Screening of Different *Actinidia* Germplasm Resources in Relation to the Tolerance of Kiwifruit Vine Decline Syndrome

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Introduction

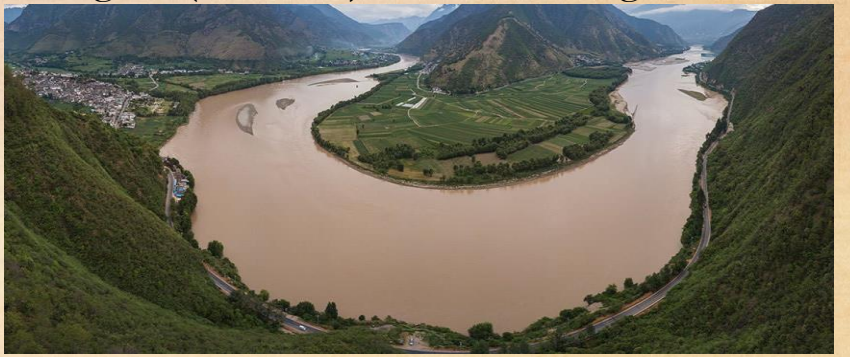
Kiwifruit Vine Decline Syndrome (KVDS): complex disease, worldwide spread. First reports in Italy since 2012 (Tacconi et al., 2012)

Aetiology: attributed soilborne pathogens (*Phytophthora*, *Pythium*, *Phytopythium*, *Fusarium etc)*, activity primary enhanced by waterlogging conditions (e.g., biotic and abiotic pathology) (Savian et al., 2020)

Up to date: disease knowledge's is poor, the disease management poorly effective as well

Example of Kiwifruit Germplasm

Yangtze (blu river), *Actinidia* Origin centre



Possible solution: screening and using tolerant/resistant species (especially for rootstocks or breeding purposes) (Testolin et al., 2014)

350 q./Ha (± 45.000 $)

25 q./Ha (± 3000 $)

Non-Infected (left) and Infected (right) Kiwifruit Orchards (author's photo)

Materials and Methods

Genotypes: *A. macrosperma*, accession number 176 (Ma176), number 183 (Ma183) and cv. Bounty71, *A. arguta* cv. Miss Green (MG), *A. polygama* (Pol) and *A. deliciosa* cv. 'Hayward' (HW)

1- Evaluation of root system (biometric indices)

2- Total aerial biomass produced (dry weight)

3- Development of a statistical model for the fitness of *Actinidia* spp. radical system (multivariate linear regression analyses)

4- Mineral Elements (ICP AES) and protein content and degradation (Bradford and SDS Page analyses) in the radical compartment

Up: *A. arguta*,
Left: *A. deliciosa*,
Right: *A. macrosperma*

Results – Radical System Indices

- Ma176, Ma183, Bounty71 and MG: full capacity to survive in KVDS inducing soils (100%). Only the 16% of HW plants survived. None *A. polygama* plant have been able to grow (0%)

- Different behavior in the root system: HW the worse, Ma176 and MG tent to be the best, others: in the middle

Genotype	Percentage of alive plants (%)
Ma176	100
Ma183	100
Bounty71	100
MG	100
HW	16
Pol	0

Alive plants (mean of 4 experimental sites)

Genotype	Volume (mL)	Depth (cm)	Width (cm)	Total roots number (100 cm²)
Ma176	407.33 c	31.34 b	47.65 B	18.64 a
Ma183	187.05 b	27.36 b	35.93 b	17.26 a
Bounty71	226.75 b	30.76 b	38.35 b	21.89 Aa
MG	389.33 c	29.80 b	36.8 b	22.93 Aa
HW	56 a	16.1 a	18.25 a	15,1 a

Root system indices. Within columns, values that are assigned by different letters are significantly different at $\alpha \leq 0.05$, 0.01, 0.001% and no significance (ns), respectively

Results – Canopy Development

Dry weight: Ma176 along with Bounty71 had the greatest value, whilst HW the lowest. Statistical significance was found in each genotype attitude to develop canopy

Genotype	Dry weight (g)	Ø (cm) trunk
Ma176	23.53 c	1.01 a
Ma183	7.12 b	0.86 a
Bounty71	22.22 c	0.96 a
MG	10.22 Bb	1.22 aA
HW	2.80 a	1.09 a

Canopy indices after one growing season. Within columns, values that are assigned by different letters are significantly different at $\alpha \leq 0.05$, 0.01, 0.001% and no significance (ns), respectively

Left: 'Bounty 71', right: *A. polygama, after one vegetative season*

Results – Statistical Models

Additive model and an Interactive one developing:

