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REVIEW ARTICLE

# How does vector diversity influence the transmission efficiency of yellow dwarf virus? Perspectives from a review

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## Abstract

Cereals are some of the most important global crops that contribute directly and indirectly to the production of food for human consumption. Cereal aphids can cause significant damage to wheat, barley and oats, particularly via the transmission of plant viruses that cause devastating plant diseases, such as yellow dwarf disease. High levels of yellow dwarf disease can result in yield losses of around 20%, rising to 80% if infection is severe. Yellow dwarf disease is caused by multiple viruses, including viruses within the families Tombusviridae and Solemoviridae. These include yellow dwarf virus species within the genus Luteovirus (Barley yellow dwarf virus) and Polerovirus (Cereal yellow dwarf virus, Wheat yellow dwarf virus, Maize yellow dwarf virus). Some yellow dwarf virus species are primarily vectored by one aphid species whereas others can be transmitted by multiple vectors. Biological diversity within a given vector species (e.g., genotype, biotype) can influence virus transmission efficiency. However, it is unclear what biological factors drive this variation within a given vector species. Understanding how biological variation in vector populations influences virus transmission efficiency can help to identify biological traits that underpin successful transmission in competent vector populations. Here, the available literature on yellow dwarf virus transmission efficiency is synthesized and significant variation in yellow dwarf virus transmission efficiency is detected between different populations for several vector species. Three biological mechanisms that potentially underpin this variation are proposed.

## KEYWORDS

cereal aphid, endosymbiont, *Solemoviridae*, *Tombusviridae*, transmission efficiency, yellow dwarf virus

## 1 | YELLOW DWARF VIRUS AND YELLOW DWARF DISEASE: A BRIEF INTRODUCTION

Cereals are some of the most important global crops that contribute directly and indirectly (e.g., as feed for livestock) to the production of food for human consumption (Marshall et al., 2013; Newton et al., 2011; Shiferaw et al., 2013); wheat (*Triticum aestivum*) alone provides 25% of daily calorific intake for the United Kingdom, with calorific provisions comparable in similar countries (e.g., 19% in Germany; Mottaleb et al., 2022). Reliance on wheat as a source of

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calories is higher (up to 61%) in countries with greater food insecurity (Mottaleb et al., 2022). Cereal crops are exposed to myriad biotic threats, including multiple herbivorous pests and diseases. Cereal aphids, including the bird cherry-oat aphid (Rhopalosiphum padi), the grain aphid (Sitobion avenae), and the rose-grain aphid (Metapolophium dirhodum), are some of the most important herbivorous pests of cereals (van Emden & Harrington, 2007). Cereal aphids are widely distributed and can cause significant damage to cereal crops. Aphid damage can be caused through direct feeding (Dedryver et al., 2010) and via the transmission of plant viruses that cause devastating plant diseases, such as yellow dwarf disease (Fabre, Dedryver, et al., 2003; Perry et al., 2000). Yellow dwarf disease can result in yield losses of around 20% (Kennedy & Connery, 2005; Liu et al., 2014; Perry et al., 2000), increasing to 80% if infection is high (Nancarrow et al., 2021). Plants are at greater risk of yellow dwarf disease infection at the early stages of plant growth; if plants become infected when mature (beyond growth stage 31), they can tolerate yellow dwarf disease infection and the disease impact is limited.

Yellow dwarf disease is caused by several distinctive viruses that are often collectively referred to as the yellow dwarf viruses (YDVs). These include barley yellow dwarf virus (BYDV, Tombusviridae, Luteovirus), cereal yellow dwarf virus (CYDV, Solemoviridae, Polerovirus), maize yellow dwarf virus (MYDV, Solemoviridae, Polerovirus), and wheat yellow dwarf virus (WYDV, Solemoviridae, Polerovirus). Yellow dwarf disease can also be caused by other viruses in these genera, including barley virus G (BVG, Solemoviridae, Polerovirus; Erickson et al., 2023; Zhao et al., 2016) and wheat leaf yellowing-associated virus (WLYaV, Solemoviridae, Polerovirus; Zhang et al., 2017). For an overview of YDV taxonomy, please see the recent comprehensive reviews by Kidanemariam and Abraham (2023) and Miller and Lozier (2022).

