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Graphical Analysis of Rootstock x Site Interaction for Two NC-140 Multi-Location Apple Rootstock Trials Using GGEbiplot

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Additional index words: GxE interaction, stability analysis, trunk cross-sectional area, yield efficiency, root suckers

Abstract

Genotype x environment interaction can alter the performance of genotypes across environments and the rootstock x site interaction is usually significant for multi-location rootstock trials. Analysis of variance is used to test the hypothesis that there is no interaction, but when the interaction is significant, it provides no information about the nature of the interaction. Biplot methodology was developed for graphical analysis of genotype x environment data and displays the genotype main effect (G) and genotype x environment interaction (GE) of a genotype-by-environment data set, where the environment (E) main effects are removed and the G main effect and the GE are retained and combined. Biplot analysis was used to graphically evaluate rootstock x site interaction using data from the 1994 and 2003 NC-140 apple rootstock trials. Data for cumulative yield from the 1994 trial was used to demonstrate some different biplots and the types of information that can be obtained with GGEbiplot software. Differences in rootstock vigor were more apparent at high-vigor sites than at low-vigor sites. Therefore, for future rootstock trials attempts should be made to include sites with a range of vigor, rather than sites with geographical diversity. For trunk cross-sectional area, cumulative yield and cumulative yield efficiency, M.9 NAKBT337 was one of the most stable rootstocks and was less sensitive to site conditions than most other rootstocks. In general, M.26 and the Geneva rootstocks (G.16, G.41 and G.935) were less stable and responded to site conditions more than M.9 NAKBT337 and B.9.

The NC-140 technical committee has performed more than 30 multisite fruit tree rootstock trials where the rootstock x site interaction is usually highly significant, but few attempts have been made to understand the nature of the interactions. Plant breeders use several statistics, reflecting various aspects of cultivar x site interaction, to evaluate the stability of cultivars grown at a number of sites for one or more years (Eberhart and Russell, 1966; Finlay and Wilkinson, 1963; Francis and Kannenberg, 1978; Kang, 1993; Lin and Binns, 1988; Shukla, 1972). Olien et al. (1991) and Marini (2020) used some of these methods to evaluate apple rootstock stability. For multilocation trials, variation is typically partitioned into three sources: genotypes (G), environments (E), and genotype x environment (GE). When the interaction is significant, rootstock means typically are compared within each site. This approach provides information about rootstock performance at each site, but it provides little information about rootstock stability and it does not identify groups of rootstocks that perform similarly within mega-environments (groups of sites where various rootstocks perform similarly).

Although environment usually explains a high proportion of variation, Yan et al. (2000) explained that only G and GE are relevant to cultivar evaluation and meg-environment identification. They described GGE biplot analysis, which is constructed by the first two symmetrically scaled principal components (PC1 and PC2) derived from singular value

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decomposition of site-centered multisite trials. Breeders of agronomic (Jalata, 2011) and horticultural (Dia et al., 2016) crops have used GGE biplots to evaluate genotype performance. But producing high-quality GGE biplots with commonly used statistical software packages is difficult. Yan (2001) developed a Windows application called GGEbiplot™ (https://www.GGEbiplot.com) to perform biplot analysis of two-way data which outputs the results as an image to allow interactive visualization of the biplot from various perspectives. Yan and Kang (2002) describe in detail the theory and practical uses of GGE biplots and provide tools to interpret biplots.

One objective of this study was to demonstrate the use of GGE biplots to interpret rootstock x site interactions for two NC-140 apple rootstock trials. A second objective was to identify groups of sites (mega-environments) where rootstocks perform similarly, so future multisite rootstock trials can be planned more efficiently. The third objective was to graphically evaluate the stability of rootstocks.

Materials and Methods

Data from two NC-140 apple rootstock trials were used to perform biplot analyses on four important response variables (trunk cross-sectional area, cumulative yield, cumulative yield efficiency, and root suckers). The 1994 trial consisted of ‘Gala’ on 18 rootstocks at 25 sites (Marini et al., 2006). For the 2003 trial, 23 rootstocks were evaluated at eight sites and the scion cultivar was ‘Golden Delicious’ (Marini et al., 2014). At some sites, some rootstocks had poor survival, so only sites and rootstocks with at least 80% tree survival were included in this study. Consequentially, there were 14 rootstocks at 17 sites for the 1994 trial and 11 rootstocks at eight sites for the 2003 trial. The experimental design for the 1994 trial was a randomized complete block design at each site with one tree per rootstock randomly assigned to each of 10 blocks. The design for the 2003 trial was a generalized randomized complete block at each site, with two trees per rootstock randomly assigned to each of four blocks. Details for the trials were previously published (Marini et al., 2006; Marini et al.,

Table 1. Names and abbreviations for sites and rootstocks used in the text and figures.

Site		Rootstock	
Name	Abreviation	Name	Abreviation
Arkansas	AR	Budagovski 9	B9
British Columbia, Ca	BC	Budagovski 491	B491
Illinois	IL	Budagovski 62396	B62396
Iowa	IA	Geneva 16	G16
Kentucky	KY	Geneva 935	G935
Maine	ME	Geneva 41	G41
Massachusetts	MA	J-TE-H	Jteh
New Brunswick, Ca	NB	Malling 9	M9
New York	NY	M.9 Nic29	Nic29
Pennsylvania, Biglerville	PAB	M.9 Pajam 1	Paj1
Pennsylvania, rock springs	PARS	M.9 Pajam 2	Paj2
New Jersey	NJ	M.9 NAKBT337	T337
North Carolina	NC	Malling 27	M27
Utah	UT	Malling 26	M26
Virginia	VA	Pi Au 51-4	Pi514
Wisconsin	WI	Pi Au 56-83	Pi5683
		Polish 2	P2
		Polish 16	P16
		Ottawa 3	O3
		Vineland 1	V1

2014). GGE biplot analyses were performed with GGEbiplot ™ using methods described by Yan and Kang (2003). Abbreviations for sites and rootstocks used in the text and figures are listed in Table 1.