- Root volume was charged and fixed as the most important parameter for plant surviving

- Volume was influenced by the total root number and the canopy dry weight

- The two models produced data not statistically different (*p* value: 0.4117)

Additive Model	*p* value	Significance
Intercept - Root Volume	2,83E-07	***
Trunk Diameter	0,3251	
Total Roots Number	0,0101	*
Canopy Dry Weight	0,6954	
Interactive model		
Intercept - Root Volume	0,00175	**
Trunk Diameter	0,18054	
Total Roots Number	0,76072	
Canopy Dry Weight	0,09775	*
Trunk Diameter * Total Roots Number	0,56566	
Trunk Diameter * Canopy Dry Weight	0,11929	
Total Roots Number * Canopy Dry Weight *	0,14616	
Total Roots Number * Canopy Dry Weight * Trunk Diameter	0,18336	
ANOVA - Additive and Interactive	0,4117	

Significant codes : 0 '***', 0.001 '**', '**' 0.01, '*' 0.05, '.' 0,1

Results – Mineral Elements

HW showed the lowest values of each element taken into consideration, apart from N. Each tested genotype had a different capability of nutrient up taking in KVDS inducing soils, however, better than HW

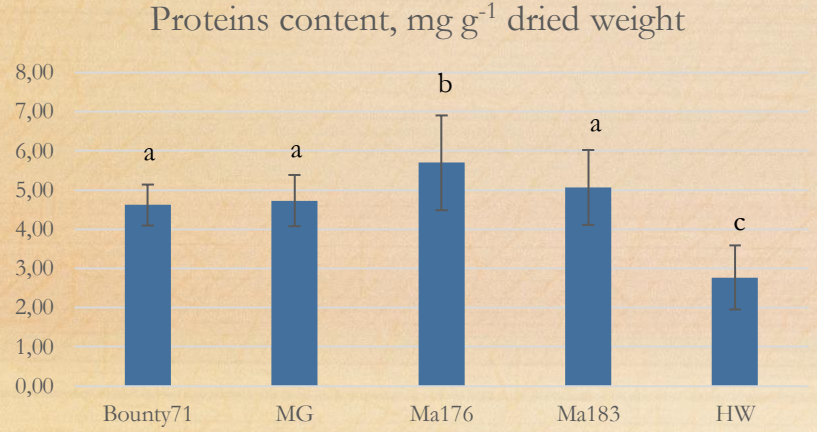
	Bounty71	MG	Ma176	Ma183	HW
N	1,96	2,14	1,78	1,80	1,74
P	45,12 *	39,97	32,28	43,17 *	1,47 ***
K	101,76	96,09	110,89	102,15	1,42 ***
C	617,10	583,40	649,53 *	632,95	37,59 ***
S	28,145	27,66	25,92	24,725	2,41 ***
Ca	4,81	6,29	7,69 *	6,7325	2,69 **
Mg	10,745	14,64 *	12,69	13,10	0,38 ***

Data: mg g^{-1} dry weight

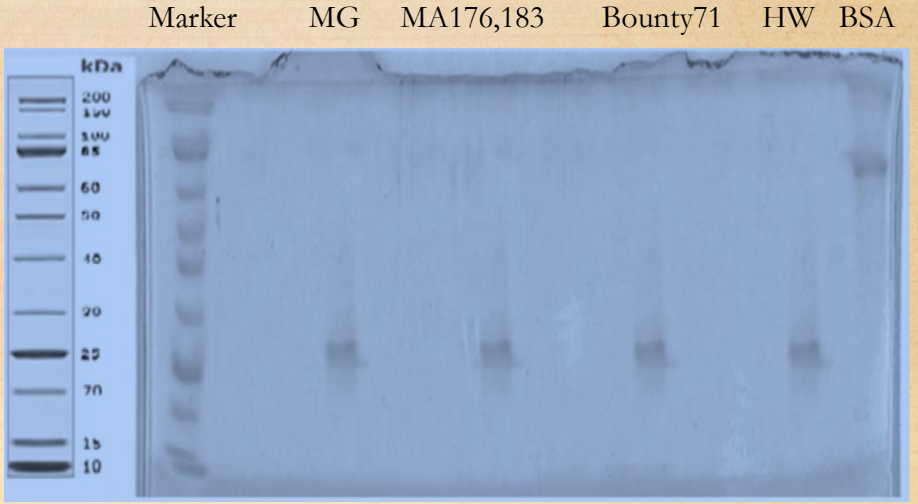
Significant codes : 0 '***', 0.001 '**', '**' 0.01, '*' 0.05, '.' 0,1

Results – Protein Content

Ma176 had the greatest value. Bounty71, MG and Ma183 were comparable but with a minor content. The lowest value was recorded for HW. No different proteins pattern were found (Bovin Siero Albumin, BSA, as positive control). The proteins identified were located between 25 and 30 kDa.



