter of lesions using Image analysis

Fig 5: Laboratory disk assay for Phytophthora colocasiae.

Methods for Linkage mapping and QTL analysis

• Linkage mapping was done using the CP option of Join Map 4.1(Van ooijjen, 2006).

• Markers were filtered for segregation distortion (markers with chi square value >3.84 were removed).

• Maps were created using Map Chart using marker positions obtained from Join Map 4.1.

• Genetic Analysis of Clonal F1 and Double cross populations (GACD) software (Zhang et al., 2015) was used to perform the QTL analysis.

• . Inclusive composite interval mapping of Additive and Dominant QTL (ICIM - ADD) was used as an algorithm for mapping the QTLs

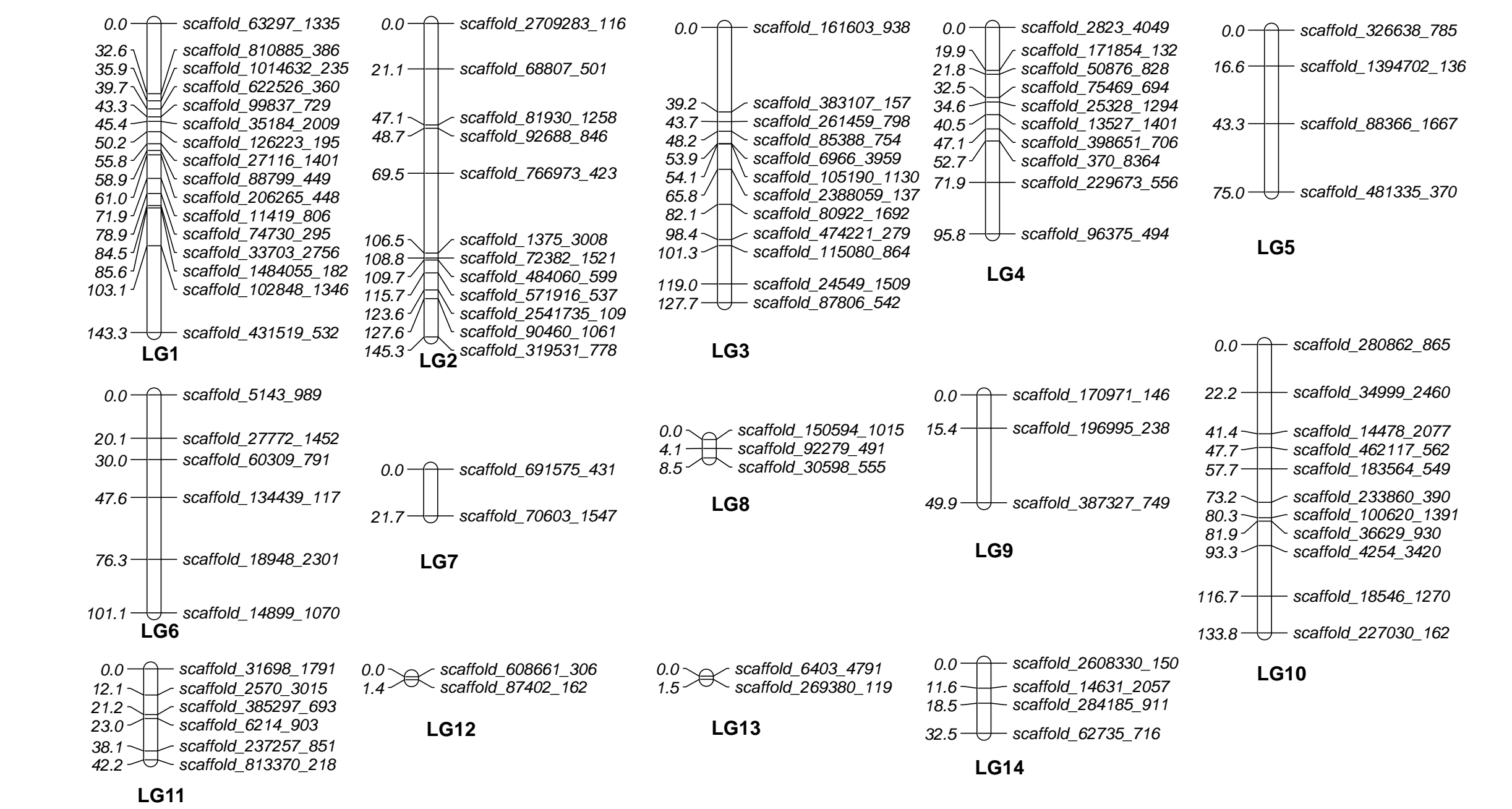## Preliminary Linkage Map

Fig 6. Preliminary linkage map with high quality SNP markers, derived from genotyping-by-sequencing.
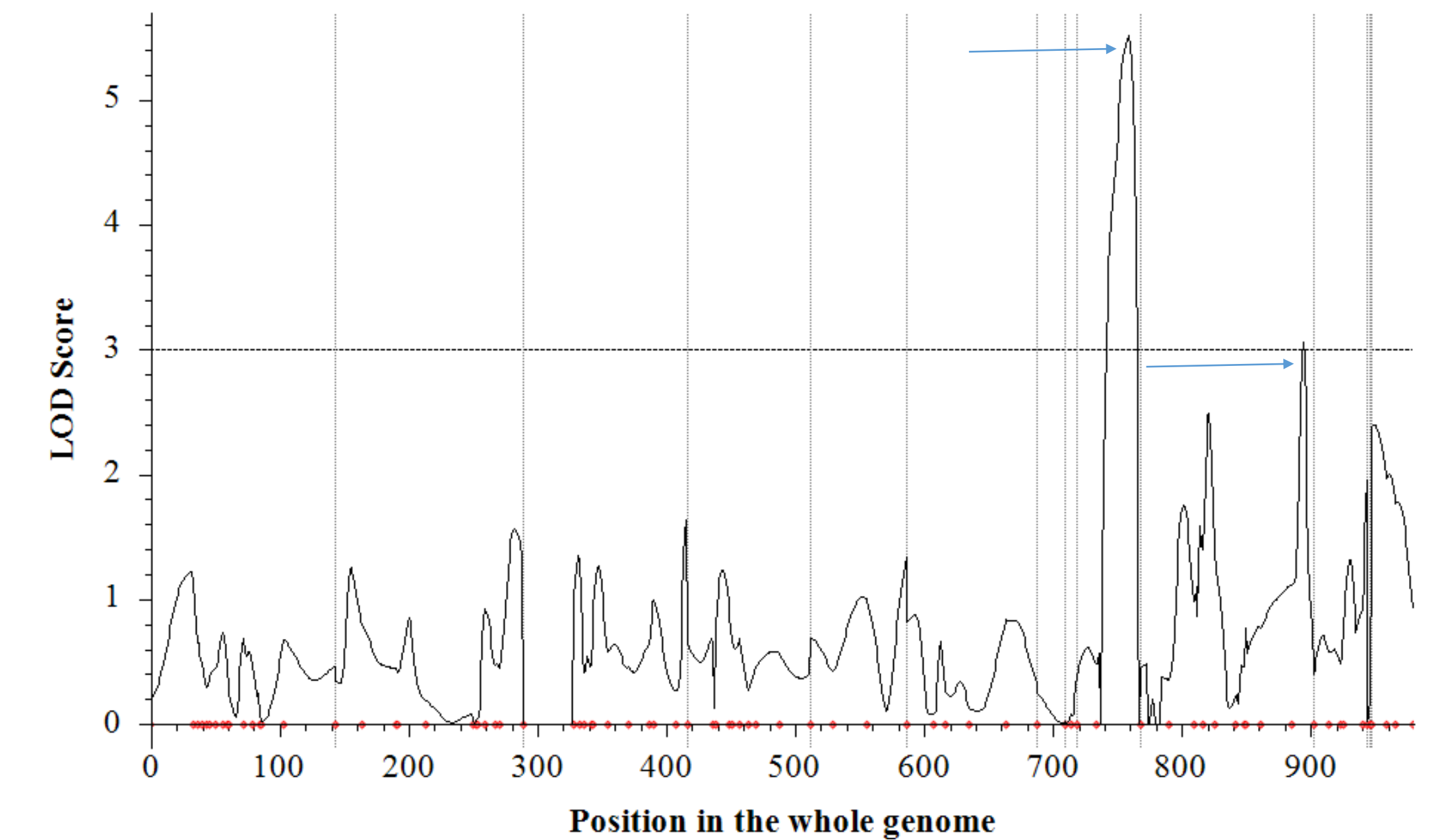
Preliminary QTL identification