Results

Biplot analysis. GGE biplots allow visualization of the interrelationship among rootstocks, sites and their interaction. Many different types of biplots can be generated to glean a great deal of information from a data set (Yan, 2001; Yan and Kang, 2003; Yan and Tinker, 2006). Cumulative yield data from the 1994 rootstock trial will be used to describe in detail several biplots that can be used to obtain various types of information.

1994 NC-140 trial.

Cumulative yield: relationships among sites. Fig. 1 shows a GGE biplot based on site-focused singular scaling and the first two principle components explained 89.8% of the total variation of the site-centered rootstock x site interaction. The lines radiating out from the biplot origin to the site markers are called site vectors. The length of the vector approximates the standard deviation within each site and is a measure of the ability to discriminate among rootstocks at that site. A short vector (BC, ME, NB, and IL) relative to the biplot size, implies that all rootstocks tend to have similar cumulative yield at that site. PARS and MA were the most discriminating sites. The angle between two site vectors provides a visual approximation of the correlation between the two sites. Sites with acute angles (<90°) are positively correlated, site vectors forming a right angle (90°) are not correlated, and site vectors with obtuse angles (>90°) are negatively correlated. For cumulative yield, all sites were positively correlated, but the correlation between UT and NJ is much stronger than for UT and NC (Fig. 1). The correlation between NC and WI was close to zero. The presence of close associations among sites suggests that the same information about rootstock yield could be obtained from fewer sites that are highly correlated and could reduce testing costs in future trials. One group of sites providing similar information for cumulative yield included UT, NJ, IA, NB and IL; a second group included PARS, MA and VA; and a third group included BC, ME and NC. The GGEbiplot software also generates a matrix of correlation coefficients for each pair of sites (data not shown). Sometimes the vector angles do not correspond well with the coefficients or even their signs because the biplot may not explain all the variation in the data set.

Cumulative yield of each rootstock at each site. The GGE biplot showing the performance of each rootstock at each site is shown in Fig. 2. The difference between Fig. 1 and Fig. 2 is that Fig. 2 also contains information about rootstocks. Vectors for both rootstocks and sites are drawn, to evaluate performance of rootstocks at specific sites and visualize specific interactions between a rootstock and a site. B.9, P.2, M.27, B.491, Mark and P.16 had lower than average yields at all sites because they have negative PC1 values. The yield for a rootstock at a site is better than average if the angle between its vector and the site's vector is <90°; its yield is below average if the angle is >90°; and it is near average if the angle is close to 90°. B.9 had slightly above average yield at NC, average yield at PARS, and slightly below

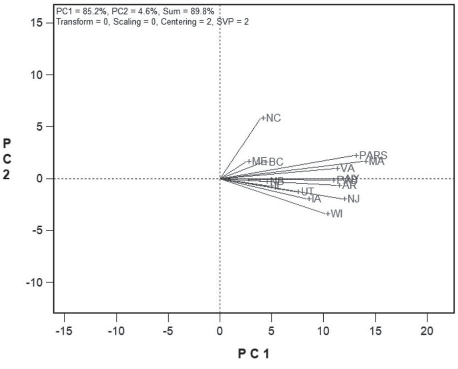

Fig. 1. Site-vector view of the GGE biplot to show cumulative yield per tree among all sites in discriminating the rootstocks in the 1994 trial.

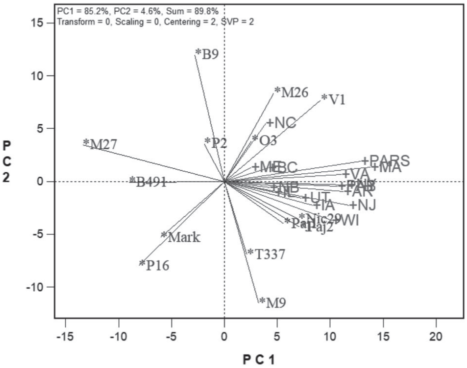

Fig. 2. The GGE biplot showing the cumulative yield of each rootstock at each site.

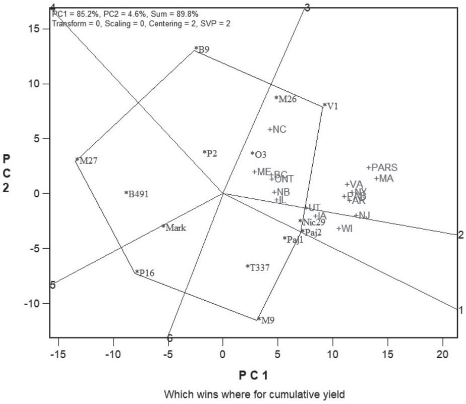

Fig. 3. The which-won-where polygon view of the GGE biplot to show which rootstocks had the highest cumulative yield per tree at which sites.

average yield at WI. In this way, Fig. 2 can be used to rank the rootstocks based on yield at any site and to rank sites on the relative yield of any rootstock.

