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Diversity of Plant Virus Populations: A Valuable Tool for Epidemiological Studies

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Abstract

Plant viruses, as any other living organisms, differ genetically from each other as a result of processes (such as mutation, recombination and other forms of genetic exchange) that generate genetic variation in each generation during their reproduction and processes (such as selection, migration and genetic drift) that modulate this variation, determine the distribution of the genetic variants within a population (i.e., the genetic structure of the population) and how it changes with time, in a dynamical phenomenon called evolution. For plant viruses, evolutionary forces that generate and modulate the genetic diversity of their populations are often associated to different phases in their biology and ecology, such as virus-host interactions and host to host transmission. Forces that shape the evolution of plant viruses are at the same time key factors affecting their pathogenic properties, including their ability to cause diseases (an aspect that is studied in the field of epidemiology). The present chapter aims to illustrate how measurement and analysis of genetic diversity and structure of plant virus populations are essential to the current knowledge on the evolutionary biology of plant viruses and how evolutionary factors have a relevant role in the dynamics of virus populations and therefore, in the epidemiology of plant virus diseases.

Keywords: genetic diversity, genetic structure, plant virus evolution, plant virus epidemiology, plant virus resistance, plant virus emergence

1. Introduction

Evolution is defined as the change with time of the frequency distribution of genetic variants in the population of an organism, what is called the genetic structure of the population. In this context, a population of plant viruses may be considered as the group of individuals of the same viral species living and reproducing in a particular and sufficiently restricted environment, so that it represents a single evolving unit (similarly as local interbreeding units of mating organisms, also called local populations or demes, are considered the fundamental evolving units in population genetics; see [1], pp. 45–46). Two different phases may be

identified along the evolutionary process: in the first one, genetic variation is generated during reproduction and the second one consists of the modulation of that variability as the result of driving evolutionary forces acting along the organism's life cycle, which are associated to its biological and ecological interactions in a particular environment.

The present chapter does not seek to be a comprehensive review on the evolutionary mechanisms that shape the diversity and genetic structure of plant virus populations, nor on the broad knowledge derived from the significant number of scientific reports published on this subject during the last decades for different groups of plant viruses. There are a number of excellent reviews covering these topics. In the first part of the chapter, these reviews will be cited in relation to the most relevant concepts that are essential to understand evolution of virus populations. This first part is aimed to serve as a general guide for the readers, who if interested, will be easily addressed to the most relevant literature on the topic. The second part of the chapter will emphasize the important implications of these evolutionary mechanisms in the population dynamics of viruses, that is, the epidemiology of virus diseases, which finally determines their development and distribution in the field.

2. Generation and modulation of genetic diversity: driving forces in evolution of plant virus populations

2.1. Generation of genetic diversity in plant virus populations

Genetic diversity of a population can be defined as the probability that two genetic variants randomly chosen from the population are different [2]. Two mechanisms are the main sources of genetic variation in viruses during their evolutionary process: mutation and genetic exchange. Both of them are presented in the following paragraphs.

Mutation is the result of errors during the replication of a genome due to the misincorporation of nucleotides in the daughter strand that do not correspond to those present in the template [3–5]. Besides its relevance in evolution as the initial step for generation of variability in populations, the mutation process has significant practical implications in the design and assessment of virus diseases control strategies (antiviral therapies, vaccinations, etc.). Also, it is a factor for the occurrence of important epidemiological phenomena, such as virus adaptation to new hosts or changes in viral virulence, which may led to the emergence or re-emergence of both animal and plant viral diseases. Therefore, the estimation of mutation rates is an important focus of research efforts [6]. Mutation rate measure the proportion of mutations generated either per round of genomic replication or per infected cell. Its calculation is often more complex than that of mutation frequency, which estimates the proportion of mutations remaining in a population after the action of selection, for instance, a fraction of mutations are deleterious and has been eliminated by purifying selection. Rates of spontaneous mutation of RNA viruses have been estimated to be several orders of magnitude higher than those of DNA viruses [5, 7] and this difference has been attributed to the lack of proof-reading activity of virus encoded RNA-dependent RNA polymerases. For plant RNA viruses, direct estimates of spontaneous mutation rates have been obtained for only two viruses,

Tobacco mosaic virus (TMV) and *Tobacco etch virus* (TEV) [7, 8]. In both cases, measurements were performed in similar experimental conditions of minimum purifying selection against deleterious mutants because the wild-type function was provided by complementation. Also in both cases, values obtained were similar and fell near the lower threshold of estimates reported for animal RNA viruses and bacteriophages, suggesting that plant RNA viruses show, indeed, lower mutation rates than animal RNA viruses [7]. In contrast, these works reported quite different spectra of mutations for the two plant viruses: preponderance (two-thirds) of insertions and deletions and a significant fraction (one-third) of multiple mutants for TMV, whereas most of TEV mutants were single-nucleotide substitutions, with the fraction of transitions being twice that of transversions. These differences could be explained by a different behavior of the respective replicases or by differences in the experimental approach [7]. Lower mutation rates in plant than in animal RNA viruses could partially explain their generally lower rates of molecular evolution and the high genetic stability of plant RNA virus populations [2]. These differences in mutation rates could derive from different selective pressures acting in the mutational strategy of RNA viruses in the two types of hosts, although the role of natural selection on the evolution of mutation still needs to be demonstrated [7]. An alternative hypothesis set out that mutation rates in RNA viruses are not adaptive but are required to replace their chemically unstable genomes [5].