Fig 7. Preliminary identification of QTL associated with TLB resistance across the entire genome in the F_1 mapping population. Peaks with LOD score>3 are identified as QTLs.
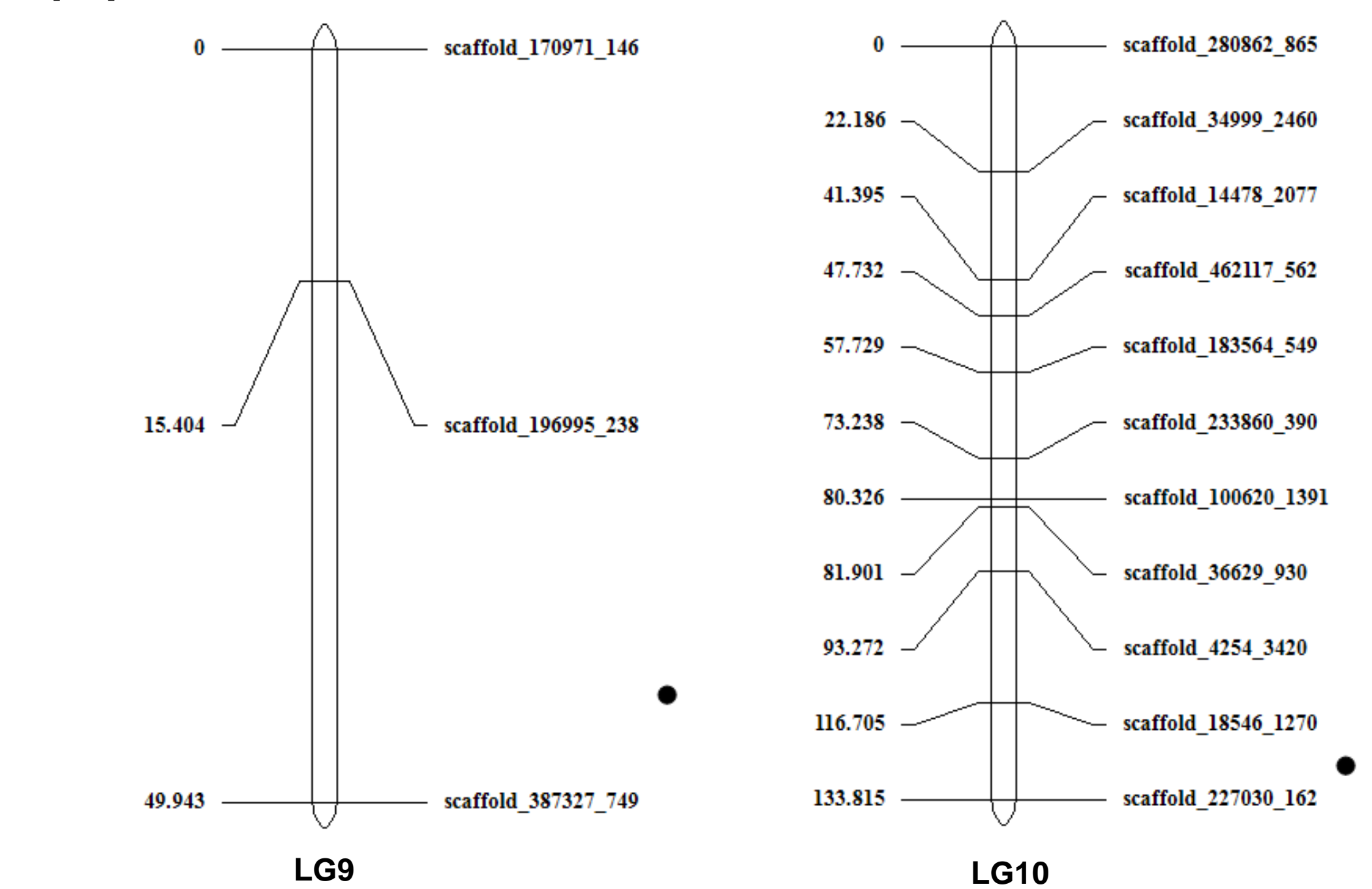

Fig 8. QTL associated with TLB resistance on linkage group 9 and 10 the F_1 mapping population.

Conclusions/Future Directions

• QTL found in non-Hawaiian material appears to have additive effect.
• Genotype new mapping population to validate initial QTL detected.
• Conduct yield trials of superior individuals.

References

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• Voorrips, R. E. (2002). MapChart: software for the graphical presentation of linkage maps and QTLs. Journal of heredity, 93(1), 77-78.
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