

Known sources of Resistance to Root-knot in *Gossypium hirsutum*

- Jackson Limbless (Orton, 1905)
- Cleviewilt-6 (Jones et al., 1958)
 - Has been used as a source of resistance in breeding programs
- Wild Mexico Jack Jones (Minton, 1962)
 - Crossed with Cleviewilt-6 to develop highly resistant Auburn and M-series sources of resistance
- 18 Primitive race stocks (Shepherd, 1983)
- 5 accessions of *G. hirsutum* from the Yucatan region of Mexico (Robinson & Percival, 1997)
- 24 primitive accessions of *G. hirsutum* (McCarty et al., 1988)
- Acala C-225 (= Acala NemX) (Oakley, 1995)

Inheritance of Resistance to Root-knot nematodes

- Cleve wilt – 6
 - one recessive gene (Bezawada, 2003)
 - one dominant gene (Shen et al., 2007)
- Auburn and M-series
 - Auburn 623: More than 2 genes, incomplete dominance (Shepherd, 1974)
 - M240: 2 dominant genes (Zhou, 1999)
 - M315: 1 dominant + 1 additive gene (McPherson et al., 2004)
 - M78: 1 dominant gene (McPherson et al., 2004)
- NemX
 - 1 recessive gene (Wang et al., 2006)

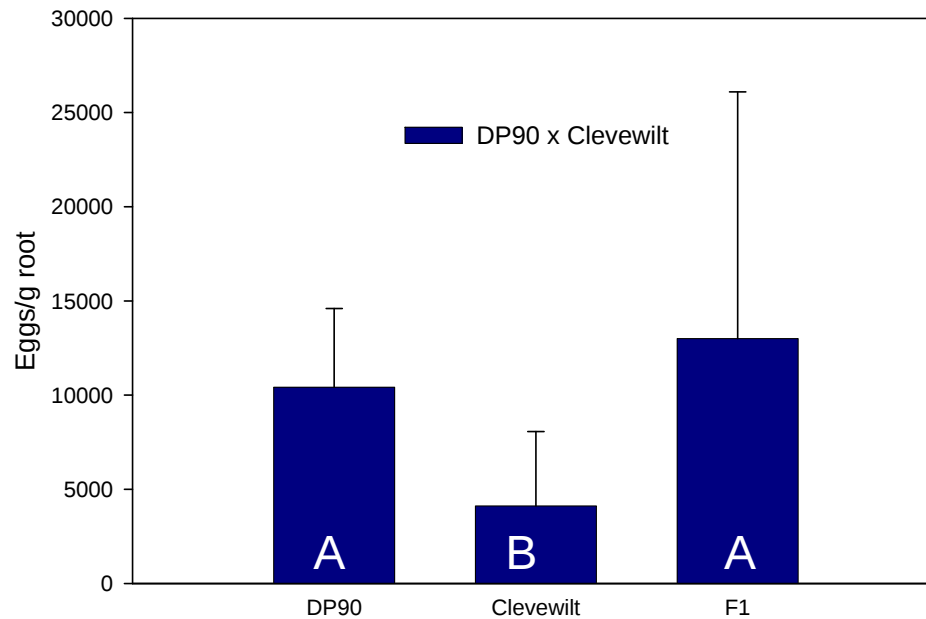
G. hirsutum is an allotetraploid with an AD genome

Diallele test to determine heritance and allelic relationships among several sources of resistance to root-knot nematodes

