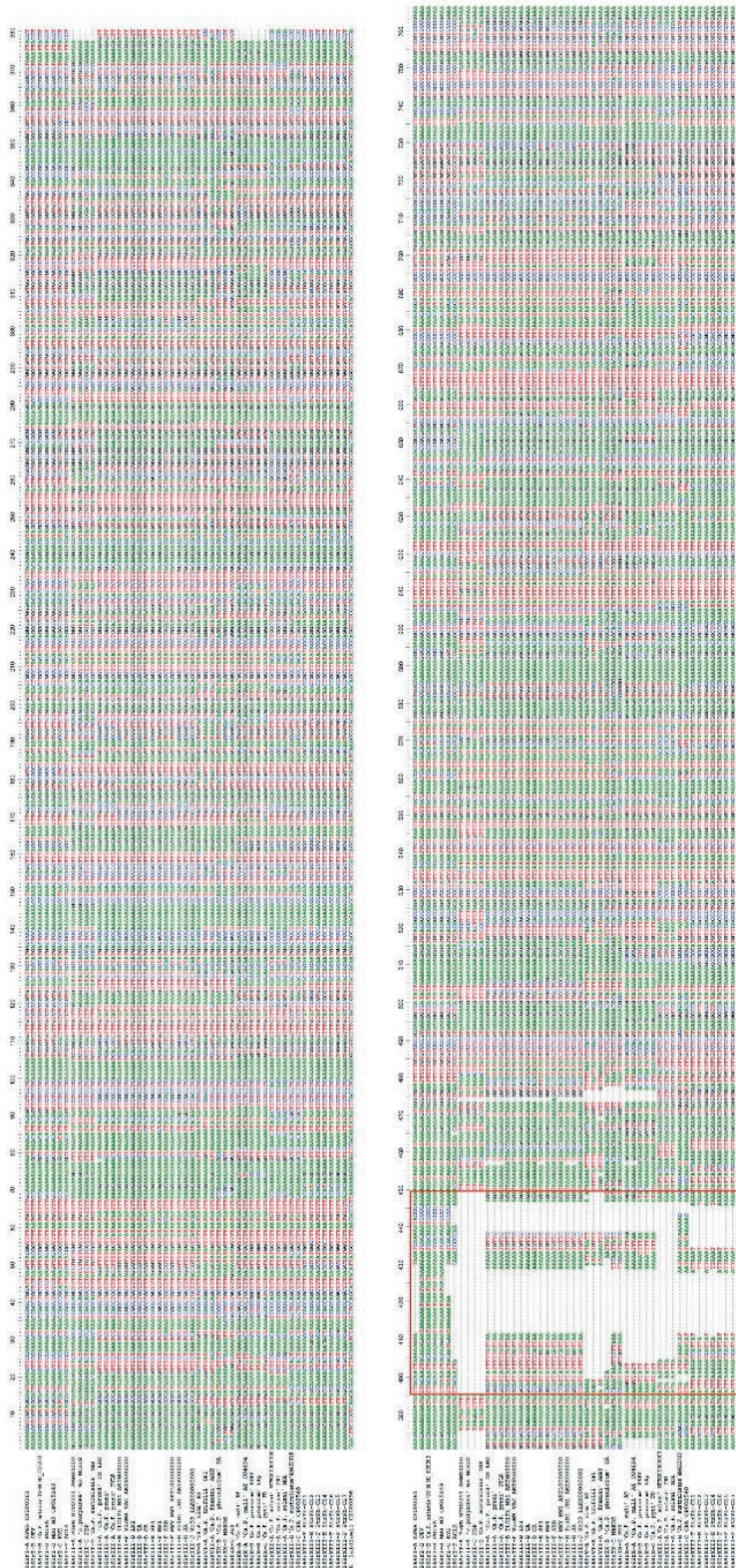
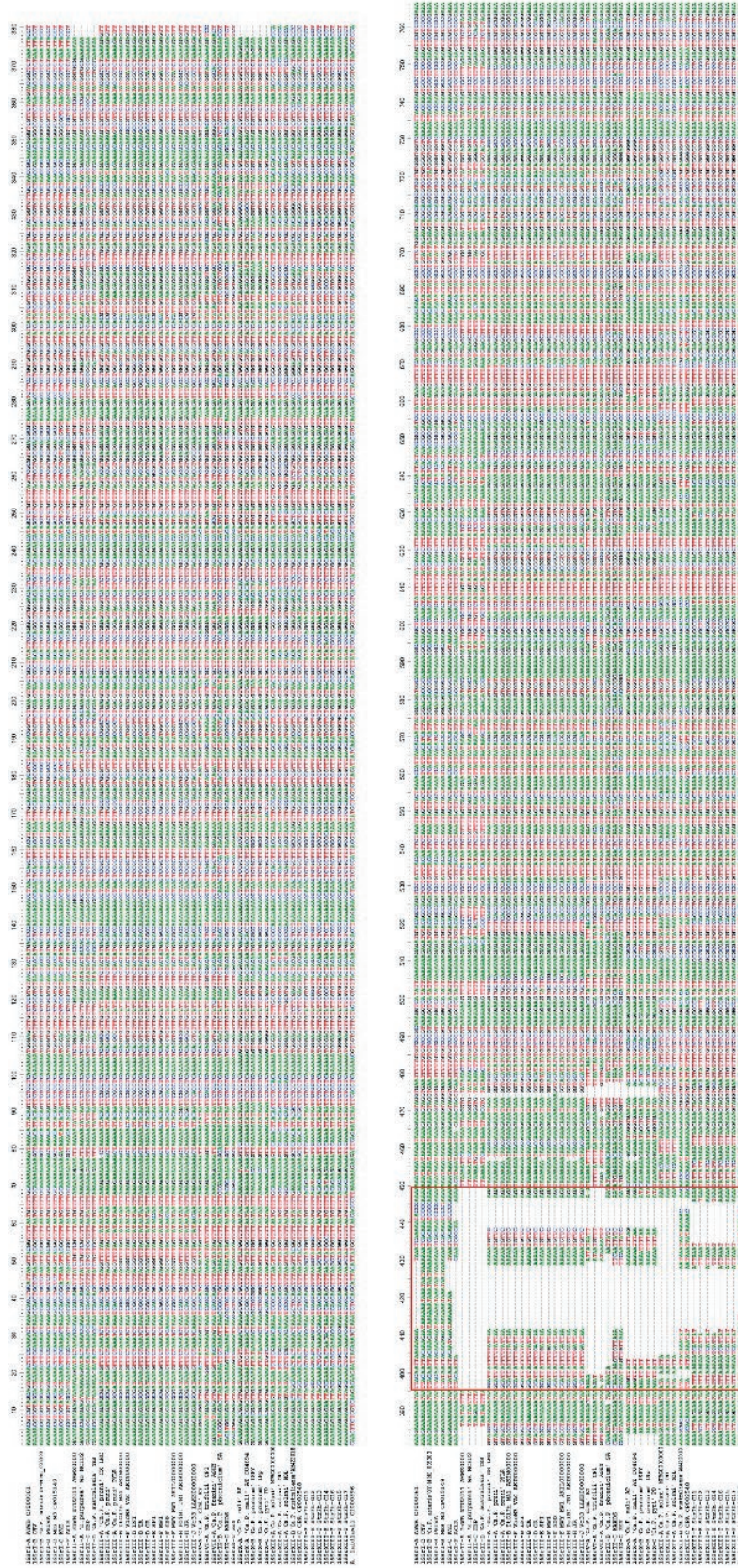


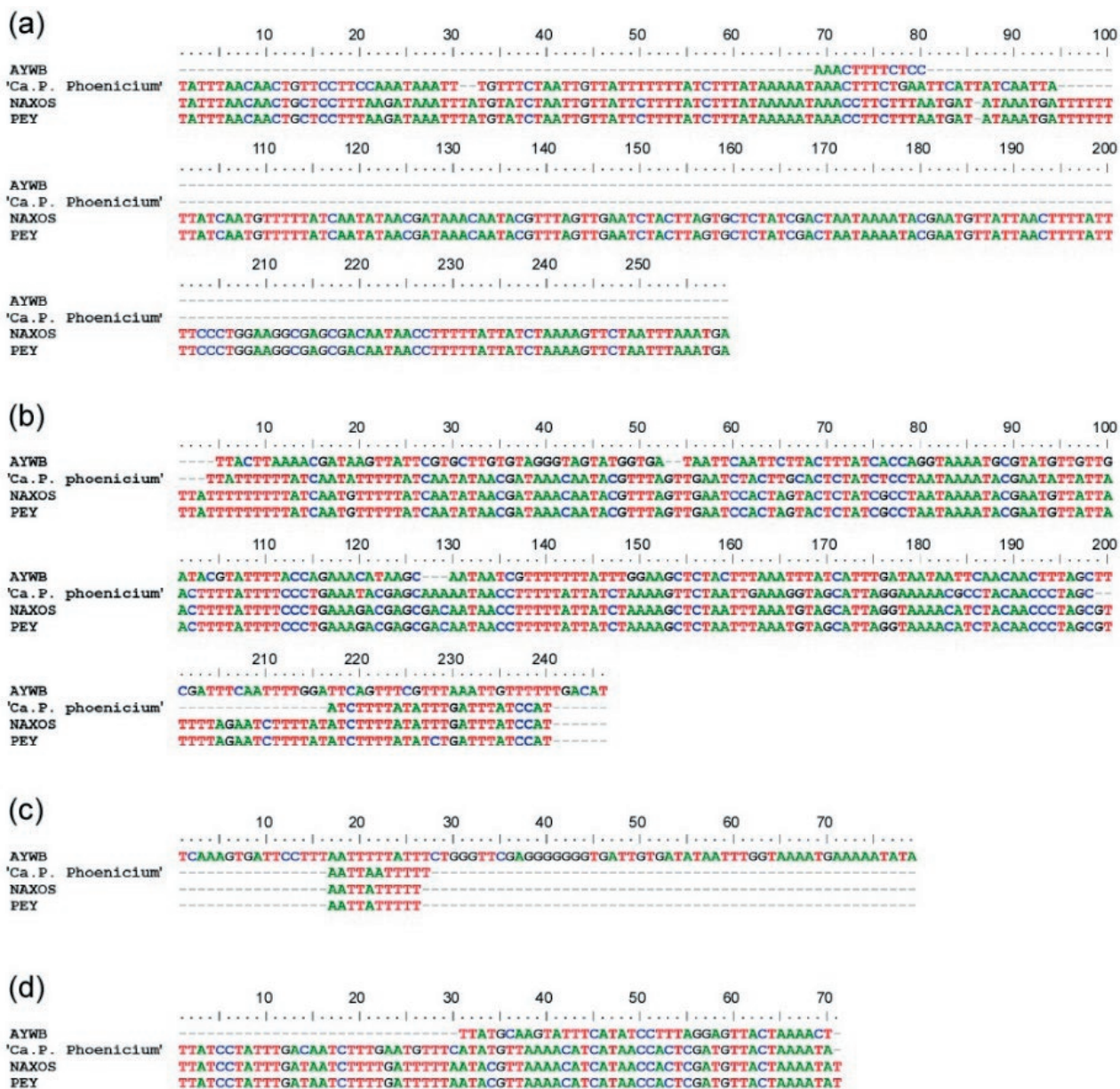
W. Cui, A. Zamorano, N. Quiroga, A. Bertaccini, N. Fiore (2021). Ribosomal protein coding genes *SSU12p* and *LSU36p* as molecular markers for phytoplasma detection and differentiation. *Phytopathologia Mediterranea* 60(2): 281-292. doi: 10.36253/phyto-11993



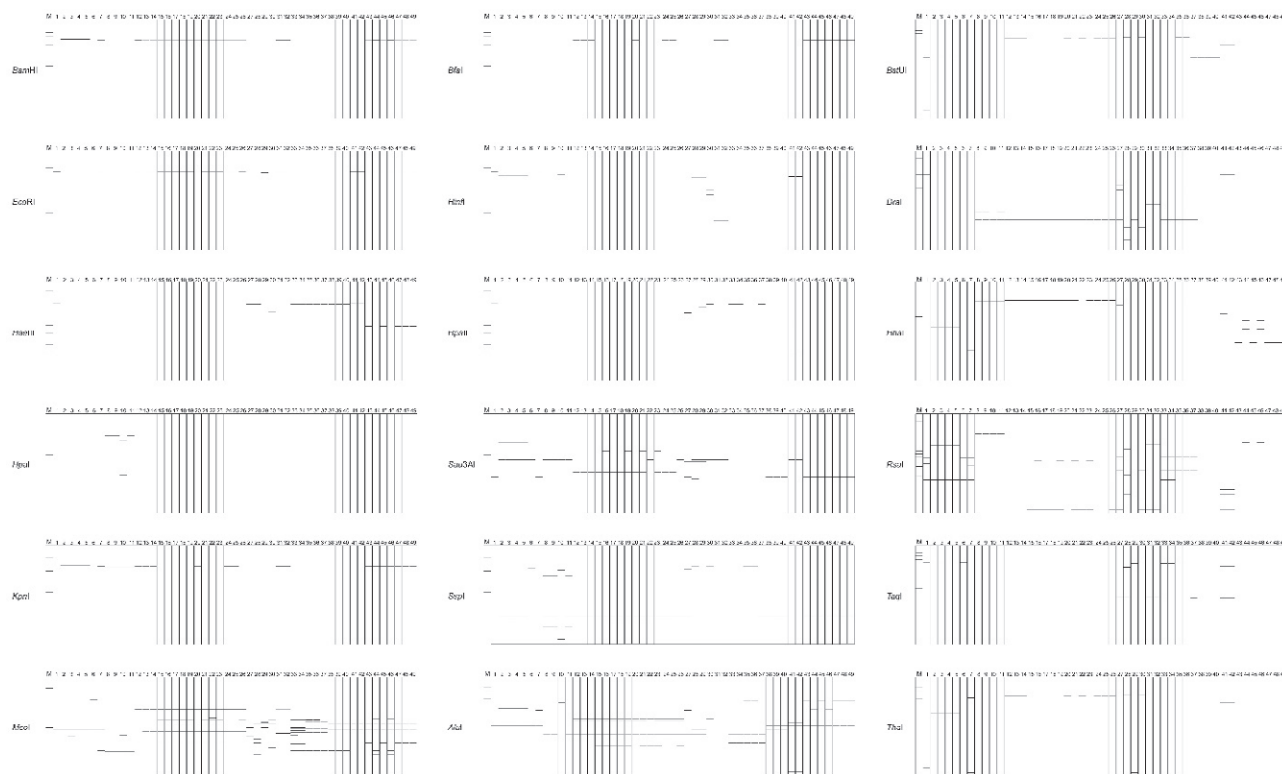
Supplementary Figure S1. Full sequence alignment of *SSU12p* sequences from the 49 samples used. The red rectangle indicates the less conserved region.



Supplementary Figure S2. Full sequence alignment of *LSU36p* sequences from the 49 samples used. The red rectangles indicate the first intergenic region, the green rectangles indicate *IF-1*, the magenta rectangles