

# Underestimating Risks & Impact of Viral Diseases on Alfalfa Health

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Alfalfa (*Medicago sativa* L.) is a major forage crop worldwide and the third most valuable field crop in the United States with an estimated worth of over \$9.3 billion. Alfalfa productivity is limited by various infectious diseases that can reduce forage yield and quality and shorten stand life. The crop can frequently be infected with a diverse array of pathogens that have distinct life cycles, biology, and modes of action. Among them are many coinfecting viruses that greatly contribute to the heterogeneity of within-host pathogenic communities, representing a ubiquitous and abundant background for all other host-pathogen interactions. Regrettably, the impact of viral diseases, their role in alfalfa health, and involvement in the severity of multi-pathogen infections are often underestimated and not well understood. Although several economically important viral diseases in alfalfa were previously described, novel viruses continue to be discovered at accelerated rates thanks to the advent of high-throughput sequencing (HTS) technologies and bioinformatics tools for interpreting massive amounts of HTS data [1,2]. Among them are emerging viruses with the capacity for serious yield losses, such as alfalfa leaf curl virus (family *Geminiviridae*), alfalfa dwarf virus (*Rhabdoviridae*), alfalfa enamovirus 1 (*Luteoviridae*), alfalfa virus S (*Alphaflexiviridae*) and others [2].

Our research has contributed to this effort, demonstrating that in agricultural production settings alfalfa plants are coinfecting with a substantial number of different viruses, including both well-known and newly discovered species, and viruses formerly described in other hosts. In a recent survey of several commercial alfalfa production fields in the U.S. Pacific Northwest, we identified a total of 45 distinct viruses, some of which were known to infect the crop prior to this study, and others that were designated as emerging, novel, and viruses integrated into the alfalfa genome [3]. The makeup of the alfalfa virome continues to expand to include new and emergent species, different geographic locations, and previously unknown adaptations to alfalfa as a new host. The extent of mixed viral infections in alfalfa, based on the HTS-derived findings, is remarkable and can reach many co-infecting viruses in a single plant. Synergetic interactions of viral coinfections can potentially threaten alfalfa production. Alfalfa may also serve as a natural reservoir for dissemination of viruses to other agriculturally important crops. In the field, viral communities are accompanied by non-viral infections and represent an essential part of the alfalfa microbiota, with which they continuously interact. Therefore, it is increasingly important to alfalfa pathology to broaden studies of single disease-causing biological organisms with research on the crop's pathobiome - a comprehensive biotic environment that not only includes a diverse community of pathogenic organisms within the plant, but also facilitates their interaction with each other, affects severity of the disease, and defines the overall impact on plant health.

## References

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