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THE VIRUS RANGE OF HOP PLANTS: IDENTIFICATION KEY

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The term "virus range" was coined by Christie and Crawford in 1978, by analogy with the term "host range", to denote all viruses that can infect a particular host species [1]. Studying the virus range of a particular host species, similar to investigating the host range of a particular virus, plays an essential role in improving the understanding of virus-host-environment interactions [2]. However, investigating the virus range of a particular host necessitates employing approaches that do not rely on *a priori* information about which viruses might be present in the sample to detect all viruses it contains. One of these approaches involves the preliminary inspection of samples under the transmission electron microscope (TEM), followed by identifying the observed viruses using serological and nucleic acid-based techniques [3]. However, identifying the virus species observed in a sample under the TEM also requires the development of identification keys, based on the shape and size of virions.

The viral diseases of the common hop (*Humulus lupulus* L.) have been studied for centuries. Numerous authors in different periods have reported various numbers of viral diseases of hop and virus species infecting this plant. For example, Schmidt and Klinkowski listed 11 viroses of hop in Europe in 1965 [4]. However, before the implementation of serological techniques, the causative agents of hop viroses were characterized by diagnostic species and a combination of symptoms of the disease they cause in those species and the hop themselves. Hence, determining the taxonomic position of the pathogens that caused diseases described during that period, such as those documented by Schmidt and Klinkowski, is impossible. For example, Adams and others revealed that arabis mosaic virus (ArMV) causes hop chlorotic disease in England, whereas Eppler indicates hop mosaic virus (HMV) as the causative agent of this disease in Germany [5, 6]. Nevertheless, many authors identified numerous virus species that infect the common hop and can be re-identified by other researchers by using serological and nucleic acid-based techniques. Thus, Pethybridge and colleagues performed a meta-analysis of studies on viruses infecting hop plants and listed 15 identifiable virus species [7].

Therefore, the study aimed to gather information about the virion size and shape of viruses belonging to the virus range of the common hop and to develop the identification key. To this end, the author was searching for information about the virion size and shape of viruses listed by Pethybridge and others [7]. The compiled information is presented in the table.

Table 1. The virion size and shape of viruses infecting hop

Species	Shape	Size, nm	Reference
Alfalfa mosaic virus, AlMV	bacilliform	30 - 56 × 19*	7
	bacilliform	61 × 17.8**	8
American hop latent virus, AHLV	filamentous	676 × 14.4	9
Apple mosaic virus, ApMV	quasi-isometric	24 × 26 - 28	10
	isometric	24	10
	isometric	22	10
	isometric	25	11
	isometric	32	11
	quasi-isometric	30 × 30 - 36	11
Arabis mosaic virus, ArMV	isometric	25 – 30*	7
	polyhedral	30***	12
Cherry leaf roll virus, CLRV	isometric	25 - 30*	7
Cucumber mosaic virus, CMV	isometric	25-30*	7
	isometric	30***	12
Hop latent virus, HLV	filamentous	678 × 15.2	9
	filamentous	650 × 13	10
Hop mosaic virus, HMV	filamentous	651 × 13.8	13
	filamentous	625 × 13	14
	filamentous	655 × 13.5	8
	filamentous	630 - 680 × 28	15
Humulus japonicus latent virus, HJLV	quasi-isometric	24 - 33	16, 17
Petunia asteroid mosaic virus, PeAMV	isometric	32 - 35*	7, 18, 19
Prunus necrotic ringspot virus, PNRSV	isometric, bacilliform	23, 25, 27*	7
	isometric	40	20
	isometric	28 - 30	21
	quasi-isometric	25**	22
	quasi-isometric	31**	22
Raspberry bushy dwarf virus, RBDV	isometric	33*	7
Strawberry latent ringspot virus, SLRSV	isometric	30*	7
Tobacco mosaic virus, TMV	rod-shaped	300 × 18*	7
Tobacco necrosis virus, TNV	isometric	28*	7
	isometric	26	23
	isometric	27 - 28	21
Tobacco ringspot virus, TRSV	isometric	25 - 30*	7

Notes: *The size and shape are listed for the virus species in general, not for the strain infecting hop [7]; **The sizes of virions were measured by the author using the website https://eleif.net/photomeasure and the micrograph published in the paper by Yu and Liu, as the authors did not specify the virion sizes [8]. The size is indicated as the average value for 5 virions and was calculated in relation to the size of the bar; ***The author consistently confuses μm with nm in its publication.

According to the table, the viruses infecting hop plants can be distinguished by reference to the following identification key.

Identification key to the virus range of hop plants

1(2). Virions are isometric and / or quasi-isometric and / or bacilliform, with the biggest dimension being less than 100 nm. – Group of isometric, quasi-isometric, and bacilliform viruses (AlMV, ApMV, ArMV, CLRV, CMV, HJLV, PeAMV, PNRSV, RBDV, SLRSV, TNV and TRSV).

2(3). Virions are rod-shaped, ca. 300 nm in length. – TMV.

3. Virions are filamentous, longer than 500 nm. – *Carlavirus compex* (AHLV, HLV, and HMV).

The identification results obtained from the key should be confirmed or specified by serological or nucleic acid-based techniques. In future work, the identification key can be supplemented with new virus species infecting hop plants if they are discovered.

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