

Supplementary data

What has changed in the outbreaking populations of the severe crop pest whitefly species in cassava in two decades?

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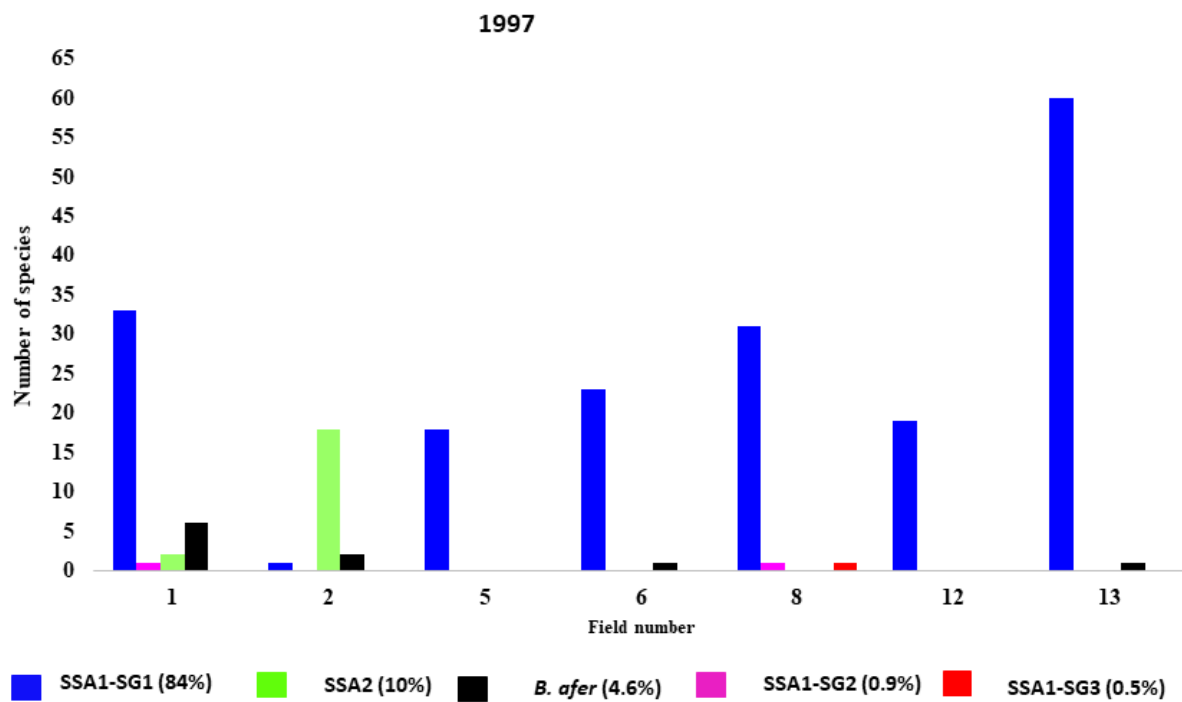
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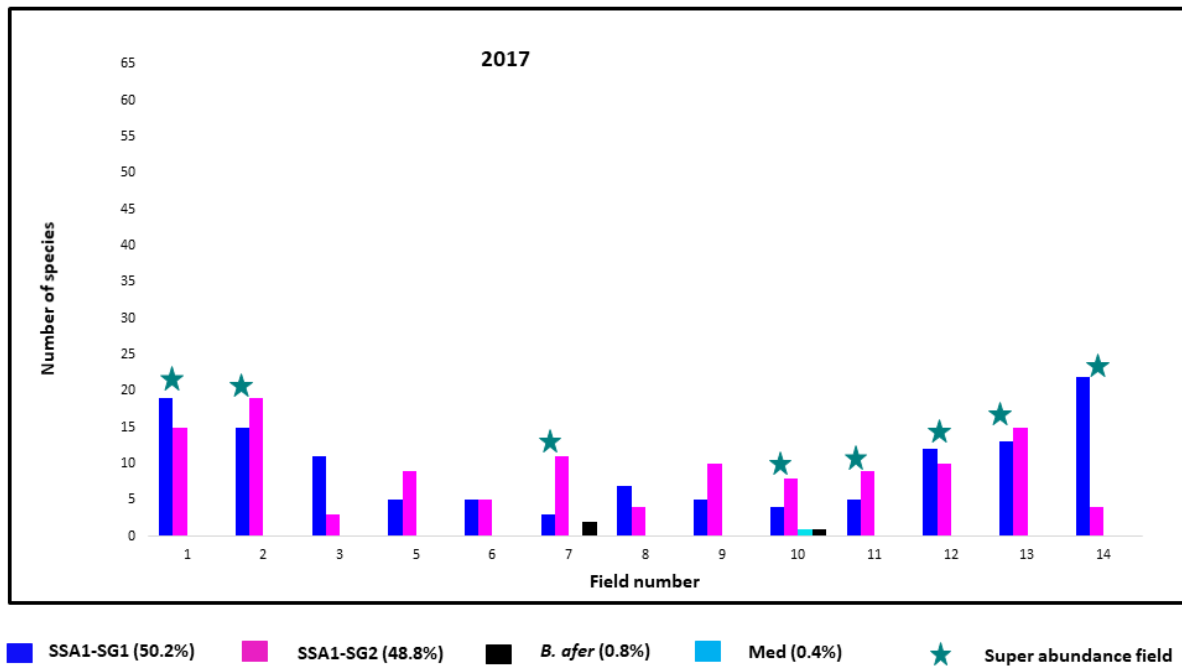
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Supp Figure 1: Species distribution per field for samples collected in Uganda 1997