indicate the second intergenic region, and the orange rectangles indicate the partial *map* gene in *AYWB* and for the three *16SrIX* strains.



Supplementary Figure S3. Sequence alignment of the first intergenic region (a), *IF-1* (b), the second intergenic region (c), and the partial *map* gene (d) separately among AYWB and the three 16SrIX strains. (a) corresponds to the red rectangles in Supplementary Figure S2, (b) corresponds to the green rectangles, (c) to the magenta rectangles and (d) to the orange ones in Figure S2.



Supplementary Figure S4. RFLP patterns of *in silico* digestion of *SSU12p* sequences from the 49 samples enclosing the strains from GenBank. The samples corresponding to the numbers are: 1, aster yellows witches' broom; 2, *Catharanthus* virescence; 3, onion yellows mild strain; 4, primula yellows; 5, maize bushy stunt; 6, clover phyllody; 7, aster yellows from apricot; 8, peanut witches' broom; 9, *Echinacea purpurea* witches' broom; 10, faba bean phyllody; 11, tomato big bud; 12 and 13, peach X disease; 14, peach yellow leaf roll; 15, Italian clover phyllody; 16, vaccinium witches' broom; 17, plum leptonecrosis; 18, *Taraxacum* leaf reddening; 19, goldenrod yellows; 20, spirea stunt; 21, milkweed yellows; 22, *Solanum* big bud; 23, milkweed yellows; 24 and 25, poinsettia branch inducing; 26, phytoplasma Vc33; 27, elm yellows; 28, clover proliferation; 29, ash yellows; 30, almond witches' broom; 31, Naxos periwinkle yellows; 32, *Picris echioides* yellows; 33 and 34, apple proliferation; 35, European stone fruit yellows; 36, plum leptonecrosis; 37, pear decline; 38 and 39, grapevine yellows; 40, Molière disease; 41, Australian grapevine yellows; 42, strawberry lethal yellows; 43–49, strawberry phyllody Chilean strains CL1, 2, 3, 4, 5, 6, and 7.

Supplementary Table S1. Diversity indices within and between different 16Sr groups used in this study, calculated using MEGA7. The “within group mean distances” were calculated as the mean pairwise distances within each group. The “between group mean distances” were calculated as the average distances between two groups. ID = identical sequences. n/c indicates that the group contains only one sample strain, so the distances within the group cannot be calculated. One-tail and two-tail t-Tests of corresponding “between group mean distance” indices were performed using the analysis tool of Office Excel.