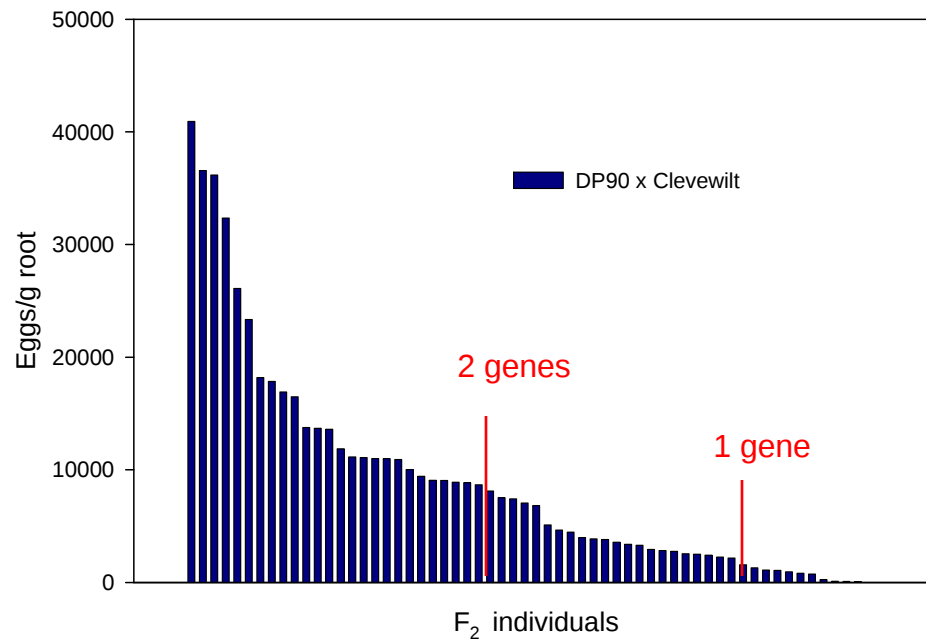
	CW	WMJJ	TX1174	TX1440	TX2076	TX2079	TX2107
DP90	X	X	X	X	X	X	X
CW		X	X	X	X	X	X
WMJJ			X	X	X	X	X
TX1174				X	X	X	X
TX1440					X	X	X
TX2076						X	X
TX2079							X

TX 1174, TX1440, TX2076, TX2079, and TX2107 identified as resistant accessions by Robinson and Percival, 1997.

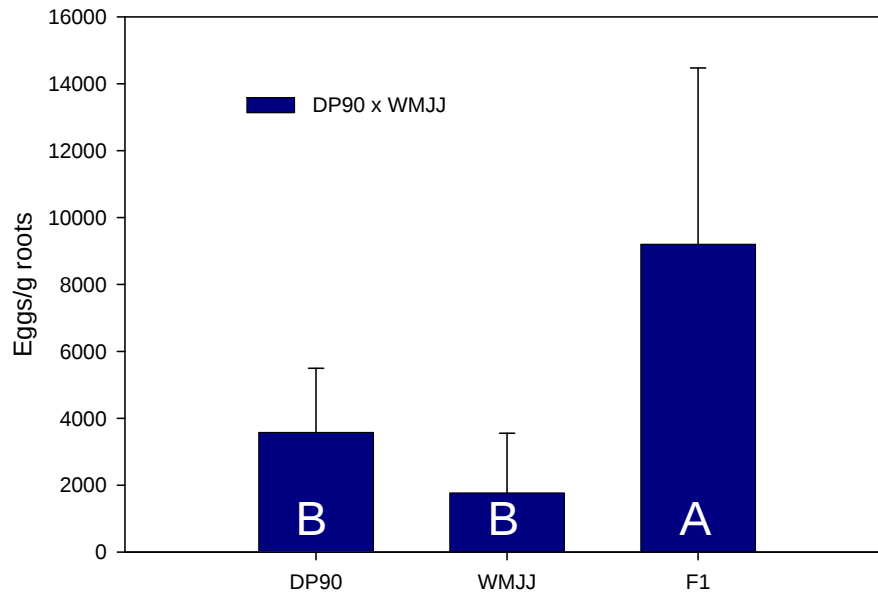
Initial crosses made at a winter nursery in Mexico (2003/04, and again in 2004/05) and most F2 populations produced in the same nursery in 2004/05. Evaluations of populations initiated in 2006.