Supp Figure 2: Species distribution per field for samples collected in Uganda 2017

Supp Table 1: Population genetic diversity indices. Population and field number where individuals collected (population/Fn), number of individual sampled (n), mean number of allele per population (NA), (Ar) allele richness, non-biased expected heterozygosity (Hnb), observed heterozygosity (Ho), and fixation indices (Fis) presented together with p value from Hardy-Weinberg equilibrium test, none of the Fis were found significant at $p < 0.05$.

Population/Fno	n	NA	Ar	Ho	Hnb	Fis
SSA1SG1/G2						
F1 - 1997	31	9	6.26	0.35 (0.22)	0.65 (0.29)	0.47
F2 - 1997	2	2	-	0.29 (0.4)	0.51 (0.33)	0.53
F5 - 1997	18	7.83	6.55	0.34 (0.3)	0.66 (0.28)	0.49
F6 - 1997	24	8	6.49	0.37 (0.23)	0.67 (0.26)	0.45
F8 - 1997	32	8.75	6.44	0.36 (0.24)	0.67 (0.24)	0.47
F12 - 1997	19	7.25	6.2	0.32 (0.23)	0.64 (0.29)	0.51
F13 - 1997	57	12.17	6.66	0.4 (0.25)	0.66 (0.28)	0.4
F1 - 2017	15	6	5.29	0.43 (0.24)	0.51 (0.32)	0.17
F2 - 2017	14	4.5	4.22	0.37 (0.26)	0.46 (0.3)	0.21
F3 - 2017	35	7.83	4.94	0.38 (0.27)	0.48 (0.3)	0.22
F5 - 2017	35	8.17	5.36	0.42 (0.28)	0.53 (0.33)	0.21
F6 - 2017	29	7.67	5.44	0.35 (0.2)	0.57 (0.28)	0.38
F7 - 2017	34	8.58	5.86	0.42 (0.23)	0.59 (0.27)	0.3
F8 - 2017	31	8.42	5.4	0.39 (0.24)	0.54 (0.27)	0.27
F9 - 2017	31	8.33	5.41	0.38 (0.25)	0.56 (0.24)	0.32
F10 - 2017	33	8.42	5.74	0.38 (0.22)	0.56 (0.29)	0.32
F11 - 2017	34	8.75	5.91	0.38 (0.24)	0.59 (0.28)	0.35
F12 - 2017	35	8.67	5.46	0.39 (0.2)	0.55 (0.27)	0.3
F13 - 2017	35	8	5.13	0.37 (0.24)	0.51 (0.32)	0.27
F14 - 2017	35	7.58	5.09	0.38 (0.25)	0.51 (0.3)	0.26
SSA2						
F1-1997	3	2.5	2.5	0.22 (0.26)	0.52 (0.27)	0.62
F2-1997	12	4.92	3.08	0.30 (0.28)	0.63 (0.25)	0.54