Which-won-where for cumulative yield. The which-won-where (sometimes called which-wins-where) polygon view of a biplot is the most succinct way of summarizing the GGE pattern of a data set (Yan and Kang, 2003) and allows one to identify mega-environments or groups of similar sites, and which rootstocks performed best in those mega-environments (Fig. 3). The plot presented in Fig. 2 is used to draw a polygon on rootstocks that are furthest from the biplot origin so that all other rootstocks are contained within the polygon. Then perpendicular lines to each side of the polygon are drawn, starting from the biplot origin. Rootstocks located on the vertices of the polygon had the highest or lowest yield at one or more sites. The perpendicular lines are equality lines between adjacent rootstocks on the polygon, which facilitate visual comparison of them. The equality lines divide the biplot into sectors, and the winning rootstocks (rootstocks with the highest yield) for each sector are those located on the respective vertex. In this example most sites fall between the second and third equality lines, where trees on V.1 had the highest cumulative yield. IA and WI fall between the first and second equality lines, where M.9 Pajam 2 had the highest yield. This pattern suggests that there are two groups of sites and, based on only cumulative yield, different rootstocks should be selected for each group.

Mean performance and stability for cumulative yield of the rootstocks. Within a single mega-environment, rootstocks may be evaluated on both mean performance and stability across sites. Fig. 4 is the average-site

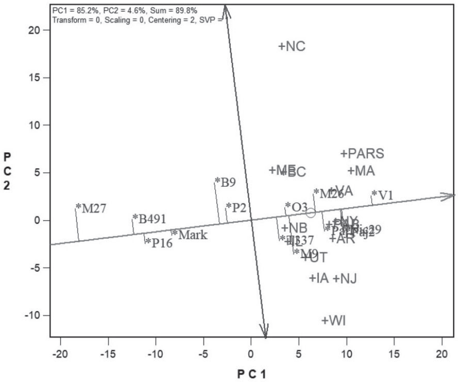

Fig. 4. The average-site coordination (AEC) view to show the mean performance and stability of the rootstocks.

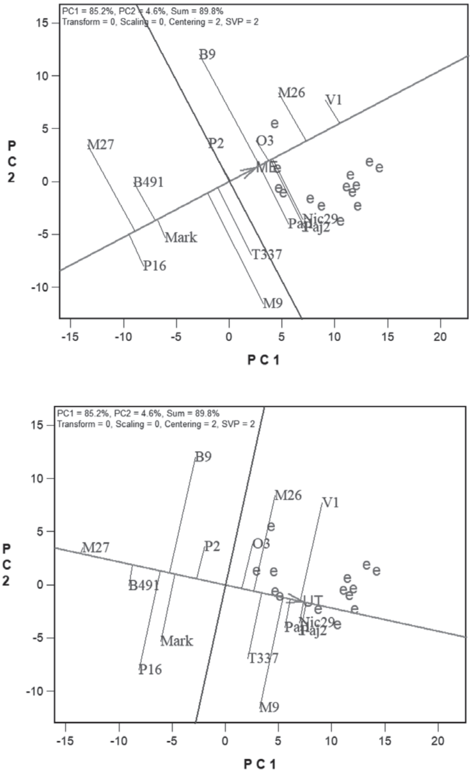

Fig. 5. Ranking rootstocks based on cumulative yield at ME (top) and UT (bottom).

coordination (AEC) view of the GGE biplot. The single-arrowed line is the AEC abscissa and passes through the average site (small circle) and the biplot origin, and points to higher mean cumulative yield across sites. Averaged over all sites, V.1 had the highest cumulative yield, followed by M.9 Pajam 2, M.9 Nic 29, and M.26, etc. M.9 NAKBT337 and P.2 had yields slightly above and below the grand mean, respectively. Trees on M.27 had the lowest yield, whereas B.491 had the second lowest yield. The double-arrowed line is the AEC ordinate and points to the greater variability (poorer stability) in either direction. Thus, Mark, P.16, and O.3 were most stable, whereas M.27, B.9 and M.9 were most unstable.

Ranking rootstocks based on cumulative yield at each site. To better evaluate the nature of the site x rootstock interaction, rootstocks can be ranked based on cumulative yield at each site. A line is drawn that passes through the biplot origin and the site. The line can have a positive or negative slope depending on the sign of PC2 in Fig. 1. Rootstock ranks for ME and UT are shown in Fig. 5. Based on the biplot in Fig. 1, ME and UT were moderately correlated, but the ranking of the rootstocks differed. For ME the ranking of the five highest-yielding rootstocks was V.1>M.26>M.9 Nic 29>M.9 Pajam 2>O.3, whereas for UT the ranking was M.9 Nic 29>M.9 Pajam 2>V.1> M.9 Pajam1>M.9. *Ranking sites based on cumulative yield for one rootstock.* To evaluate the specific adaptation of a rootstock, sites can be ranked based on the relative cumulative yield per tree of a rootstock by drawing a line that passes through the biplot origin and the rootstock in Fig. 2. Plots for M.9 NAKBT337 and M.26 are shown in Fig. 6. The plots show that trees on M.9 NAKBT337 had the highest yields at WI>NJ>IA>AR, but trees on M.26 had highest cumulative yields at MA and PARS, followed by NC and VA.

Ranking sites based on both discriminating ability and representativeness. For future rootstock trials it is useful to identify sites that discriminate between rootstocks, but the ideal test site is one that is both discriminating and representative. Figure 7 is similar to Fig. 1 except the “Average-Environment Axis” [AEA, or average-site-axis, Yan (2001)] has been added. The average site, represented by the small circle at the end of the arrow, has the average coordinates of all sites and the AEA is the line that passes through the average site and the biplot origin. The site that has the smallest angle with the AEA is more representative of the other sites. Thus, NB, PAB and NY are most representative, whereas NC and WI are least representative. Sites that are both discriminating (furthest from the biplot origin), and representative (small angles with the AEA) are good test sites for selecting generally adapted rootstocks.