Genetic exchange occurs when genetic information from different genetic variants infecting the same cell is switched between them to form a new variant. It may take place through **recombination**, when the switched information consists on segments of nucleotide strands of different genetic variants, or through **reassortment** of whole genomic segments in viruses with segmented genomes, a process which is also known as pseudorecombination [9].

Once some initial level of genetic variation is created by mutations, the opportunities of genetic exchange between different genetic variants may increase, contributing to the generation of new variability. Recombination and reassortment are frequent in populations of plant-infecting viruses with either RNA or DNA genomes [2, 5, 10]. Analysis of their sequences indicates that both mechanisms contribute significantly to the generation of variability in the evolution and diversification of certain taxonomic groups [11–16]. Recombination and reassortment events may involve members of the same plant virus species [17–19], members of different species [20–24] or even genus [25]. Genetic exchange by recombination or reassortment may have important epidemiological implications of practical relevance, even more than mutation, as it has been associated to host jumps, host range expansion, changes in virulence, breaking of host resistance and finally, the emergence of new viral plant diseases. Outstanding examples of that are the contribution of recombination and reassortment in the development of a severe epidemic of Cassava mosaic disease in Uganda [26] and the appearance of several new recombinant species of begomoviruses in the Mediterranean Basin associated to the Tomato yellow leaf curl disease in tomato [27]. However, in spite of the relevant epidemiological role of genetic exchange, till date, little information is available on the rates with which it occurs in plant viruses in the absence of selection. Recombination rates have been experimentally estimated in coinfections of different genotypes of *Brome mosaic virus* [28, 29], *Cauliflower mosaic virus* (CaMV) [30] and TEV [31]. Although results obtained should be compared with caution,

they are similar (particularly those of CaMV and TEV) and as high as mutation rates (at least for TEV), indicating that recombination may be as relevant as mutation in creating variability [31]. It has been shown that selection against heterologous gen combinations increases as host colonization progresses along the infection cycle of *Cucumber mosaic virus* [32], affecting the frequency of genetic exchange. This explains that recombinants and reassortants are often found at low frequencies [33, 34], although the frequency of particular combinations may be dependent on agro-ecological factors [17, 19], and support the hypothesis of co-adaptation of gene complexes within the viral genomes [32, 35].

It has been exposed above that creation of variability is an initial and required step in the evolution of populations. On the other hand, variability may also contribute to effects of evolution that may be detrimental for populations. For instance, a population may become extinct because of an excessive accumulation of mutations, a phenomenon known as lethal mutagenesis [36], which also takes place in viruses and is an interesting mechanism for antiviral therapies [37]. Also, high mutation rates combined to small sizes of asexual populations (as a result of genetic bottlenecks, see below) may lead to the progressive accumulation of deleterious mutations and the loss of mutation-free individuals, with a consequent reduction in fitness in populations, which is called the "Muller's ratchet" [9, 38]. In addition to the adaptive relevance of genetic exchange to create beneficial genomic combinations, recombination and reassortment may represent a sexual mechanism contributing to compensate the accumulation of deleterious mutations and the effect of "Muller's ratchet" in populations, and it has been postulated as a theory of evolution of sex in RNA viruses [9, 39]. Alternatively, it could be that recombination, together with mutation, had evolved as consequences of the fast incorporation rate of RNA-dependent RNA polymerases in RNA viruses. It might be the case at least for several RNA viruses, including TEV, for which a highly significant correlation was found between their recombination and mutation rates [31]. Possibilities for evolution of recombination in RNA viruses were reviewed in [9].

2.2. Evolutionary forces that determine the genetic diversity of populations of plant viruses

A key concept to understand evolution, that is, the change with time of the genetic structure of a population, is the fitness of an individual or genetic variant. **Fitness** is a measure of the reproductive ability of each individual or genetic variant with which it contributes to the next generation in a particular environment [40]. Therefore, in an ideal population of infinite size (to ensure that every single variant contributes to the next generation), an estimate of the fitness of a variant is the frequency at equilibrium with which this variant is present in the progeny. Fitness and population size define the meaning of the two main evolutionary forces, selection and genetic drift. **Selection** represents the changes in the frequency of variants in the ideal population: it is positive (adaptive selection) for fittest variants which increase their frequency and negative (purifying selection) for less fit variants which decrease their frequency. **Genetic drift** occurs when the population is not large enough for each variant to have progeny, so that variants might pass to the next generation rather by chance (random effects), not by their respective fitness [2]. Thus, population demography may influence, and even inhibit, the effects of selection through genetic drift. As mentioned above, RNA viruses, including those of plants, are characterized by a high ability to genetic variation, and their populations are

subjected to high variations in size along the infection cycle due to fast replication rates (expansions) and transmission between hosts or between tissues within a host (reductions). Consequently, conditions at which mutation, selection and genetic drift operate are determinant for the adaptation or extinction of RNA viruses [36].

