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BEGOMOVIRUS QUASISPECIES ADAPT TO HOSTS BY EXPLORING DIFFERENT SEQUENCE SPACE WITHOUT CHANGING THEIR CONSENSUS SEQUENCES

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Geminiviruses possess single-stranded circular DNA genomes that depend on cellular polymerases for replication in the host nucleus. In plant hosts, geminivirus populations behave as ensembles of mutant and recombinant genomes. This favours the emergence of new geminivirus strains able to produce new diseases or overcome the genetic resistance of cultivars. In warm and temperate areas several whitefly-transmitted geminiviruses of the genus *Begomovirus* cause the tomato yellow leaf curl disease (TYLCD) with important economic consequences. TYLCD is frequently controlled in commercial tomato production using the *Ty-1* resistance gene. Over a 45 day period we studied the evolution of infectious clones from three TYLCD-associated begomoviruses: *Tomato yellow leaf curl Sardinia virus*, *Tomato yellow leaf curl virus* and the recombinant *Tomato yellow leaf curl Axarquia virus*. The evolution of their viral progeny was examined in susceptible tomato (*ty1/ty1*), resistant tomato (*Ty1/ty1*), common bean, and the wild reservoir *Solanum nigrum*. We found that in addition to affecting viral accumulation kinetics, the host influenced the sequence space explored by these begomoviruses. In tomato, viral dynamics was not influenced by the presence of the *Ty-1* gene. Interestingly, positive adaptation of the coat protein gene was only observed in the common bean and *S. nigrum*, which correlates with these plants having viral quasispecies with the highest degree of complexity and heterogeneity. Our results underline the importance of analysing the mutant spectra of begomovirus infections, especially in wild reservoirs, which have the potential to give rise to large numbers of emergent variants in spite of the invariance of their consensus sequences.