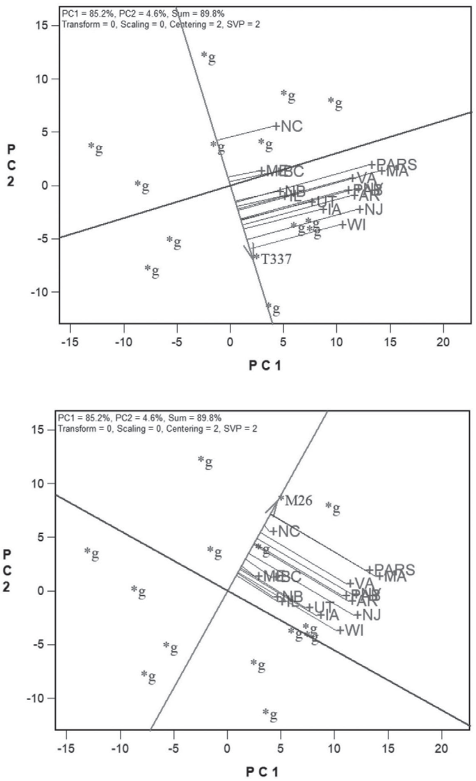

Fig. 6. Ranking of sites based on relative cumulative yield of T.337 (top), M.26 (bottom).

Based on only cumulative yield per tree, future rootstock trials should include NY, PAB and possibly VA, because they are more discriminating than NB. Discriminating, but non-representative sites (WI, PARS and NJ) are useful for identifying specifically adapted rootstocks if the sites can be divided into groups.

Trunk cross-sectional area (TCA). The GGE biplot for TCA explained 95.9% of the total variation of the environment-centered G and E table. All the sites were positively correlated. ME, NC, and BC were highly correlated, and UT, AR and IL were highly correlated, but the two groups were poorly correlated with each other (Fig. 8). UT, PAB, NJ and IL were the most discriminating sites, whereas BC, NB, ME and ONT were the least discriminating. Averaged over all sites, V.1 had the largest trunks and M.27 had the smallest trunks. The least stable rootstocks were V.1, Mark and M.26, whereas P.2 was extremely stable. Pairs of rootstocks that were highly correlated included M.9 NAKB.337 and M.9; P.16 and B.491; M.9 Nic 29 and M.9 Pajam 1; and B.9 and Mark (Fig. 8). M.9 NAKBT337 was slightly negatively correlated with M.26, V.1, O.3, B.9, and Mark.

The which-won-where view of the GGE biplot shows that sites fell into two sectors

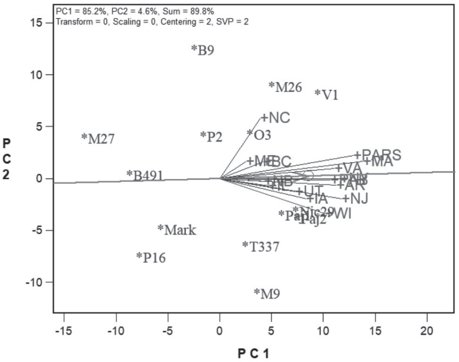

Fig. 7. The discrimination and representativeness view of the GGE biplot to show the discriminating ability and representativeness of the sites for evaluating cumulative yield per tree in the 1994 trial.

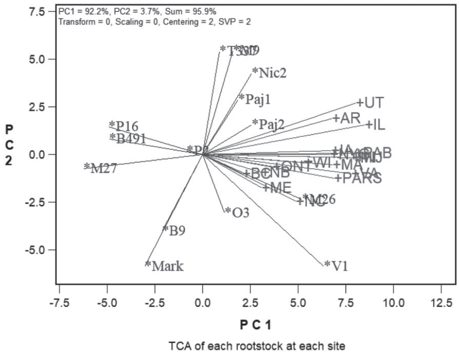

Fig. 8. The GGE biplot showing the trunk cross-sectional area of each rootstock at each site.

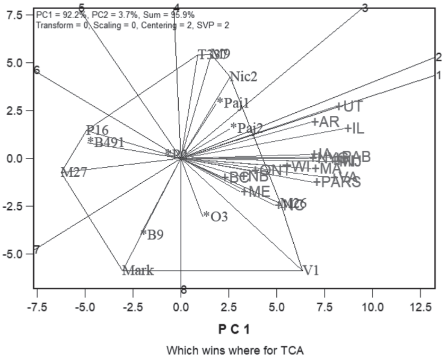

Fig. 9. The which-won-where view of the GGE biplot to show which rootstocks had the largest TCA at which sites.

for TCA (Fig. 9). One sector contained UT and all other sites fell into a different sector. In the sector with most sites, trees on V.1 had the largest TCA. The average-site coordination (AEC) view was generated to show the mean performance and stability of the rootstocks and trees on V.1 had the largest trunks followed by M.26> M.9 Pajam 2> M.9 Nic 29> M.9 Pajam 1> M.9> O.3>M.9 NAKBT337> P.2> B.9> Mark> B.491> P.16>M.27 (data not shown). M.9 NAKBT337 was slightly above average and P.2 was slightly below average. V.1, O.3 and P.2 were very stable, and M.9 NAKBT337, M.9 and Mark were least stable. To better understand the nature of the interaction, plots of rootstock ranks for TCA were evaluated for nine sites (data not shown). The relative ranking of rootstocks was similar for most sites. Trees on B.491, P.16 and M.27 were the smallest at all sites, but at UT Mark also fell into this group. Rootstocks with largest TCA included V.1, M.26 and O.3 at most sites. However, at IA and UT M.9 Nic 29 was larger than O.3, whereas at PARS, M.9 Pajam 2 was larger than O.3. The least stable rootstocks at ME included M.9 NAKBT337, M.9, Mark and B.9; at UT the least stables rootstocks were V.1, M.9 NAKBT337, M.9 and Mark. Based on discrimination and representativeness for TCA, WI was closest to the average site, followed by NY, IA and MA. The least desirable sites were UT, AR, ME and NC (data not shown).