2.2.1. Selection

Fitness, the parameter that determines selection, is dependent on the environment. Therefore, changes in environmental conditions (for instance, a change of host) may be determinant for a variant generated by mutation to be eliminated from or fixed in the population, giving it a chance for adaptation. In a population, the proportion of mutations that are beneficial, neutral, deleterious or lethal is known as the **distribution of mutational fitness effects**. For RNA viruses, a large proportion of mutation and recombination events are deleterious or lethal [41, 42]. For neutral and deleterious mutations, the **mutation-selection balance** refers to the relationship between the mutation rate and selective pressures that define the frequency of these mutations in the population (they can be continuously created by mutagenesis). On the other hand, **genetic robustness** refers to a kind of molecular mechanisms that minimize the phenotypic effects of mutations and may become a successful strategy against deleterious mutations or may hinder opportunities of adaptation. Robustness has been observed to occur in experimental populations of a plant viroid [43].

Comparative analysis of genetic diversity of populations in different phases of the infection cycle of plant viruses has allowed the identification of selective pressures associated to each of them, although selection is often difficult to distinguish from genetic drift, as both mechanisms result in the decrease in population diversity. Phases of viral cycle associated to selection were reviewed in [2] and [44]. In summary, selective pressures are related to: i) the maintenance of functional structures, that is, certain amino acids involved in the stability of viral particles or in the secondary and tertiary molecular structures required for replication or other interactions; ii) interactions of viruses with their hosts, resulting in the genetic differentiation of natural populations according to the host, the overcoming of host resistance genes, changes in virulence and co-evolution of plants and viruses [45]; iii) interactions between viruses and their vectors for transmission and between hosts and vectors. The sequence analysis of genes related to some of the functions mentioned above for several plant DNA and RNA viruses indicated that selection on plant virus encoded proteins is mostly negative, as measured by the ratio between nucleotide diversities at non-synonymous and synonymous positions (d_{NS}/d_S) (this estimates the degree of functional constraint for the maintenance of the encoded protein). Two major conclusions were derived from the analysis [2]. First, the degree of negative selection is similar for plant RNA and DNA viruses and does not depend on the function of the encoded protein (in contrast to some proteins of cellular organisms, which are more conserved than others). This suggest the existence of epistatic effects of selection in multifunctional virus-encoded proteins or in genes with overlapping open reading frames, so that proteins are never optimized just for one of the functions. Second, the degree of negative selection in plant viruses falls in the same range of that of proteins of their eukaryotic hosts and vectors, suggesting that selection arise from the necessary triple interaction virus-host-vector.

Observation of changes in the genetic structure of within-host populations that are associated to different degree of compatibility between the virus and the host provides insights into the host-adaptive process (reviewed in [3]). In compatible interactions of highly host-adapted viruses, negative selection tends to maintain virus population in equilibrium, resulting in a high stability of its genetic structure, as found in intra-host populations of *Tobacco mild green mosaic virus* and other plant viruses infecting their susceptible hosts. In contrast, more variability was found in small intra-host populations of *Beet necrotic yellow vein virus* (BNYVV) in partially resistant plants, expected to be under virus-host adaptation, than in large BNYVV populations in susceptible plants. This contributes to explain the sudden stochastic diversification of BNYVV populations in sugar beet after the deployment of resistant plant genotypes in the field, and the higher diversity observed in populations of other plant viruses in their centers of origin, where they are in phase of adaptation to a new host [3]. Similarly, higher between-hosts diversities were found in host-adapting populations in virus' centers of origin (*Wheat streak mosaic virus* in North America; *Rice yellow mottle virus*, RYMV, in eastern Tanzania) or in virus emerging areas (resistance breaking variants of BNYVV in the Imperial Valley of California) than in well-adapted virus populations in other areas (other regions in Africa for RYMV or in USA for BNYVV, see references 3, 51, 114 and 130 in [3]).

Another interesting topic on host-adaptive process is that concerning host-range evolution for those viruses that behave as multi-host parasites. Multi-host parasitism is common among plant viruses, leading to the consideration of generalist and specialist plant viruses [46, 47]. Different hosts represent, indeed, different environments for viruses and, accordingly, fitness differences should be expected for viruses across their host range. Genetic differentiation of virus populations according to the host may indicate host adaptation and detailed analysis show evidence of host adaptation in populations of a particular virus sampled from different hosts, or even from new hosts in which the virus has acquired the capacity to infect [48]. More clear indication is obtained when a virus from an original host is serially transferred to other host and it is observed virus adaptation to the new host but associated to a fitness loss in the original host. This type of host selectivity has been shown even in cases of generalist viruses, supporting the theory of trade-offs across hosts, that is, the virus cannot simultaneously maximize its fitness in all of its alternative hosts [48]. Antagonistic pleiotropy, that is, mutation with positive effects in a given host are deleterious in another one, seems to be the major cause of across-host fitness trade-offs, as reviewed in [48, 49].

In a population, the success in the adaptive process to a new host, that means that any beneficial mutation in the new host become fixed, depends on the distribution of mutational fitness effects (see above), which is highly affected by the environment (the new host species), so that there is a larger proportion of beneficial mutations as the taxonomic relatedness of the new host to the original one decreases. This process is in part explained by antagonistic pleiotropy and may be significantly sensitive to genetic drift [50]. Adaptation is also dependent on **epistasis**, defined as the effect of a mutation in one gene on the expression of other gene in the same genome, being this effect often negative (antagonistic epistasis), that is, the combined effect of both mutations is less pronounced than their individual effects would be, and also dependent on the environment (the host) [51, 52].

