

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

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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 these two populations using single nucleotide on polymorphisms (SNP) markers to identify QTLs linked with TLB resistance, both in field trials and laboratory assays.

#### Taro leaf blight



Fig 4: TLB affected plant at Pepeekeo, Hawaii.



0.0 scaffold_63297_1335 32.6 scaffold_810885_386 35.9 scaffold_1014632_235 39.7 scaffold_622526_360 43.3 scaffold_99837_729 45.4 scaffold_35184_2009 50.2 scaffold_126223_195 55.8 scaffold_27116_1401 58.9 scaffold_206265_448 71.9 scaffold_11419_806 78.9 scaffold_74730_295 50.4 50 scaffold_74730_295	0.0 scaffold_2709283_116 21.1 scaffold_68807_501 47.1 scaffold_81930_1258 48.7 scaffold_92688_846 69.5 scaffold_766973_423 106.5 scaffold_1375_3008	0.0 scaffold_161603_938 39.2 scaffold_383107_157 43.7 scaffold_261459_798 48.2 scaffold_85388_754 53.9 scaffold_6966_3959 54.1 scaffold_105190_1130 65.8 scaffold_2388059_137 82.1 scaffold_80922_1692 98.4 scaffold_474221_279 101.2 scaffold_115080_964		0.0 scaffold_326638_785 16.6 scaffold_1394702_136 43.3 scaffold_88366_1667 75.0 scaffold_481335_370 LG5
84.5 85.6 103.1 143.3 LG1 scaffold_33703_2756 scaffold_1484055_182 scaffold_102848_1346 scaffold_431519_532 LG1	108.8 scaffold_72382_1521   109.7 scaffold_484060_599   115.7 scaffold_571916_537   123.6 scaffold_2541735_109   127.6 scaffold_90460_1061   145.3 LG2	101.3 scaffold_115080_864 119.0 scaffold_24549_1509 127.7 scaffold_87806_542 LG3	LG4	0.0
0.0 scaffold_5143_989 20.1 scaffold_27772_1452 30.0 scaffold_60309_791 47.6 scaffold_134439_117	0.0 scaffold_691575_431 21.7 scaffold_70603_1547	0.0 4.1 8.5 LG8 scaffold_150594_1015 scaffold_92279_491 scaffold_30598_555	0.0 scaffold_170971_146 15.4 scaffold_196995_238 49.9 scaffold_387327_749 LG9	22.2 scaffold_34999_2460   41.4 scaffold_14478_2077   47.7 scaffold_462117_562   57.7 scaffold_183564_549   73.2 scaffold_233860_390   80.3 scaffold_100620_1391   81.9 scaffold_36629_930   93.3 scaffold_4254_3420
76.3 scaffold_18948_2301 101.1 scaffold_14899_1070 LG6 0.0 scaffold_31698_1791 12.1 scaffold_2570_3015 21.2 scaffold_385297_693 23.0 scaffold_6214_903	LG7 0.0	0.0 1.5 scaffold_6403_4791 scaffold_269380_119 LG13	0.0 scaffold_2608330_150 11.6 scaffold_14631_2057 18.5 scaffold_284185_911	116.7 scaffold_18546_1270 133.8 scaffold_227030_162 LG10
38.1 scaffold_237257_851 42.2 scaffold_813370_218		2010	32.5 — — scaffold_62735_716 LG14	

#### Fig 6. Preliminary linkage map with high quality SNP markers,

## **Breeding of Taro and Mapping Population**



Fig 1: How breeding of taro occurs.

Mapping population #1





- 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



derived from genotyping-by-sequencing.

## **Preliminary QTL identification**



#### Position in the whole genome

Fig 7. Preliminary identification of QTL associated with TLB resistance across the entire genome in the F<sub>1</sub> mapping population. Peaks with LOD score>3 are identified as QTLs.



#### Population 1025

Population 1060

Fig 2: Mapping populations used to identify TLB resistance.

# Segregating population for TLB resistance



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.



Fig 8. QTL associated with TLB resistance on linkage group 9 and 10 the F<sub>1</sub> 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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### Acknowledgements





#### colocasiae isolate. The smaller the lesion diameter, the greater



Inclusive composite interval mapping of Additive and

Dominant QTL (ICIM - ADD) was used as an algorithm for