Yield efficiency. For cumulative yield efficiency *(CYE)*, IL and BC were most discriminating, whereas AR, NB and ME were least discriminating (Fig. 10). NC and AR were negatively correlated. Sites that were highly correlated included IL and ONT; PAB and UT; ME, MA and WI; VA and PARS; and BC and IA. Trees on P.16 and B.491 had the highest average CYE, whereas trees on M.26 and V.1 had the lowest CYE. Groups of rootstocks that were highly correlated included V.1 and M.26; M.27 and P.2; B.9, O.3 and Mark; B.491 and P.16; and all the others (Fig. 10). The least stable rootstocks included P.16, B.9, M.27, M.26, V.1 and T.337, whereas O.3 was very stable. AT NC, CYE was greater than average for P.2, M.27, Mark and B.9, but CYE was below average for M.9 Pajam 1 and M.9 Pajam 2, M.9, M.9 Nic 29 and M.9 NAKBT337 (data not shown). At IL, CYE was greater than average for B.9, Mark, O.3, and B.491, but below average for M.26, V.1, M.9 Pajam1, M.9 Pajam 2, M.9, M.9 Nic29 and M.9 NAKBT337 (data not shown). For NY, the only rootstocks with above average CYE were P.16, B.491, B.9, O.3 and Mark (data not shown). The which-won-where

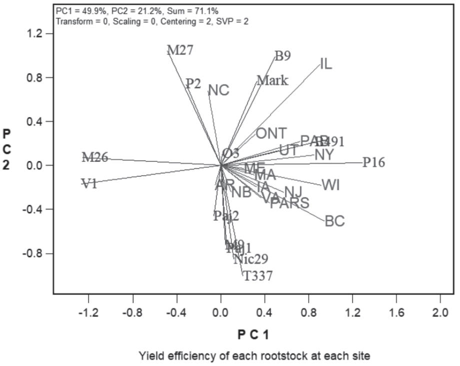

Fig. 10. The GGE biplot showing cumulative yield efficiency of each rootstock at each site.

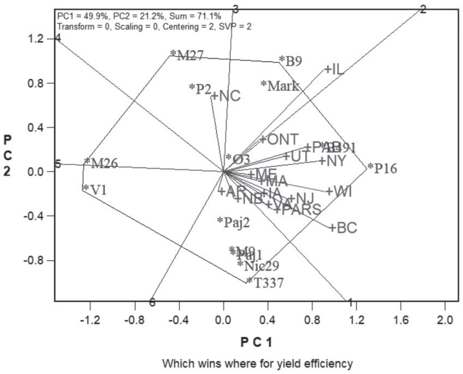

Fig. 11. The which-won-where view of the GGE biplot to show which rootstocks had the highest cumulative yield efficiency at which sites for the 1994 rootstock trial.

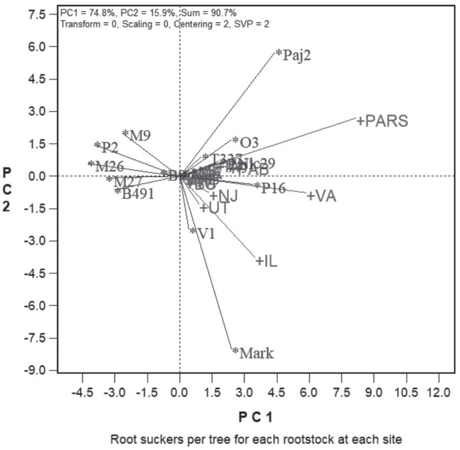

Fig. 12. The GGE biplot showing number of root suckers per tree for each rootstock at each site for the 1994 rootstock trial.

plot shows six sectors (Fig. 11) and one or more sites fell into four sectors. One group included AR and NB, where M.9 NAKBT337 had the highest CYE. The second group contained only NC, where M.27 had the highest CYE. IL fell into the third sector, where B.9 had the highest CYE. The fourth sector contained the remaining sites, where P.16 had the highest CYE. The AEC view of the biplot showed that, when averaged over all sites, trees on P.16, B.491 and B.9 had the highest CYE, whereas M.26 and V.1 had the lowest CYE (data not shown). The most unstable rootstocks included B.9, M.9 NAKBT337 and M.27, whereas P.16, O.3, M.26 and V.1 were the most stable. Ranking rootstocks based on CYE at individual sites allows visualization of the interactions (data not shown), and results were similar to those generated by the which-won-where biplot in Fig. 11. For example, trees on M.27, B.9 and P.2 had the highest CYE in the sector at NC, whereas trees on B.9, P.16 and B.491 had the highest CYE for the sector containing ONT and IL. Trees on M.9 NAKBT337, M.9 Nic 29 and M.9 Pajam 1 had the highest CYE for the sector containing AR and NB, whereas trees on P.16, B.491, and sometimes M.9 NAKBT337 had the highest CYE for the sector containing the other 11 sites. At most sites M.9 NAKBT337 ranked in the top five rootstocks for CYE, but it ranked last at NC. Based on discrimination and representativeness for CYE, the most desirable sites included ME, MA and NY, and the least desirable sites included IL, NC and BC (data not shown).