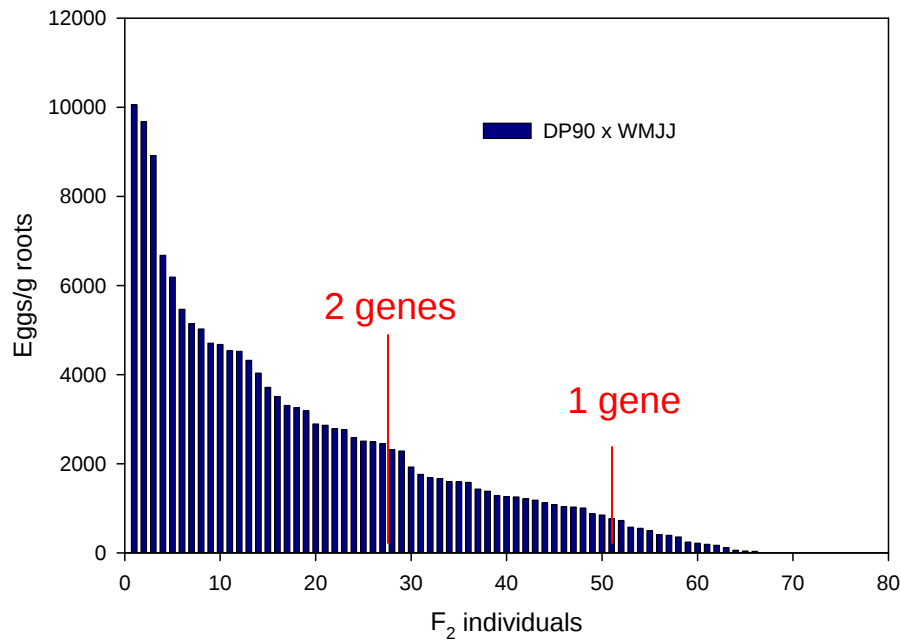
High level of reproduction on F_1 indicates recessive inheritance



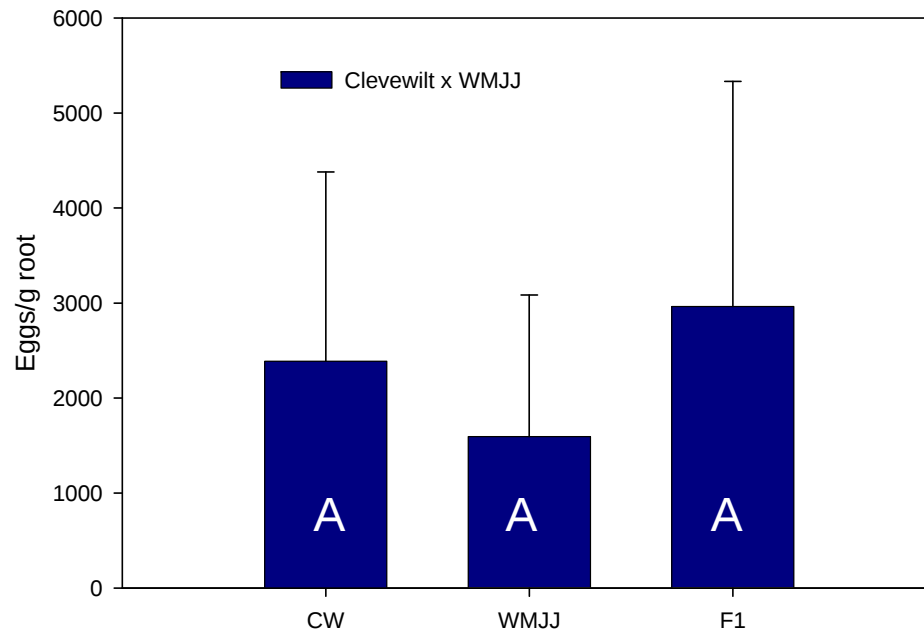
Two recessive genes (9:7 ratio) model gives best fit to observed segregation in F_2



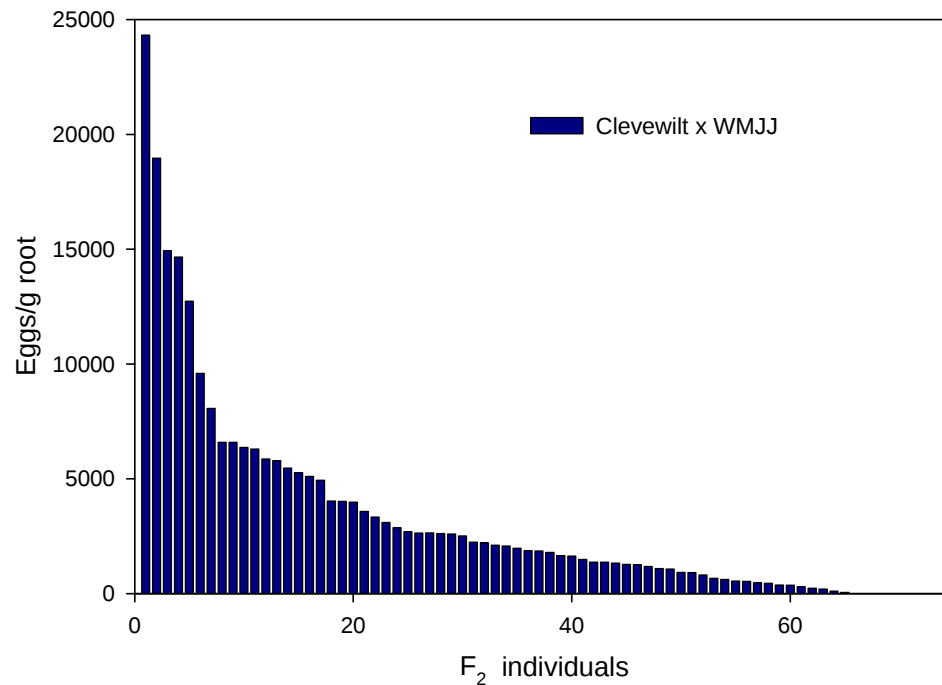
High level of reproduction on F1 indicates recessive inheritance