Yellow dwarf disease symptoms vary between cereal species, with stark symptomatic differences between oats (Avena sativa) and barley (Hordeum vulgare). Disease symptoms are also influenced by the age of the plant when initially infected (Armand et al., 2023). Table 1 summarizes the known yellow dwarf disease symptoms for the main cereal crops (wheat, barley and oats). However, it is important to note that there may be differences in symptoms between crop cultivars, the virus transmitted, and even between variants within a virus species. Yellow dwarf disease is a widespread crop disease of international importance and is of concern to cereal producers worldwide. A recent molecular evolution study has suggested that yellow dwarf disease originated from the United States and potentially spread outward from North America to China, Europe and Australia, before spreading to additional countries (Malmstrom et al., 2007; Wei et al., 2023). Human activity, for example via the movement of virus-carrying vectors or virus-infected plants, is the most likely mechanism behind this dispersal (Malmstrom et al., 2007; Wei et al., 2023; Yao et al., 2019). In Europe R. padi, S. avenae and M. dirhodum are the main YDV vectors of concern in agricultural systems (McNamara et al., 2020), and vector demographics and immigration are key foci for ongoing research efforts (Holland et al., 2021; Morales-Hojas et al., 2020).

#### 1.1 Overview of the disease cycle

YDV is a circulative, non-propagative, persistent virus (Ng & Perry, 2004). Essentially, this means YDV is able to circulate within and between the tissue and organs of the vector (Blanc et al., 2014; Gildow & Gray, 1993; Paliwal & Sinha, 1970); YDV is unable to reproduce, or propagate, within the vector (Paliwal & Sinha, 1970); and YDV remains present within the vector, and therefore the vector remains infective, for prolonged periods (Guo et al., 1997a; Paliwal & Sinha, 1970; Rochow, 1959). YDV can be present in the gut, hemolymph and salivary glands of virus-carrying aphids (Gildow & Gray, 1993; Paliwal & Sinha, 1970), although the virus is only transmitted to plants when present in the salivary glands (Gildow & Gray, 1993). As a persistent virus, aphids carrying YDV remain infective for long periods and the virus is not lost upon aphid moulting (Paliwal & Sinha, 1970; Rochow, 1959).

Virus particles are acquired from virus-infected plants during aphid ingestion of the plant phloem. Following ingestion from infected phloem cells, the viral particles traverse the food canal and foregut into the mid- and hindgut where they are transported across gut epithelial cells into the hemocoel (Li et al., 2001). Virions circulate in the hemolymph and are then selectively taken up by accessory salivary gland cells (Gildow & Gray, 1993). Salivary gland selectivity is thought to be modulated, to a certain extent, by the basal lamina of the accessory salivary gland (Gildow & Gray, 1993). The capsid proteins of the virus are also key determinants of viral selectivity and movement across the epithelial barriers, and as such the capsid proteins of the virus are thought to contribute toward vector specificity.

Virus particles are inoculated into the phloem of uninfected plants during salivation by virus-carrying aphids (Gildow & Grav. 1993; Jiménez et al., 2020; Ng & Perry, 2004; Prado & Tjallingii, 1994). The length of time required for successful transmission is highly variable (Power et al., 1991; Watson & Mulligan, 1960) and transmission success increases with infestation time (Power et al., 1991). Until recently it was believed that successful YDV transmission required a prolonged period of phloem contact, with seminal research indicating that YDV transmission can occur after 2h of aphid infestation, increasing gradually to a plateau of transmission efficiency around 24h (Lowles et al., 1996). However, recent observations have indicated that YDV can be successfully transmitted following brief contact between the stylet of an infected aphid and a sieve element cell (Jiménez et al., 2020). In terms of transmission efficiency (i.e., the percentage of plants infected with B/CYDV), Jiménez et al. (2020) found a transmission efficiency of around 15% following brief intracellular probe of a sieve element cell with the aphid stylet and a transmission efficiency of 33% following a period of brief salivation into a probed sieve element cell. The highest transmission efficiency (c. 56%) occurred after a sustained period of salivation into the phloem (Jiménez et al., 2020).

Within the plant tissue, YDV is phloem-limited (Esau, 1957; Jensen, 1969), although occasional secondary infection of adjacent vascular tissue (xylem and parenchyma) has been observed after necrosis of neighbouring phloem cells (Esau, 1957). Viral particles reduce meristematic activity in the vascular tissue of infected plants

TABLE 1 Summary of the common yellow dwarf disease symptoms of barley, oat, and wheat.