Root suckers. PARS was the most discriminating site for root suckers, and VA and IL were moderately discriminating (Fig. 12). Trees on M.9 Pajam 2 had the most suckers and trees on M.26, P.2, M.27, B.491 and M.9 produced the fewest suckers. M.9 Pajam 2 and Mark were the least stable, and B.9 was very stable for root suckers. The which-won-where biplot segregated the sites into two sectors (Fig. 13). One sector contained PARS, MA, VA, IA, ME AR, PAB and NC, where M.9 Pajam 2 had the most suckers; Mark had the most suckers at the other sites.

2004 NC-140 trial.

Trunk cross-sectional area. TCA for all eight sites were positively correlated and UT and KY were the most discriminating (Fig. 14). Among rootstocks, TCA was positively correlated for the two Pi Au rootstocks, but

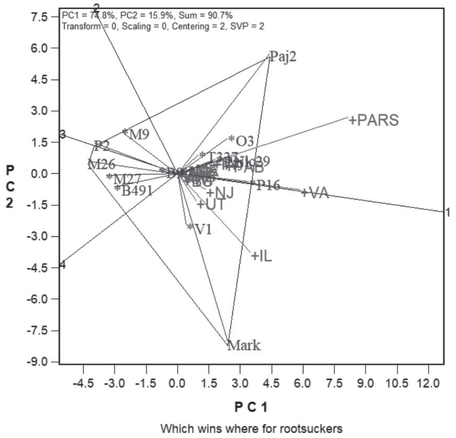

Fig. 13. The which-won-where view of the GGE biplot to show which rootstocks had the most root suckers which sites for the 1994 rootstock trial.

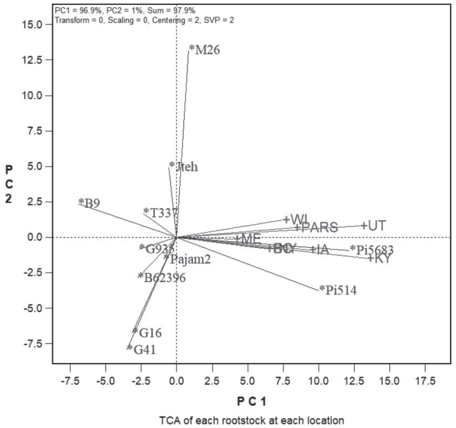

Fig. 14. The GGE biplot showing trunk cross-sectional area for each rootstock at each site for the 2004 rootstock trial.

they were negatively correlated with all other rootstocks except M.26, G.41 and G.16 with which they were poorly correlated. Based on the vector angles, the Pi Au rootstocks were largest at all sites, and B.9 and G.935 were smallest at most sites. The least stable rootstocks included M.26 and the two Pi Au rootstocks, whereas G.935, M.9 Pajam 2 and M.9 NAKBT337 were most stable (Fig. 14). The which-won-where biplot showed that all eight sites fell into the same sector, and in that sector the Pi Au rootstocks had the largest trunks, whereas B.9 had the smallest trunks (data not shown). When rootstocks were ranked at each site, the interaction was not very strong because trees on Pi Au 56-83, Pi Au 51-4 and M.26 always had the largest trunks and B.9 always had the smallest trunks. The other rootstocks had similar size trunks and the order of the rankings changed only slightly for different sites (data not shown). Based on the biplot for discrimination and representation, WI and IA were the most ideal sites, and ME was the least ideal for evaluating TCA (data not shown).

Cumulative yield. Yield was positively correlated for all sites, but the correlation was weakest for KY and UT (Fig. 15). Yield was most variable between rootstocks at KY and least variable at IA (data not shown). Yield was above average for the two Pi Au rootstocks and J-T-EH, slightly above average for B.62396 and M.9 Pajam 2, and below average for the other rootstocks (Fig. 15). The least stable rootstocks included G.935, M.9 Pajam2 and the two Pi Au rootstocks, whereas G.41 and M.9 NAKBT337 were most stable (Fig. 15). The which-won-where

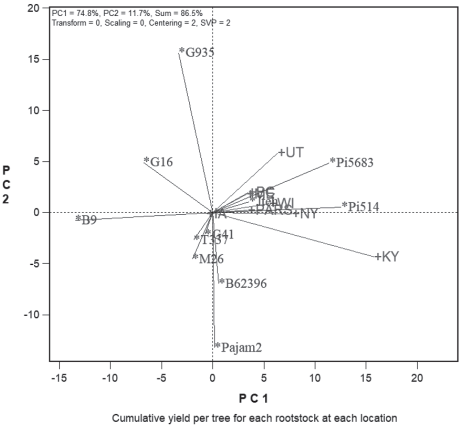

Fig. 15. The GGE biplot showing cumulative yield per tree for each rootstock at each site for the 2004 rootstock trial.

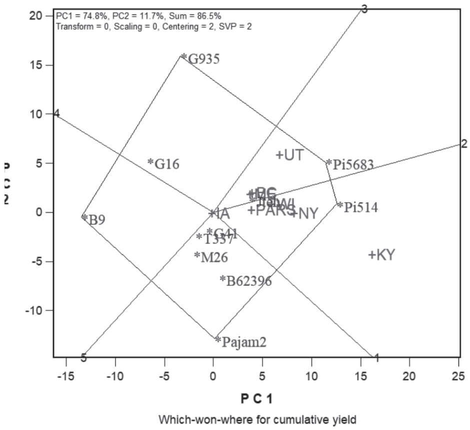

Fig. 16. The which-won-where view of the GGE biplot to show which rootstocks had the highest cumulative yield at which sites for the 2004 rootstock trial.

biplot divided the eight sites into three different sectors (Fig. 16). IA was in one sector, where B.9 had the lowest cumulative yield. UT, BC and ME fell into a second sector, where Pi Au 56-83 had the highest yield. WI, PARS, NY and KY fell into the third sector, where Pi Au 51-4 had the highest yield (Fig. 16). When the average ranks were plotted, the two Pi Au rootstocks had the highest yield and B.9 had the lowest yield (data not shown). The ranking of rootstocks in the M.26 size class from high to low was G.935 > M.9 NAKBT337 = G.41 > B.62396 > M.26. Biplots of rootstock rankings at each site indicated mild interaction (data not shown). The two Pi Au rootstocks had the highest yield at all sites, but the order sometimes changed. B.9 had the lowest yield at all sites. G.935 probably contributed most to the interaction, because it had the third highest yield at UT, ME and BC, but it had the third lowest yield at NY, KY and IA (data not shown). The most ideal sites for evaluating the effect of rootstock on cumulative yield were PARS and WI, whereas ME was least ideal (data not shown).