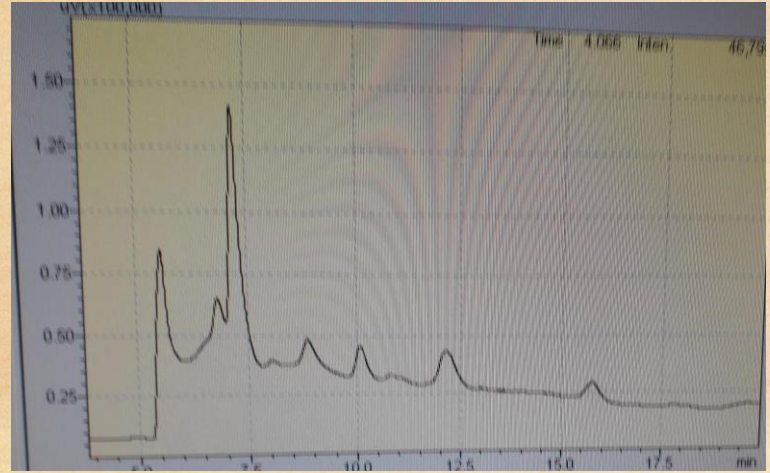
Different letters (e.g., a, b, c,) are significantly different at $\alpha \leq 0.05$, 0.01, 0.001 % and no significance (ns), respectively.



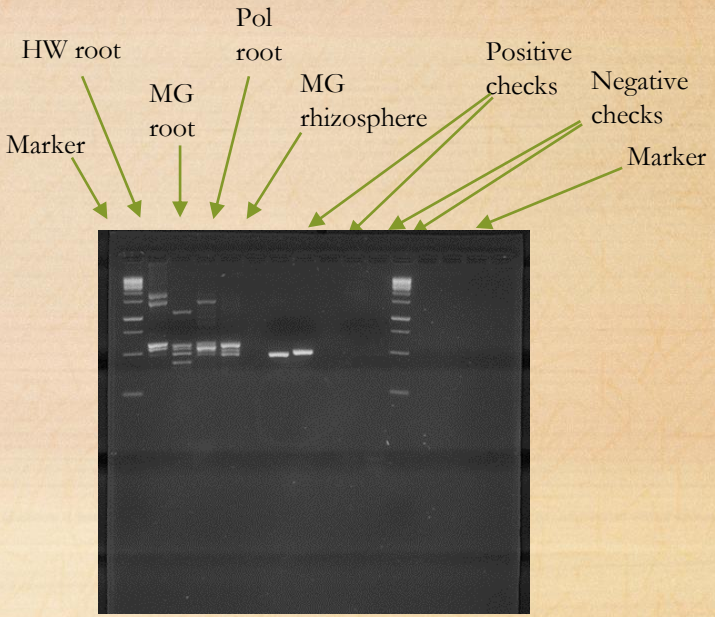
SDS PAGE

Ongoing Activities

Left: detection of radical exudates (HPLC): succinic, acetic, malic etc. acids (chromatogram)
Right: metabarcoding approach to investigate microbial communities associated with root endosphere and rhizosphere of different *Actinidia* genotypes. Example of amplicons to submit to Miseq sequencing obtained with specific primers for *Oomycetes* from rhizosphere and endosphere samples of some tested *Actinidia* species



HPLC chromatogram



Electrophoresis run

Conclusions

Several genotypes were able to survive in the tested KVDS inducing soil. Hayward confirmed to decline rapidly. Nevertheless, *A. polygama* was the most sensitive. Lots of differences emerged for traits related to root and canopy development in decline inducing soils

Both statistical models demonstrated that root number and canopy dry weight seemed to be the most effective indices in determining the root volume

Protein content: Ma176 had the highest value while HW the lowest (degradation). The other genotypes showed similar content and patterns

Capability of mineral up taking: Hayward cv. was not able to grow and not even to supply the mineral demand for the plant nutrition. The other genotypes had a similar behavior with only some specificities

The significant differences among *A. macrosperma* genotypes in each analyses carried out, suggested us that the germplasm of this specie deserve to be more carefully evaluated (QTL for resistance, physiology, agronomy, biochemistry, grafting attitude, etc.)

Thanks for the Kind Attention and Let's Eat Kiwis!

ersa
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