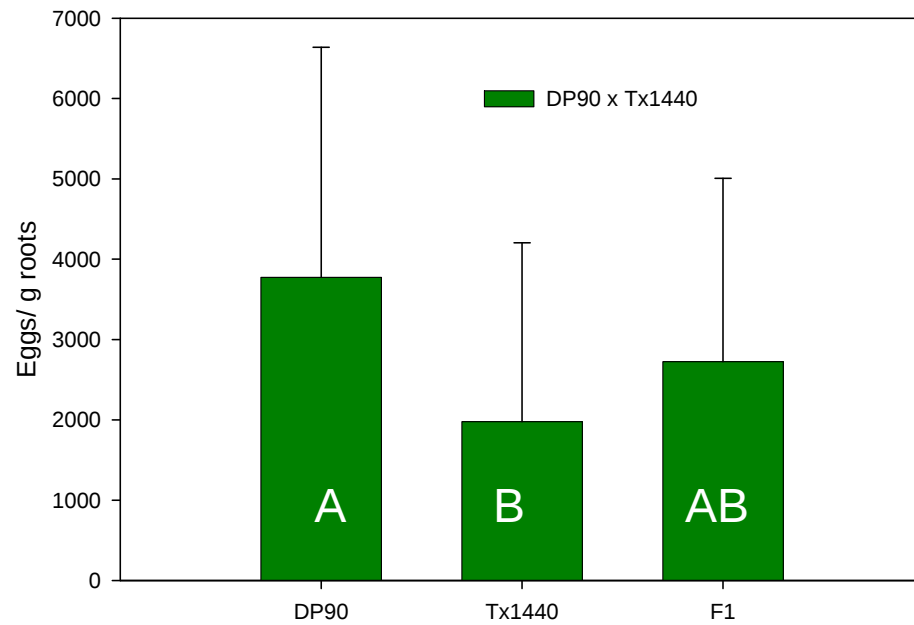
Two recessive genes model gives best fit to observed segregation in F₂



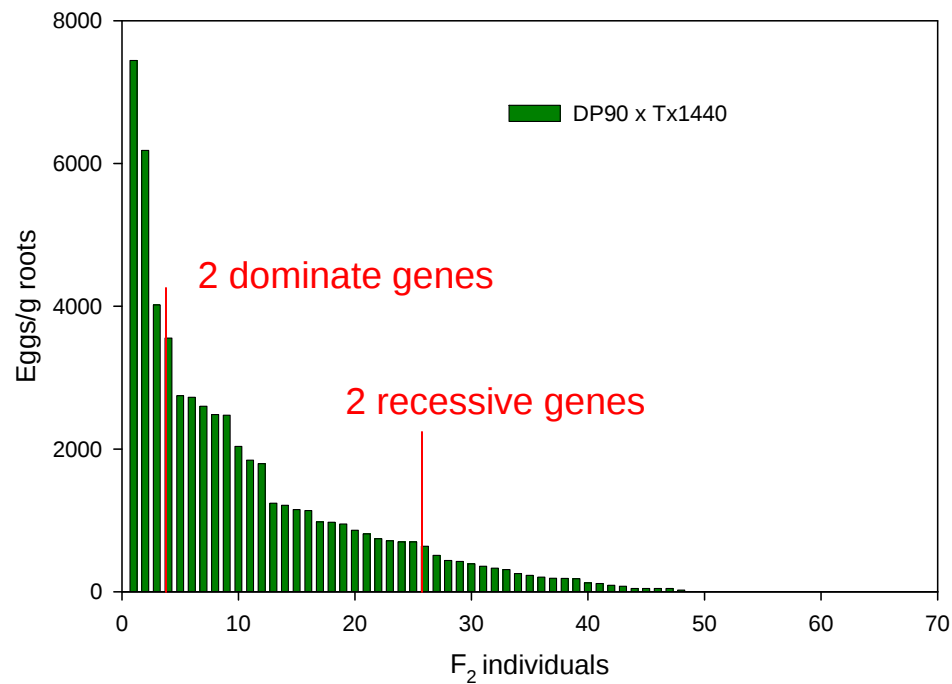
Resistance of F_1 is similar to that of parents as expected for two resistant parents with at least some of same resistance genes in each parent.