Selection pressures are also associated to the transmission process. Many plant viruses depend on vectors for transmission. Thus, virus-vector interaction is a probable source of selective pressures. Evidence of virus-vector selection comes from the loss of vector transmission capacity for viruses that have been mechanically transmitted in experiments of serial inoculations (reviewed in [2]). This phenomenon also suggests that might exist trade-offs for adaptation to transmission, as already commented for host adaptation. Virus-vector negative selection is supported by the lower d_{NS}/d_S ratio observed in the coat protein gene, a determinant for vector transmission of many viruses, for vectored viruses compared to that of nonvectored viruses [53]. More complex interaction among viruses, hosts and vectors may also play a role in selection for transmission. For instance, plant viruses may have mutualistic interactions with their vectors, so that infected plants become more attractive for transmission vectors [54], viruliferous vectors increase their fecundity by partial suppression of plant defense mechanisms against feeding vectors [55] and some circulative-propagative viruses seem to modify their vectors' feeding behavior to increase their transmission rate [56, 57].

2.2.2. Genetic drift

Genetic drift refers to the random effects that result from reductions in the population size. In that context, one must consider what is called the effective population size, defined as the number of individuals that give rise the next generation. Plant viruses exhibit high replication rates; therefore, they may reach large population sizes in infected cells or plants. Though, the effective population size of their populations may be several orders of magnitude smaller, as estimated for TMV, TMGMV and WSMV [2, 44]. This may be considered a probable reason to explain the low genetic diversity commonly found in their natural populations, in spite of their high replication and mutation rates [44].

As shown for selection, genetic drift may be associated to almost every step of the virus life cycle and genetic bottlenecks, which are severe reductions in the effective population size, have been shown to operate during virus colonization of a host and transmission between hosts [58–65]. The multiplicity of infection (MOI), that is, the number of virus particles or genomes that infect a cell, has been estimated for some plant viruses either in local infections or along the systemic colonization of a host [66–68], giving roughly similar results, and showing that MOI may vary during systemic infection. Also, estimates of the size of genetic bottlenecks have been reported to be very low, associated to the systemic invasion of leaves [65], aphid transmission [58, 69] and contact transmission [64] between hosts. In addition, the size of bottlenecks is dependent on the viral load, at least during colonization of the host [70, 71].

Above estimates of MOI and of size of genetic bottlenecks are highly relevant to many important processes in virus evolution. For instance, MOI influence the opportunities for genetic exchange to take place, which at least require two different genotypes coinfecting a cell. Also, the efficiency of complementation of defective genomes may occur at high MOI levels, which may be particularly important when deleterious mutants have pleiotropic effects on other viral functions or on other environments (host jumps) [72]. The direct consequence of a severe population bottleneck (an effective population size very low compared to the total census population, which may be very large [2]) is known as "founder effect", an extreme type

of genetic drift implying that the new population (generation) is started (founded) by a few genetic variants randomly sampled from the original population. The overall evolutionary consequence of reductions in the effective population size is a decrease in the genetic diversity within each founded population and a strong spatial structure, derived from the increase in genetic diversity between daughter populations, as observed for TMV even at relatively high MOI [66], with a stochastic spatial distribution of genotypes [73, 74]. Finally, as already indicated in the end of Section 2.1, when bottlenecks lead the population to an effective size below the threshold needed for selection to eliminate deleterious mutations and ensure the transmission of the fittest variants, the fitness of the population may decrease by progressive accumulation of deleterious mutants, leading the population to extinction by mutational meltdown (the "Muller's ratchet" phenomenon) [9, 36, 75]. Interactions between viruses may promote extinction of one of the viruses by mutational meltdown: coinfection of TMV with TMGMV in *Nicotiana glauca* plants from Australia resulted in a reduction in size of the TMV population which led this population to extinction [76].

3. Dynamics of genetic diversity and structure of plant virus populations: implications of evolutionary factors in the epidemiology of diseases

The term evolutionary epidemiology has been coined to denote the link between evolutionary biology and epidemiology [44, 77], which basically describes the integration of ecological and evolutionary concepts, as those already reviewed in this chapter, to better understand specific epidemiological components of host-parasite interactions. Conversely, epidemiological dynamics is also an important factor influencing evolutionary dynamics. This framework is at the base of the most recent advances in the areas of evolutionary biology and epidemiology, some of which are commented below, pointing to the most relevant reviews covering those subjects.

Two of the most important properties of pathogens, with evident implications in epidemiology of diseases, are pathogenicity and virulence. Pathogenicity is defined as the qualitative capacity of a pathogen to infect and cause disease on a host. Virulence is the degree of damage that the pathogen infection causes to the host, but in the context of evolution, it refers to the decrease in fitness of the host caused by the pathogen. Hosts may exert selective pressures on both virulence and pathogenicity of the pathogen, as it happens in agricultural systems in which humans manipulate the host genetic structure by the deployment of host genetic resistance in the field, with the consequent risk of appearance of resistance-breaking variants. On the other hand, the genetic structure of host populations may change in response to the pathogen selective pressures, but mostly in natural ecosystems. The reciprocal evolutionary interaction between hosts and pathogens brings the concept of host-pathogen coevolution. In spite of a broad collection of theoretical models regarding host-parasite coevolution, experimental evidences are scant and some advances have been made in this field to test theoretical hypotheses, which have been recently reviewed [45, 78].