Supp Table 2. Fst matrix of SSA1 Ugandan populations from 1997 and 2017. All bolded numbers are significant.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	
F1-SG1-1997	1	0																														
F5-SG1-1997	2	0.054	0																													
F6-SG1-1997	3	0.052	0.015	0																												
F8-SG1-1997	4	0.032	0.02	0.023	0																											
F12-SG1-1997	5	0.044	0.008	0.034	0.032	0																										
F13-SG1-1997	6	0.026	0.029	0.016	0.012	0.024	0																									
F1-SG1-2017	7	0.104	0.104	0.125	0.149	0.116	0.074	0																								
F1-SG2-2017	8	0.08	0.06	0.099	0.096	0.073	0.058	0.014	0																							
F2-SG1-2017	9	0.086	0.096	0.135	0.123	0.103	0.07	0.056	-0.001	0																						
F2-SG2-2017	10	0.098	0.118	0.145	0.152	0.12	0.069	0.039	-0.006	0.011	0																					
F3-SG1-2017	11	0.102	0.09	0.127	0.117	0.097	0.077	0.05	0.012	0.001	0.011	0																				
F5-SG1-2017	12	0.082	0.091	0.113	0.112	0.083	0.068	0.081	0.015	0.003	0.037	0.035	0																			
F5-SG2-2017	13	0.078	0.072	0.106	0.108	0.078	0.055	0.027	-0.01	0	-0.011	0.004	0.013	0																		
F6-SG1-2017	14	0.053	0.043	0.084	0.068	0.061	0.041	0.042	0	0.009	0.032	0.022	0.016	0.013	0																	
F6-SG2-2017	15	0.05	0.065	0.095	0.065	0.068	0.038	0.058	0.023	0.013	0.04	0.033	0.024	0.022	0.013	0																
F7-SG1-2017	16	0.049	0.042	0.07	0.056	0.046	0.026	0.081	0.01	0.002	0.049	0.026	0.001	0.014	0.003	-0.006	0															
F7-SG2-2017	17	0.057	0.065	0.1	0.079	0.069	0.039	0.051	0.024	0.024	0.034	0.038	0.02	0.02	0.017	0.004	0	0														
F8-SG1-2017	18	0.064	0.068	0.085	0.076	0.057	0.038	0.047	0.016	0.005	0.012	0.025	0.023	0.013	0.018	0.014	0.006	0.006	0													
F8-SG2-2017	19	0.06	0.082	0.109	0.093	0.07	0.054	0.073	0.018	-0.003	0.03	0.019	0.009	0.014	0.01	-0.001	0	0.01	0.008	0												
F9-SG1-2017	20	0.042	0.077	0.095	0.067	0.063	0.048	0.098	0.033	0.007	0.052	0.048	0.023	0.036	0.032	0.012	-0.001	0.024	0.008	-0.003	0											
F9-SG2-2017	21	0.052	0.088	0.104	0.091	0.074	0.045	0.079	0.043	0.031	0.043	0.05	0.024	0.032	0.043	0.024	0.022	0.022	-0.003	0.005	0.002	0										
F10-SG1-2017	22	0.078	0.082	0.095	0.094	0.074	0.053	0.084	0.043	0.045	0.07	0.039	0.015	0.034	0.031	0.012	0.008	0.012	0.022	0.009	0.028	0.02	0									
