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Chapter 1

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

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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 that those of DNA viruses [5, 7] and this difference has been attributed to the lack of proofreading 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 led 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 BYNVV, 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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