Other epidemiological implications of the evolutionary dynamics of plant viruses deal with the improvement of disease management strategies. Acosta-Leal [3] evaluated possible opportunities

for virus-disease control, as resistance genes, natural plant resistance mechanisms, control of coinfection dynamics, modeling virus robustness, etc. and discussed about research advances and needs in relation to a simple theoretical model, which states that an assembly of management measures should be addressed to altogether reduce the effective population size of virus populations, increase their genetic diversity and maximize bottleneck effects, so that a virus population could be gradually excluded from its hosts species.

Finally, a highly relevant epidemiological consequence of plant virus evolutionary dynamics is the risk of emergence of virus diseases, which seriously compromise agriculture production worldwide. Emergence of new diseases may occur either by appearance of new virus species that spill over from wild plant reservoirs or of well known viruses that suddenly show new pathogenic and epidemiological properties (host jumps, resistance-breaking variants). The risk of resistance-breaking was evaluated for a set of representative plant viruses and pathosystems in relation to an index of evolutionary potential, based on the effective population size, the degree of genetic exchange and the amount of gene flow, which was proposed as an important determinant of the durability of resistance against plant viruses [46]. Ecological and epidemiological factors of plant virus emergence often have their origin at the interface between managed and natural ecosystems and are mostly related to a rapid expansion of human activity, including the worldwide distribution of crop species far from their geographic origins, the intensiveness of agricultural practices and the international trade facilitating the spread of damaging viral species, all of them under the effect of global climate change [79]. Factors favoring emergence derive from complex interactions among host plants, viruses and their vectors (for vector-borne viruses) and have been analyzed in the context of evolutionary ecology, genetics and epidemiology [80]. In summary, they result in changes in the ecology and genetic composition of host plant, virus and vector populations during three different temporal phases that describe the process of emergence. In a first phase, viruses spill over from host reservoirs in which they are well-adapted (often reservoirs of wild plants) and jump to the same host species in a new ecological environment or to a new host species. In this phase, ecological conditions for plant hosts, viruses (and vectors) must favor the contact between the original and the new host populations for emergence to occur. This includes the introduction of hosts, viruses (and vectors), often by human activity, in areas where they were not present before. Other factor facilitating new contacts is ecosystem simplification [81], characterized by reduced species diversity in agricultural compared to natural ecosystems, a concomitant reduction in the genetic diversity of crops compared to wild populations and a higher host density. A second phase consists on the evolutionary process of virus adaptation to the new host or environment to the point that new infections and transmission in the new host is ensured, making between-host transmission independent from the original reservoir. As indicated in Section 2.2.1, adaptation to a new host is a process governed by an assembly of evolutionary factors, such the generation of beneficial mutations (and genetic exchange in cases of cellular coinfection), the interaction between beneficial mutations (epistasis) in a favorable environment (a particular new host) that may results in trade-offs across hosts and obviously, stochastic effects. Here, it is important to stress that the symplast, where plant viruses must replicate and evolve, is a high structured environment where virus populations adopt a metapopulation structure, a set of subpopulations, each one occupying different

tissues and organs. This metapopulation structure is probably generated by the effect of genetic bottlenecks and might affect the efficiency of natural selection [80]. In the third phase, an efficient epidemiology should optimize between-host transmission in the new host and environment, which implies new adaptation to vectors in the case of vectored viruses. As predicted by theoretical models, the epidemiological potential of a pathogen depends on its basic reproductive ratio (R_0), which represents the number of new infections per infected host in a susceptible population. R_0 value must be larger than unity for an epidemic to occur. Consequently, during this phase of emergence, evolutionary factors determining virus competence for transmission (and adaptation to new vectors in vectored viruses) should maximize transmission rate and reduce virulence.

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References

- [1] Hartl DL, Clark AG. Principles of population genetics. 4th ed. Sunderland, MA 31375 USA: Sinauer Associates Inc. Publishers; 2007. 669 p. ISBN: 978-0-87893-308-2
- [2] Garcia-Arenal F, Fraile A, Malpica JM. Variability and genetic structure of plant virus populations. *Annual Review of Phytopathology*. 2001;39:157–186.
- [3] Acosta-Leal R, Duffy S, Xiong Z, Hammond RW, Elena SF. Advances in plant virus evolution: translating evolutionary insights into better disease management. *Phytopathology*. 2011;101:1136–1148.
- [4] Garcia-Arenal F, Fraile A, Malpica JM. Variation and evolution of plant virus populations. *International Microbiology*. 2003;6:225–232.
- [5] Gibbs A, Gibbs M, Ohshima K, Garcia-Arenal F. More about plant virus evolution: past, present, and future. In: Domingo E, Parrish CR, Holland JJ, editors. *Origin and Evolution of Viruses* 2nd ed. London: Elsevier; 2008. p. 229–249. DOI: 10.1016/B978-0-12-374153-0.00011-4
- [6] Sanjuan R, Nebot MR, Chirico N, Mansky LM, Belshaw R. Viral mutation rates. *Journal of Virology*. 2010;84:9733–9748.
- [7] Tromas N, Elena SF. The rate and spectrum of spontaneous mutations in a plant RNA virus. *Genetics*. 2010;185:983–989.