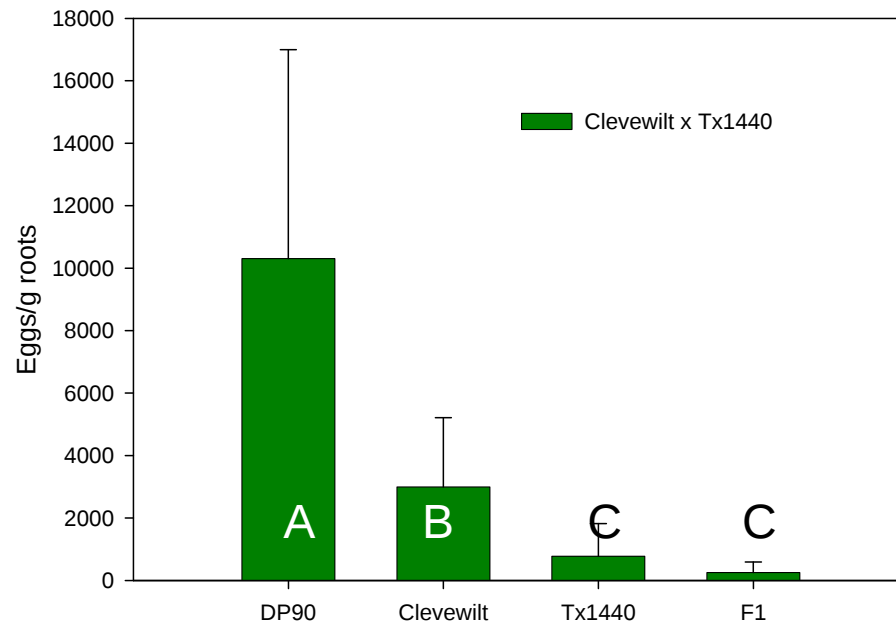
That some of the F_2 are highly susceptible indicates that some of the genes for resistance in Clevevilt are different from those in Wild Mexico Jack Jones.



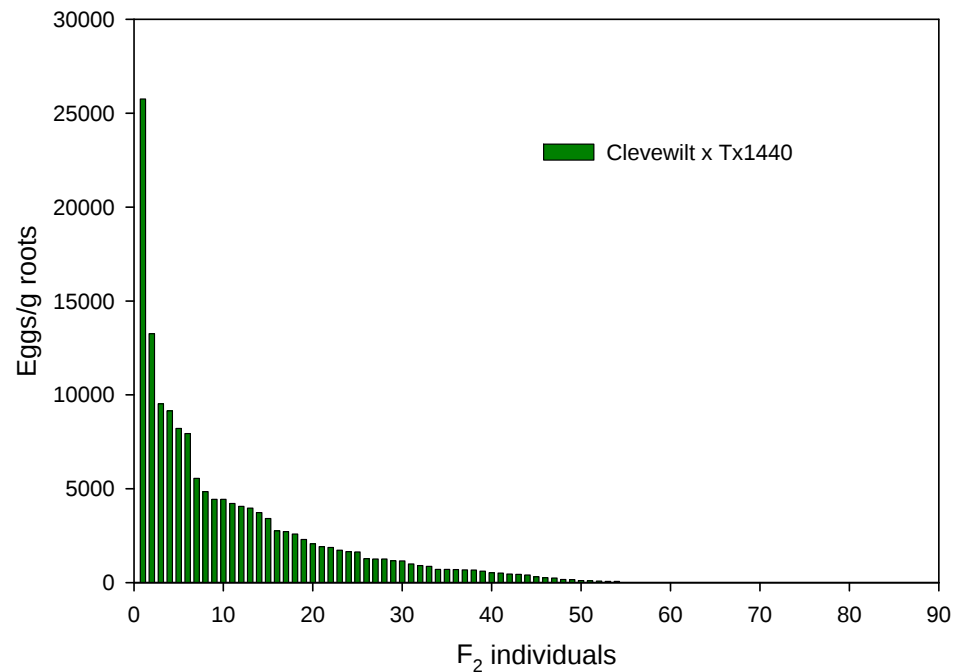
High variation precludes clear separation of parental and F_1 populations.