F10-SG2-2017	23	0.062	0.063	0.076	0.072	0.061	0.044	0.076	0.035	0.027	0.044	0.034	0.021	0.026	0.023	0.007	0.005	0.013	0.009	0.007	0.017	0.013	0.007	0								
F11-SG1-2017	24	0.059	0.062	0.089	0.085	0.063	0.042	0.058	0.014	-0.008	0.025	0.016	0.009	0.01	0.011	0.002	0.003	0.007	-0.004	-0.008	0.008	0.01	0.005	-0.002	0							
F11-SG2-2017	25	0.045	0.043	0.081	0.053	0.045	0.024	0.068	0.03	0.012	0.043	0.035	0.025	0.026	0.024	-0.002	0.001	0.005	0.007	0.005	0.015	0.021	0.019	0.012	-0.002	0						
F12-SG1-2017	26	0.062	0.078	0.098	0.082	0.072	0.044	0.085	0.035	0.021	0.027	0.038	0.011	0.025	0.027	0.007	0.005	0.009	-0.001	0.002	0.008	0.004	0.012	-0.002	0	0.011	0					
F12-SG2-2017	27	0.054	0.075	0.11	0.092	0.086	0.053	0.058	0.022	-0.007	0.015	0.021	0.017	0.018	0.021	0.012	0.004	0.007	0	0.008	0.01	0.013	0.028	0.016	0.001	0.006	0.005	0				
F13-SG1-2017	28	0.075	0.071	0.107	0.1	0.075	0.04	0.059	0.022	0.023	0.033	0.031	0.004	0.02	0.026	0.009	0.009	0.013	-0.001	0.002	0.024	0.01	-0.005	0.013	0.005	0.015	0.002	0.017	0			
F13-SG2-2017	29	0.082	0.106	0.13	0.124	0.105	0.058	0.096	0.029	0.032	0.036	0.03	0.01	0.022	0.02	0.014	0.014	0.018	0.01	0.008	0.025	0.021	0.013	0.016	0.018	0.027	-0.002	0.012	0	0		
F14-SG1-2017	30	0.084	0.084	0.122	0.11	0.095	0.065	0.068	0.01	0.001	0.022	0.02	0.009	0.014	0.036	0.013	0.009	0.022	0.007	0.002	0.018	0.021	0.029	0.012	-0.001	0.018	0.006	0.002	0.021	0.016	0	
F14-SG2-2017	31	0.05	0.07	0.106	0.1	0.071	0.031	0.078	0.014	0.024	0.011	0.024	-0.006	0	0.018	0.017	0.005	0.003	-0.016	-0.003	0.005	-0.009	-0.006	0.002	-0.006	0.006	-0.009	-0.001	-0.013	-0.013	0.018	0

Supp Table 3: Probability values of one-tailed Wilcoxon sign-rank tests to verify significant heterozygosity (H) deficit or excess as expected after recent expansion or reduction of population sizes performed on 2017 samples. Analyses were performed under the single step mutation model (SMM) and the two-phased model of mutation (TPM). Significant values ($\alpha=0.05$) are in bold.

	H excess		H deficit	
	SMM	TPM	SMM	TPM
F1	0.997	0.966	0.009	0.083
F2	0.998	0.973	0.007	0.067
F3	1	0.999	0.001	0.002
F5	0.999	0.992	0.003	0.021
F6	0.999	0.998	0.002	0.005
F7	1	0.998	0.001	0.006
F8	1	0.999	0.001	0.002
F9	1	0.998	0.001	0.005
F10	1	0.999	0	0.002
F11	1	0.998	0.001	0.005
F12	1	0.999	0	0.003
F13	1	1	0	0.001
F14	1	0.999	0.001	0.003