- [8] Malpica JM, Fraile A, Moreno I, Obies CI, Drake JW, Garcia-Arenal F. The rate and character of spontaneous mutation in an RNA virus. *Genetics*. 2002;162:1505–1511.
- [9] Simon-Loriere E, Holmes EC. Why do RNA viruses recombine? *Nature Reviews Microbiology*. 2011;9:617–626.
- [10] Chare ER, Holmes EC. A phylogenetic survey of recombination frequency in plant RNA viruses. *Archives of Virology*. 2006;151:933–946.
- [11] Chenault KD, Melcher U. Phylogenetic-relationships reveal recombination among isolates of cauliflower mosaic-virus. *Journal of Molecular Evolution*. 1994;39:496–505.
- [12] Harrison BD, Robinson DJ. Natural genomic and antigenic variation in whitefly-transmitted geminiviruses (Begomoviruses). *Annual Review of Phytopathology*. 1999;37:369–398.
- [13] MacFarlane SA. Natural recombination among plant virus genomes: evidence from tobnaviruses. *Seminars in Virology*. 1997;8:25–31.
- [14] Ohshima K, Tomitaka Y, Wood JT, Minematsu Y, Kajiyama H, Tomimura K, et al. Patterns of recombination in turnip mosaic virus genomic sequences indicate hotspots of recombination. *Journal of General Virology*. 2007;88:298–315.
- [15] Padidam M, Sawyer S, Fauquet CM. Possible emergence of new geminiviruses by frequent recombination. *Virology*. 1999;265:218–225.
- [16] Roossinck MJ. Evolutionary history of Cucumber mosaic virus deduced by phylogenetic analyses. *Journal of Virology*. 2002;76:3382–3387.
- [17] Bergua M, Luis-Arteaga M, Escribe F. Genetic diversity, reassortment and recombination in Alfalfa mosaic virus population in Spain. *Phytopathology*. 2014;104:1241–1250.
- [18] Garcia-Arenal F, Escribe F, Aranda MA, Alonso-Prados JL, Malpica JM, Fraile A. Molecular epidemiology of Cucumber mosaic virus and its satellite RNA. *Virus Research*. 2000;71:1–8.
- [19] Tentchev D, Verdin E, Marchal C, Jacquet M, Aguilar JM, Moury B. Evolution and structure of tomato spotted wilt virus populations: evidence of extensive reassortment and insights into emergence processes. *Journal of General Virology*. 2011;92:961–973.
- [20] Desbiez C, Lecoq H. The nucleotide sequence of Watermelon mosaic virus (WMV, Potyvirus) reveals interspecific recombination between two related potyviruses in the 5' part of the genome. *Archives of Virology*. 2004;149:1619–1632.
- [21] Garcia-Andres S, Accotto GP, Navas-Castillo J, Moriones E. Founder effect, plant host and recombination shape the emergent population of begomoviruses that cause the tomato yellow leaf curl disease in the Mediterranean basin. *Virology*. 2007;359:302–312.
- [22] Monci F, Sanchez-Campos S, Navas-Castillo J, Moriones E. A natural recombinant between the geminiviruses Tomato yellow leaf curl Sardinia virus and Tomato yellow

- leaf curl virus exhibits a novel pathogenic phenotype and is becoming prevalent in Spanish populations. *Virology*. 2002;303:317–326.
- [23] Valli A, Lopez-Moya JJ, Garcia JA. Recombination and gene duplication in the evolutionary diversification of P1 proteins in the family Potyviridae. *Journal of General Virology*. 2007;88:1016–1028.
- [24] White PS, Morales F, Roossinck MJ. Interspecific reassortment of genomic segments in the evolution of cucumoviruses. *Virology*. 1995;207:334–337.
- [25] Klute KA, Nadler SA, Stenger DC. Horseradish curly top virus is a distinct subgroup II geminivirus species with rep and C4 genes derived from a subgroup III ancestor. *Journal of General Virology*. 1996;77:1369–1378.
- [26] Pita JS, Fondong VN, Sangare A, Otim-Nape GW, Ogwal S, Fauquet CM. Recombination, pseudorecombination and synergism of geminiviruses are determinant keys to the epidemic of severe cassava mosaic disease in Uganda. *Journal of General Virology*. 2001;82:655–665.
- [27] Diaz-Pendon JA, Canizares MC, Moriones E, Bejarano ER, Czosnek H, Navas-Castillo J. Tomato yellow leaf curl viruses: menage a trois between the virus complex, the plant and the whitefly vector. *Molecular Plant Pathology*. 2010;11:441–450.
- [28] Bruyere A, Wantroba M, Flasiński S, Dzianott A, Bujarski JJ. Frequent homologous recombination events between molecules of one RNA component in a multipartite RNA virus. *Journal of Virology*. 2000;74:4214–4219.
- [29] Urbanowicz A, Alejska M, Formanowicz P, Blazewicz J, Figlerowicz M, Bujarski JJ. Homologous crossovers among molecules of brome mosaic bromovirus RNA1 or RNA2 segments in vivo. *Journal of Virology*. 2005;79:5732–5742.
- [30] Froissart R, Roze D, Uzest M, Galibert L, Blanc S, Michalakakis Y. Recombination every day: Abundant recombination in a virus during a single multi-cellular host infection. *PLoS Biology*. 2005;3:389–395.
- [31] Tromas N, Zwart MP, Poulain M, Elena SF. Estimation of the in vivo recombination rate for a plant RNA virus. *Journal of General Virology*. 2014;95:724–732.
- [32] Escriu F, Fraile A, Garcia-Arenal F. Constraints to genetic exchange support gene coadaptation in a tripartite RNA virus. *PLoS Pathogens*. 2007;3:67–74.
- [33] Bonnet J, Fraile A, Sacristan S, Malpica JM, Garcia-Arenal F. Role of recombination in the evolution of natural populations of Cucumber mosaic virus, a tripartite RNA plant virus. *Virology*. 2005;332:359–368.
- [34] Lin HX, Rubio L, Smythe AB, Falk BW. Molecular population genetics of Cucumber mosaic virus in California: evidence for founder effects and reassortment. *Journal of Virology*. 2004;78:6666–6675.