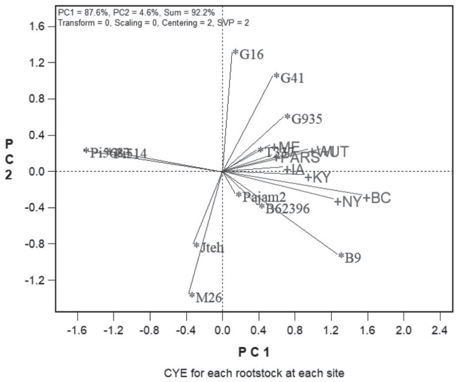

Fig. 17. The GGE biplot showing cumulative yield efficiency for each rootstock at each site for the 2004 rootstock trial.

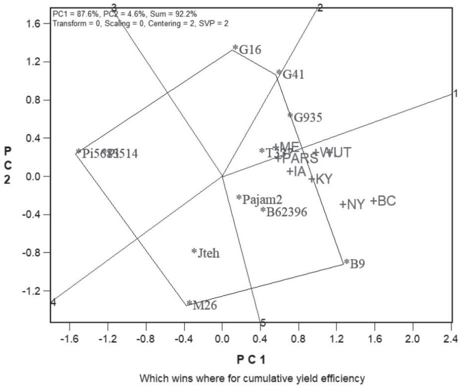

Fig. 18. The which-won-where view of the GGE biplot to show which rootstocks had the highest cumulative yield efficiency at which sites for the 2004 rootstock trial.

Cumulative yield efficiency. For CYE, all sites were positively correlated, but CYE was most positively correlated for UT, WI and PARS and least correlated for NY and ME (Fig. 17). BC was the site that best discriminated between rootstocks, and ME and PARS were least discriminating. At ME, M.9 NAKBT337 had higher than average CYE, and CYE was higher than average for B.9 at NY (data not shown). The lack of wide angles between sites indicates mild interaction (Fig. 17). The which-won-where biplot segregated the eight sites into two groups (Fig. 18). ME was in one sector, where trees on G.935 had the highest CYE. The other seven sites fell into the other sector, where trees of B.9 had the highest CYE. The two Pi Au rootstocks had the lowest CYE. When averaged over all sites, CYE was ranked as B.9 > G.935 > G.41 > M.9 NAKBT337 > B.62396 > G.16 > M.9 Pajam 2 > JTEH > M.26 > Pi Au 51-4 > Pi Au 56-83 (data not shown). The two Pi Au rootstocks and B.9 were least stable, whereas M.9 Pajam 2, B.62396, and M.9 NAKBT337 were most stable. ME is likely the site most responsible for the interaction because the rootstock ranking for CYE was G.41 > G.395 > G.16 > G935 but at the other seven sites the ranking was B.9 > G.935 > G.41 or B.9 > G.41 > G.935 (data not shown). The most ideal sites for evaluating rootstock effects on CYE were KY, IA and ME; BC and NY were least ideal (data not shown).

Root suckers. UT was the most discriminating site for root suckers, whereas ME, NY and KY were least discriminating (Fig. 19). Pi Au 51-4 and G.935 were least stable and M.9 NAKBT337 was most stable. Root sucker production was least well correlated for PARS and BC. Root sucker production was most highly correlated for J-TE-H, G.41, M.26 and Pi Au 56-83. M.9 NAKBT337 and Pi Au 51-4 produced above average root suckers at ME, IA, and PAR (data not shown). The which-won-where biplot separated the sites into two groups (data not shown). UT and BC were in the same group, where G.935 produced the most root suckers. The other six sites fell into the other sector where Pi Au 51-4 produced the most suckers and M.26 produced the fewest suckers (data not shown). The biplot for means and instability showed that Pi Au 51-4, M.9 Pajam 2 and G.935 produced the most suckers; G.935 was least stable, and G.16 and M.9 NAKBT.337 were most stable (data not shown). Biplots for rootstock rankings for each site indicate that BC and UT were different than the other sites, which supports the which-won-where biplot (data not shown). The ranking for root suckers at BC was G.395 > M.9 Pajam 2 > Pi Au 51-4; at UT the ranking was G.935 > Pi Au 5-14 > M.9 Pajam 2. At all the other sites the ranking was Pi Au 51-4 > B.9 or M.9 NAKBT337 > M.9 Pajam 2>B.9 (data not shown). The most ideal sites for evaluating the effect of rootstocks on root suckers were KY and ME, and the least ideal sites were PARS, NY and BC (data not shown).

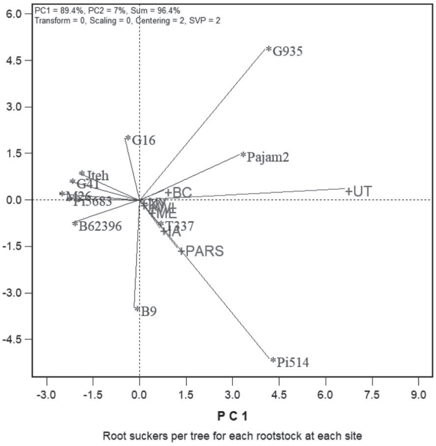

Fig. 19. The GGE biplot showing root sucker production for each rootstock at each site for the 2004 rootstock trial.