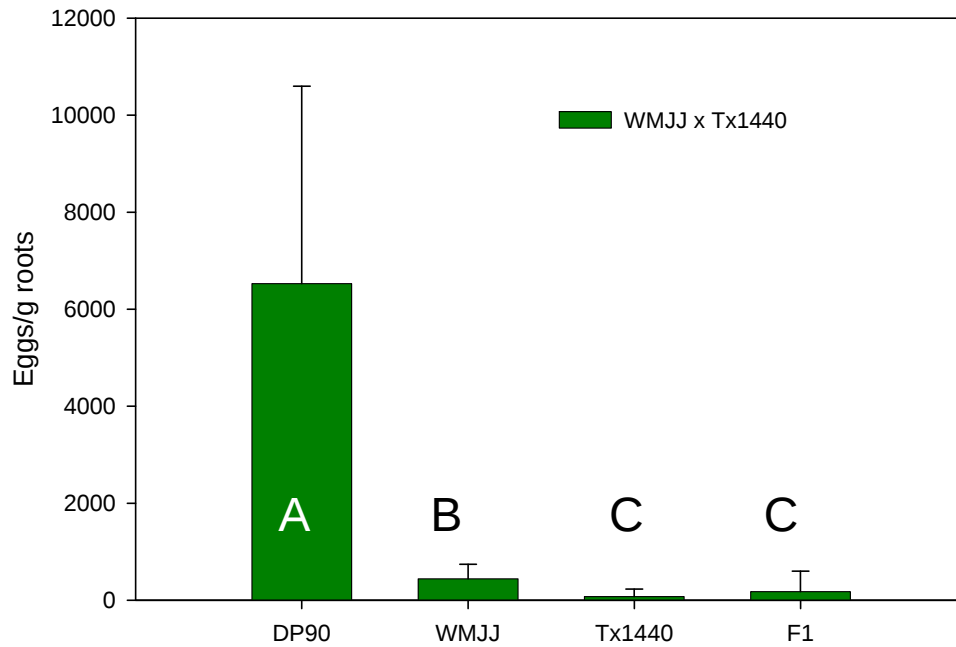
If one assumes dominance, then data fits a model for 2 dominate genes. Poor fit to either 1 or 2 recessive gene models



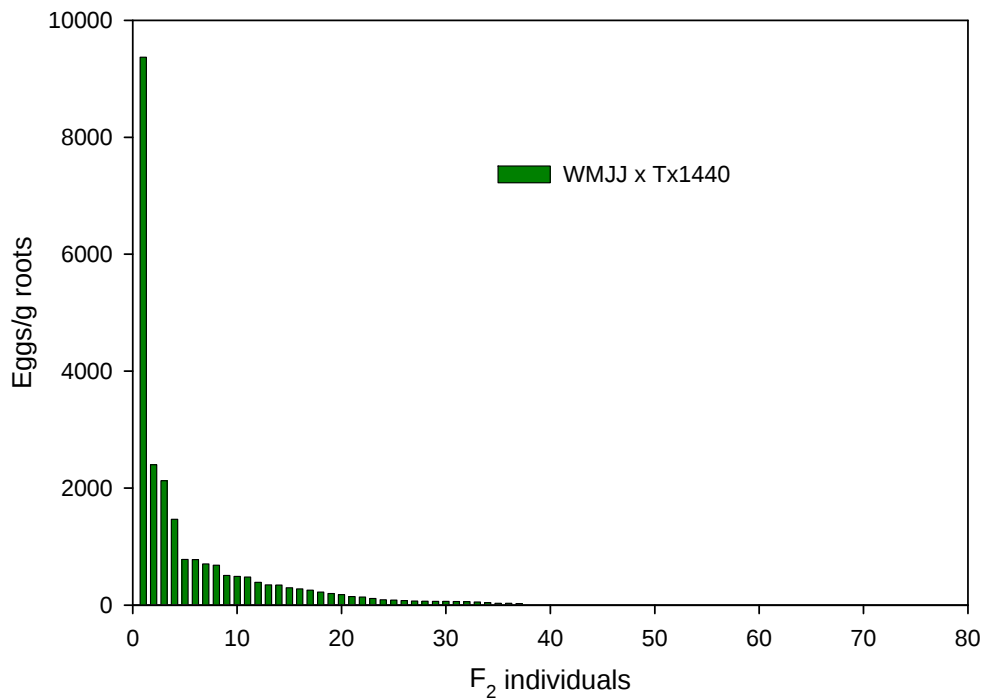
Reproduction on F_1 similar to that of resistant parents. Supports previous conclusion that resistance in TX1440 is inherited as a dominant trait.