- [35] Martin DP, van der Walt E, Posada D, Rybicki EP. The evolutionary value of recombination is constrained by genome modularity. *PLoS Genetics*. 2005;1:475–479.
- [36] Elena SF, Miralles RF, Cuevas JM, Turner PE, Moya A. The two faces of mutation: extinction and adaptation in RNA viruses. *Iubmb Life*. 2000;49:5–9.
- [37] Bull JJ, Sanjuan R, Wilke CO. Theory of lethal mutagenesis for viruses. *Journal of Virology*. 2007;81:2930–2939.
- [38] Muller HJ. The relation of recombination to mutational advance. *Mutation Research*. 1964;1:2–9.
- [39] Chao L. Evolution of sex in RNA viruses. *Trends in Ecology & Evolution*. 1992;7:147–151.
- [40] Maynard Smith J. *Evolutionary Genetics*. Oxford, UK: Oxford University Press; 1989. ISBN: 0198502311
- [41] Carrasco P, de la Iglesia F, Elena SF. Distribution of fitness and virulence effects caused by single-nucleotide substitutions in tobacco etch virus. *Journal of Virology*. 2007;81:12979–12984.
- [42] Sanjuan R, Moya A, Elena SF. The distribution of fitness effects caused by single-nucleotide substitutions in an RNA virus. *Proceedings of the National Academy of Sciences of the United States of America*. 2004;101:8396–8401.
- [43] Codoñer FM, Daros JA, Sole RV, Elena SF. The fittest versus the flattest: Experimental confirmation of the quasispecies effect with subviral pathogens. *PLoS Pathogens*. 2006;2:1187–1193.
- [44] Jeger MJ, Seal SE, Van den Bosch F. Evolutionary epidemiology of plant virus disease. *Plant Virus Epidemiology. Advances in Virus Research*. 2006;67:163–203.
- [45] Fraile A, Garcia-Arenal F. The Coevolution of Plants and Viruses: Resistance and Pathogenicity. *Advances in Virus Research*. 2010;76:1–32.
- [46] Garcia-Arenal F, McDonald BA. An analysis of the durability of resistance to plant viruses. *Phytopathology*. 2003;93:941–952.
- [47] Power AG, Flecker AS. Virus specificity in disease systems: are species redundant? In: Kareiva P, Levin SA, editors. *The importance of species: Perspectives on expendability and triage* Princeton, New Jersey 08540: Princeton University Press; 2003. p.330–346.
- [48] Garcia-Arenal F, Fraile A. Trade-offs in host range evolution of plant viruses. *Plant Pathology*. 2013;62:2–9.
- [49] Elena SF, Agudelo-Romero P, Lalic J. The evolution of viruses in multi-host fitness landscapes. *The Open Virology Journal*. 2009;3:1–6.
- [50] Lalic J, Cuevas JM, Elena SF. Effect of Host Species on the Distribution of Mutational Fitness Effects for an RNA Virus. *PLoS Genetics*. 2011;7:e1002378.
- [51] Lalic J, Elena SF. Magnitude and sign epistasis among deleterious mutations in a positive-sense plant RNA virus. *Heredity*. 2012;109:71–77.