Discussion

The biplot analyses presented here are more informative than the traditional stability analyses (Olien et al., 1991; Marini, 2020) and ANOVAs more commonly used to analyze data from rootstock trials. There are no reports in the literature where biplot analyses were performed on more than one set of data and there are few reports where more than one response variable was analyzed for a single trial. Dia et al. (2016) performed biplot analyses for 40 watermelon genotypes at eight locations over three years. Their results from the polygon view of the GGE biplot was similar to ours, where the best genotypes for an environment or set of environments depended on the response variable being considered.

Biplot analysis can be used by pomologists to graphically identify sites that discriminate between rootstocks or cultivars, sites that are representative, and groups of sites that provide similar information. The results can be considered while planning future multi-location trials. In addition, information can be obtained concerning the average performance of rootstocks or cultivars as well as their performance at individual sites and their stability. Such information is important for developing regional rootstock or cultivar recommendations. It is not possible to compare results from different studies because the relative performance of rootstocks depends on the unique combination of rootstocks, sites, and the horticultural skills of the collaborators for each data set. In addition, the results usually differed for each response variable. Most published biplot analyses report only yield of agronomic crops, but in the current study four important response variables were analyzed and this complicated the interpretation of the results, but some general patterns were obvious. For both trials, UT was above average for discriminating between rootstocks for most response variables, whereas ME was among the least discriminating sites. Unexpectantly for TCA, sites with short growing seasons (ME, ONT, NY, BC, and WI) usually did not fall into the same mega-environment. Ideal sites are both discriminating and representative. There were 8 combinations of trials and response variables. Sites that were desirable for at least two of these combinations included IA, KY, MA, ME, NY, and WI, whereas ME and BC were least desirable for more than one combination. A factor that is difficult to evaluate but may potentially affect data from multisite trials is differences in horticultural management. Although cooperators are supposed to follow a protocol, I have observed that yield may double when a new cooperator assumes responsibility for a planting. Assuming management is not an important factor influencing rootstock vigor, attempts should be made to include WI and IA in future trials because they were desirable in both trials. For CYE, only ME was desirable in both trials.

Identification of groups of sites where rootstocks perform similarly would be desirable while planning future rootstock trials and for developing commercial rootstock recommendations. Sites with similar length of growing season or sites within a geographic region might be expected to segregate rootstock vigor similarly, but this was not always the case. Only seven sites were common to both trials. For TCA in both trials, BC and ME were very highly correlated, and WI and PARS were highly correlated. Therefore, it is not important to include both BC and ME or both WI and PARS in future trials. UT was discriminating in both trials, whereas the low vigor sites (ME, BC, ONT, and NB) were nondiscriminating in both trials. Therefore, ME, BC, ONT and NB are not very good sites for evaluating rootstock vigor.

For cumulative yield and cumulative yield efficiency, results for the two trials were inconsistent. Only ME and BC were highly correlated in both trials. UT was the most desirable site for the 1994 trial, but PARS and WI were most desirable for the 2004 trial. For cumulative yield, all sites fell into the same group for the 1994 trial, but for the 2004 trial there were three groups (UT, BC and ME; NY, PARS, WI and KY; and IA), so sites within a group should provide similar information about cumulative yield.

For CYE there were four groups of sites for the 1994 trial and two groups for the 2004 trial, but no two sites were grouped together for both trials. Desirability of sites for evaluating CYE was inconsistent for the two trials. For the 1994 trial, the most desirable sites included ME, MA and UT, whereas BC was among the least desirable sites for both trials.

For root suckers, PARS and IL were discriminating for the 1994 trial and UT was most discriminating for the 2004 trial, whereas ME, NY and WI were nondiscriminating for both trials. Therefore, ME, NY and WI are not good sites for evaluating the effect of rootstocks on root sucker production.

In another study, using the same data sets, Marini (2020) calculated five stability statistics to evaluate rootstock stability. As expected, results from the previous study did not always agree with results from biplot analysis; however results were often similar. Stability statistics indicated that for most response variables B.9 and M.27 were above average in stability, whereas the two Pi Au rootstocks were less stable than average. Biplot analysis indicated that the Geneva rootstocks and M.26 were often less stable than average, but the stability statistics indicated that stability for G.16 was above average for cumulative yield, and G.41 and G.935 were above average for cumulative yield efficiency.

Biplots were able identify rootstocks that were stable for each rootstock trait. Except for M.9 NAKBT337, which was stable for cumulative yield, cumulative yield efficiency and root suckers, no rootstock had above average stability for more than two traits in the 2004 trial. However, M.9 NAKBT337 was not more stable for any trait than the other rootstocks tested in the 1994 trial. The relatively new Geneva rootstocks are of particular interest, especially compared to the standard Malling rootstocks, because they are being widely planted. For TCA, G.935 and M.9 Pajam 2 were the most stable, but M.26, G.41 and G.16 were unstable. For cumulative yield M.9 NAKBT337 and G.41 were most stable, whereas G.935, B.9 and M.9 Pajam 2 were unstable. For cumulative yield efficiency, M.9 NAKBT337 and M.9 Pajam 2 were most stable and B.9, M.26, G.16 and G.41 were unstable. For root suckers, G.16 and M.9 NAKBT337 were most stable and G.935 was least stable. Taken together these results indicate that the Geneva rootstocks may be more responsive to site conditions than M.9 NAKBT337 or B.9.

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