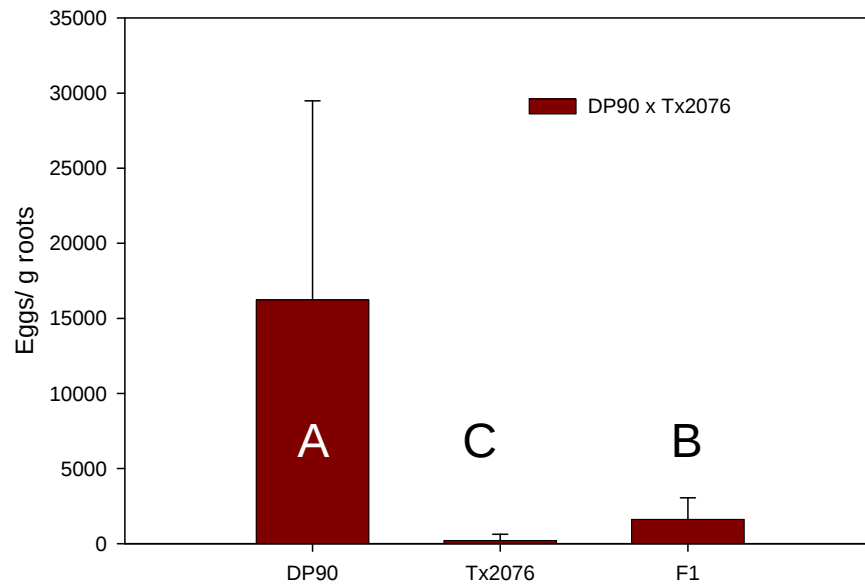
That some of the F_2 are highly susceptible indicates that Cleve wilt and TX1440 Jones have different resistance genes



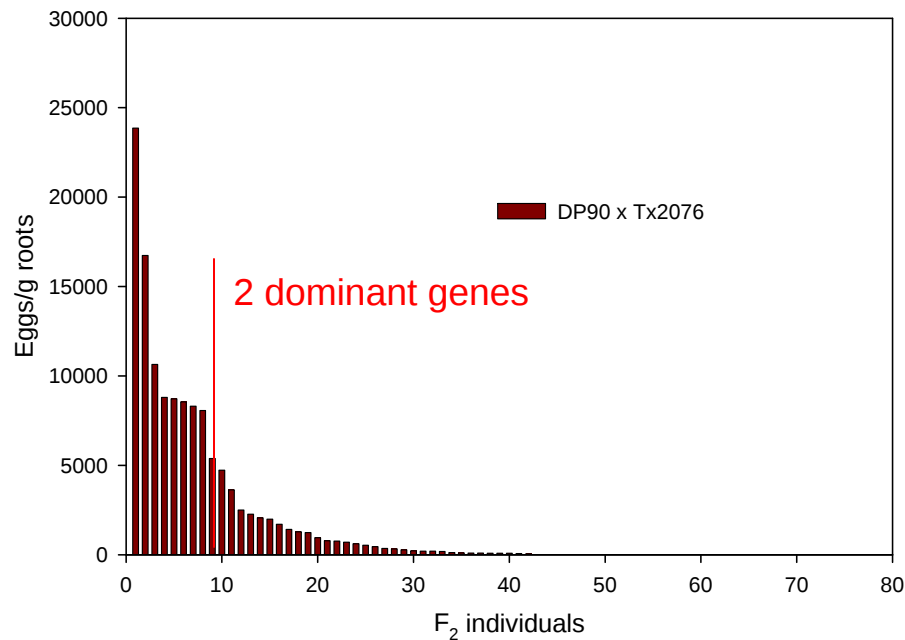
Behavior of F_1 similar to that observed in cross with Cleve wilt.