- [52] Lalic J, Elena SF. Epistasis between mutations is host-dependent for an RNA virus. *Biology Letters*. 2013;9:20120396.
- [53] Chare ER, Holmes EC. Selection pressures in the capsid genes of plant RNA viruses reflect mode of transmission. *Journal of General Virology*. 2004;85:3149–3157.
- [54] Mauck K, Bosque-Perez NA, Eigenbrode SD, De Moraes CM, Mescher MC. Transmission mechanisms shape pathogen effects on host-vector interactions: evidence from plant viruses. *Functional Ecology*. 2012;26:1162–1175.
- [55] Abe H, Tomitaka Y, Shimoda T, Seo S, Sakurai T, Kugimiya S, et al. Antagonistic plant defense system regulated by phytohormones assists interactions among vector insect, thrips and a tospovirus. *Plant and Cell Physiology*. 2012;53:204–212.
- [56] Moreno-Delafuente A, Garzo E, Moreno A, Fereres A. A Plant Virus Manipulates the Behavior of Its Whitefly Vector to Enhance Its Transmission Efficiency and Spread. *PLoS One*. 2013;8:e61543.
- [57] Poulin R. Manipulation of host behaviour by parasites: a weakening paradigm? *Proceedings of the Royal Society of London B-Biological Sciences*. 2000;267:787–792.
- [58] Betancourt M, Fereres A, Fraile A, Garcia-Arenal F. Estimation of the effective number of founders that initiate an infection after aphid transmission of a multipartite plant virus. *Journal of Virology*. 2008;82:12416–12421.
- [59] French R, Stenger DC. Evolution of wheat streak mosaic virus: Dynamics of population growth within plants may explain limited variation. *Annual Review of Phytopathology*. 2003;41:199–214.
- [60] Jridi C, Martin JF, Marie-Jeanne V, Labonne G, Blanc S. Distinct viral populations differentiate and evolve independently in a single perennial host plant. *Journal of Virology*. 2006;80:2349–2357.
- [61] Li HY, Roossinck MJ. Genetic bottlenecks reduce population variation in an experimental RNA virus population. *Journal of Virology*. 2004;78:10582–10587.
- [62] Monsion B, Froissart R, Michalakakis Y, Blanc S. Large Bottleneck Size in Cauliflower Mosaic Virus Populations during Host Plant Colonization. *PLoS Pathogens*. 2008;12: e1005512.
- [63] Nolasco G, Fonseca F, Silva G. Occurrence of genetic bottlenecks during citrus tristeza virus acquisition by *Toxoptera citricida* under field conditions. *Archives of Virology*. 2008;153:259–271.
- [64] Sacristan S, Diaz M, Fraile A, Garcia-Arenal F. Contact transmission of tobacco mosaic virus: a quantitative analysis of parameters relevant for virus evolution. *Journal of Virology*. 2011;85:4974–4981.

- [65] Sacristan S, Malpica JM, Fraile A, Garcia-Arenal F. Estimation of population bottlenecks during systemic movement of Tobacco mosaic virus in tobacco plants. *Journal of Virology*. 2003;77:9906–9911.
- [66] Gonzalez-Jara P, Fraile A, Canto T, Garcia-Arenal F. The multiplicity of infection of a plant virus varies during colonization of its eukaryotic host. *Journal of Virology*. 2009;83:7487–7494.
- [67] Gutierrez S, Yvon M, Thebaud G, Monsion B, Michalakis Y, Blanc S. Dynamics of the Multiplicity of Cellular Infection in a Plant Virus. *PLoS Pathogens*. 2010;6:e1001113.
- [68] Miyashita S, Kishino H. Estimation of the size of genetic bottlenecks in cell-to-cell movement of soil-borne wheat mosaic virus and the possible role of the bottlenecks in speeding up selection of variations in trans-acting genes or elements. *Journal of Virology*. 2010;84:1828–1837.
- [69] Moury B, Fabre F, Senoussi R. Estimation of the number of virus particles transmitted by an insect vector. *Proceedings of the National Academy of Sciences of the United States of America*. 2007;104:17891–17896.
- [70] Gutierrez S, Yvon M, Pirolles E, Garzo E, Fereres A, Michalakis Y, et al. Circulating Virus Load Determines the Size of Bottlenecks in Viral Populations Progressing within a Host. *PLoS Pathogens*. 2012;8:e1003009.
- [71] Zwart MP, Daros J-A, Elena SF. One Is Enough: In Vivo Effective Population Size Is Dose-Dependent for a Plant RNA Virus. *PLoS Pathogens*. 2011;7:e1002122.
- [72] Tollenaere C, Susi H, Laine A-L. Evolutionary and epidemiological implications of multiple infection in plants. *Trends in Plant Science*. 2016;21:80–90.
- [73] Ali A, Li H, Schneider WL, Sherman DJ, Gray S, Smith D, et al. Analysis of genetic bottlenecks during horizontal transmission of Cucumber mosaic virus. *Journal of Virology*. 2006;80:8345–8350.
- [74] French R, Stenger DC. Population structure within lineages of Wheat streak mosaic virus derived from a common founding event exhibits stochastic variation inconsistent with the deterministic quasi-species model. *Virology*. 2005;343:179–189.
- [75] de la Iglesia F, Elena SF. Fitness declines in Tobacco etch virus upon serial bottleneck transfers. *Journal of Virology*. 2007;81:4941–4947.
- [76] Fraile A, Escriu F, Aranda MA, Malpica JM, Gibbs AJ, GarciaArenal F. A century of tobamovirus evolution in an Australian population of *Nicotiana glauca*. *Journal of Virology*. 1997;71:8316–8320.
- [77] Grenfell BT, Pybus OG, Gog JR, Wood JLN, Daly JM, Mumford JA, et al. Unifying the epidemiological and evolutionary dynamics of pathogens. *Science*. 2004;303:327–332.
- [78] Sacristan S, Garcia-Arenal F. The evolution of virulence and pathogenicity in plant pathogen populations. *Molecular Plant Pathology*. 2008;9:369–384.

- [79] Jones RAC. Plant virus emergence and evolution: origins, new encounter scenarios, factors driving emergence, effects of changing world conditions and prospects for control. *Virus Research*. 2009;141:113–130.
- [80] Elena SF, Fraile A, Garcia-Arenal F. Evolution and Emergence of Plant Viruses. *Advances in Virus Research*. 2014;88:161–191.
- [81] Roossinck MJ, Garcia-Arenal F. Ecosystem simplification, biodiversity loss and plant virus emergence. *Current Opinion in Virology*. 2015;10:56–62.