Within group mean distance		Between group mean distance											t-Test results		
		16SrI	16SrII	16SrIII	16SrV	16SrVI	16SrVII	16SrIX	16SrX	16SrXII	16SrXIII		P one-tail	P two-tail	
SSU12p															
16SrI	0.034	16SrI	ID										SSU12p-LSU36p	2.38377E-14	4.76754E-14
16SrII	0.037	16SrII	0.633	ID									SSU12p-16Sr	7.32639E-24	1.46528E-23
16SrIII	0.026	16SrIII	0.383	0.426	ID								SSU12p-tuf	0.11260869	0.22521738
16SrV	n/c	16SrV	0.410	0.436	0.218	ID							LSU36p-16Sr	2.75265E-23	5.5053E-23
16SrVI	n/c	16SrVI	0.457	0.444	0.268	0.154	ID						LSU36p-tuf	7.08502E-16	1.417E-15
16SrVII	n/c	16SrVII	0.430	0.454	0.264	0.136	0.167	ID					16Sr-tuf	1.58453E-24	3.16905E-24
16SrIX	0.074	16SrIX	0.436	0.489	0.289	0.250	0.269	0.273	ID						
16SrX	0.041	16SrX	0.404	0.575	0.364	0.285	0.380	0.328	0.360	ID					
16SrXII	0.149	16SrXII	0.234	0.648	0.403	0.410	0.449	0.431	0.482	0.400	ID				
16SrXIII	0.023	16SrXIII	0.238	0.569	0.365	0.345	0.365	0.381	0.388	0.309	0.216	ID			
LSU36p															
16SrI	0.018	16SrI	ID												
16SrII	0.075	16SrII	0.770	ID											
16SrIII	0.041	16SrIII	0.889	0.699	ID										
16SrV	n/c	16SrV	0.788	0.838	0.669	ID									
16SrVI	n/c	16SrVI	0.759	0.719	0.562	0.322	ID								
16SrVII	n/c	16SrVII	0.656	0.609	0.572	0.347	0.256	ID							
16SrIX	0.053	16SrIX	1.055	1.116	1.082	1.111	0.988	0.904	ID						
16SrX	0.061	16SrX	0.625	0.789	0.691	0.936	0.709	0.712	1.171	ID					
16SrXII	0.087	16SrXII	0.353	0.722	0.821	0.783	0.718	0.581	1.189	0.639	ID				
16SrXIII	0.012	16SrXIII	0.280	0.679	0.715	0.787	0.667	0.609	1.057	0.583	0.228	ID			
16Sr															
16SrI	0.004	16SrI	ID												
16SrII	0.008	16SrII	0.105	ID											
16SrIII	0.005	16SrIII	0.094	0.079	ID										
16SrV	n/c	16SrV	0.094	0.103	0.061	ID									
16SrVI	n/c	16SrVI	0.093	0.092	0.057	0.026	ID								
16SrVII	n/c	16SrVII	0.095	0.094	0.063	0.034	0.026	ID							
16SrIX	0.003	16SrIX	0.113	0.093	0.057	0.057	0.057	0.056	ID						
16SrX	0.008	16SrX	0.073	0.106	0.094	0.093	0.094	0.092	0.094	ID					
16SrXII	0.009	16SrXII	0.033	0.108	0.097	0.105	0.101	0.100	0.109	0.073	ID				
16SrXIII	0.008	16SrXIII	0.037	0.104	0.093	0.100	0.093	0.098	0.106	0.071	0.036	ID			
tuf															
16SrI	0.023	16SrI	ID												
16SrII	0.035	16SrII	0.601	ID											
16SrIII	0.032	16SrIII	0.346	0.503	ID										
16SrV	n/c	16SrV	0.432	0.545	0.316	ID									
16SrVI	n/c	16SrVI	0.440	0.443	0.324	0.141	ID								
16SrVII	n/c	16SrVII	0.376	0.499	0.321	0.170	0.136	ID							
16SrIX	0.076	16SrIX	0.481	0.455	0.385	0.331	0.323	0.301	ID						
16SrX	0.045	16SrX	0.368	0.583	0.415	0.388	0.428	0.401	0.446	ID					
16SrXII	0.089	16SrXII	0.138	0.559	0.343	0.409	0.390	0.378	0.476	0.371	ID				
16SrXIII	0.018	16SrXIII	0.176	0.568	0.325	0.375	0.361	0.320	0.476	0.363	0.159	ID			