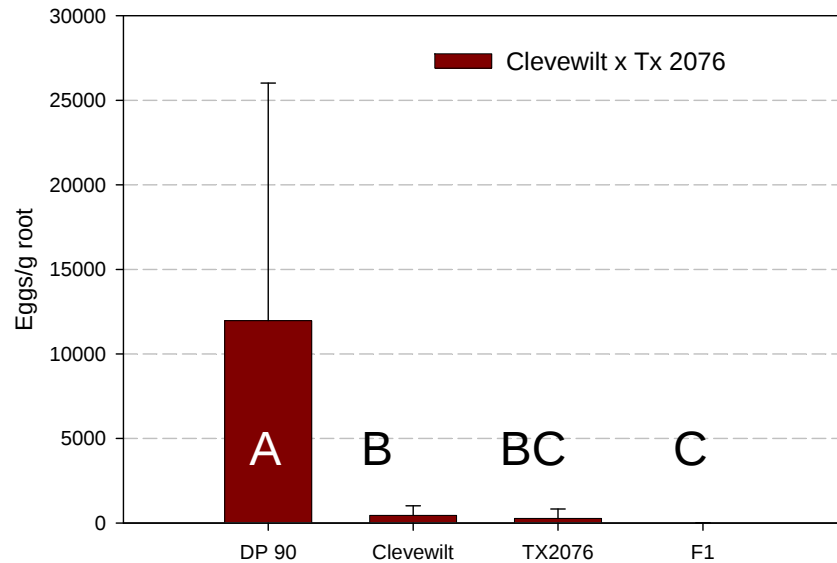
That some of the F_2 are highly susceptible indicates that Wild Mexico Jack Jones and Tx1440 have different resistance genes



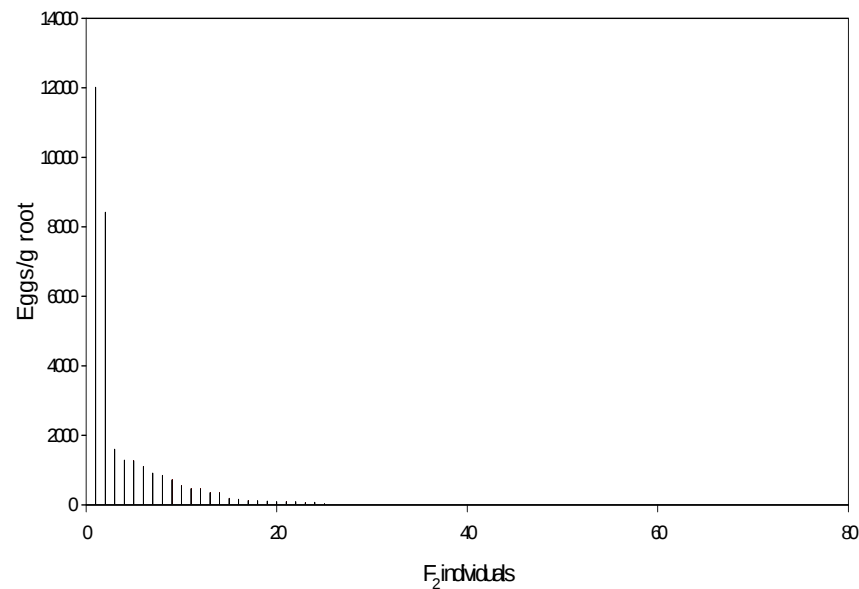
Low reproduction on F1 indicates dominate inheritance of resistance



Segregation pattern fits a 2 gene model slightly better than it does a 1-gene model.



Resistance in F_1 supports previous conclusion that resistance is inherited as a dominant trait.



That some of the F_2 are highly susceptible indicates that Cleviewilt and TX2076 have different resistance genes

Preliminary Conclusions

- The four resistant accessions examined to date each appear to have at least some unique genes for resistance
- Resistance in Cleviewilt and Wild Mexico Jack Jones inherited as a recessive trait
- Resistance in TX1440 and TX 2076 inherited as a dominant trait.