	Common symptom													
Crop	Impact on aboveground crop physiology	Impact on below- ground crop physiology	Impact on leaf discolouration	Impact on leaf anatomy										
Barley (Hordeum vulgare)	Crop stunting <sup>1,2,6,7,10</sup> ; delayed maturity <sup>1</sup> ; shrivelled grain <sup>1,7</sup> ; abortion of florets and sterile flowers <sup>1</sup> ; excessive tillering in severe infection <sup>1</sup> ; lower transpiration <sup>2</sup> ; chlorosis <sup>6,10</sup>	Reduced root mass <sup>1,10</sup> ; lower root:shoot ratio <sup>2</sup>	Often turn chrome yellow <sup>1,2,6,7,10</sup>	Leaf edges can become distorted, curled or serrated <sup>1</sup> ; reduced leaf area <sup>1,7</sup>										
Oat (Avena sativa)	Severe crop stunting <sup>2,6,7</sup> ; increased number of weak tillers; reduced tillering <sup>1</sup> ; abortion of florets and sterile flowers <sup>1</sup> ; lower transpiration <sup>2</sup> ; chlorosis <sup>2,6</sup>	Reduced root mass <sup>1</sup> ; lower root:shoot ratio <sup>2</sup>	Often turn red, orange or purple <sup>1,2,6,7</sup>											
Wheat (Triticum aestivum)	Crop stunting <sup>5,6,8</sup> ; increased number of undeveloped tillers <sup>5</sup> ; abortion of florets and sterile flowers <sup>1,9</sup> ; reduced tillering <sup>1,4,9</sup> ; delayed maturity <sup>5</sup> ; shrivelled grain <sup>9</sup> ; chlorosis <sup>6</sup> ; reduced chlorophyll content <sup>5</sup>	Reduced root length <sup>3</sup> ; lower root:shoot ratio <sup>3</sup> ; reduced root mass <sup>1,4</sup>	Often turn yellow or red (especially flag leaf) <sup>1,6,7,8</sup> ; leaf yellowing can vary between cultivars from minimal to severe with chlorosis											
<sup>1</sup> Agrios (2005).														
<sup>2</sup> Erion and Riedell (2	012).													
<sup>3</sup> Hoffman and Kolb (	1997).													
<sup>4</sup> Vandegeer et al. (20	016).													
<sup>5</sup> Moreno-Delafuente	e et al. (2020).													
	1987), Kojima et al. (1983).													
<sup>7</sup> Doodson and Saund	ders (1970).													
<sup>8</sup> Liang et al. (2019).														
<sup>9</sup> Smith and Sward (1	982).													

<sup>10</sup>Kiesling (1985).

(Esau, 1957), which can disrupt differentiation and development of cellular organelles in infected phloem cells (Jensen, 1969), resulting in stunted growth and eventual necrosis of infected cells (Esau, 1957), culminating in the symptoms detailed in Table 1. Persistent infestation with virus-carrying vectors can increase the severity of disease observed (Liang et al., 2019).

## **1.2** | The aphid vectors and virus species of economic importance

There are many cereal aphid species that can vector YDV, and a summary of the species of economic importance is provided in Table 2. There is significant biological diversity within YDV species, with multiple variants described for each species. In total, there are around seven described BYDV species, two CYDV species, one MYDV species, one WYDV species, and a related species that is currently unassigned a genus (Aradottir & Crespo-Herrera, 2021). Multiple variants for a given virus species can also exist, adding a further level of biological complexity. Furthermore, some virus species are vectored by multiple aphid species (e.g., *R. padi, S. avenae, M. dirhodum*, and *Sitobion. fragariae* are vectors of BYDV-PAV and BYDV-MAV) whereas other species are primarily vectored by one or two aphid species (e.g., Schizaphis graminum, S. avenae, and BYDV-GAV). This indicates that there are several compatible (competent or efficient) and incompatible (incompetent or inefficient) vector-virus combinations within the aphid-YDV system. The mechanisms behind this vector-variant specificity are believed to involve compatible and incompatible interactions between different virus variants and the basal lamina of the salivary gland of a given vector species, leading to selective uptake of the virus by the vector (Gildow & Gray, 1993); selectivity can also occur in the midgut and hindgut (Gray et al., 2014). Specific proteins are also thought to aid virus uptake and retention and contribute toward transmission efficiency (Cilia, Howe, et al., 2011; Wang et al., 2015). Vector (aphid) and host (plant) proteins can also interact to influence virus uptake and transmission (Cilia et al., 2012). However, the evolutionary mechanism behind high specificity and selectivity, particularly within different variants of a virus species, is unclear.

Note that the International Committee on Taxonomy of Viruses (ICTV) is currently reassigning and renaming multiple virus species (Walker et al., 2022), including many plant viruses. Several YDV species have been updated, and where taxonomy has been recently revised the new genus and species name are provided in Table 2.

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 TABLE 2
 Overview of the main vectors of each yellow dwarf virus species.

Virus species	Virus strain (updated name, if applicable)	Main vectors (average transmission efficiency >10%)	References
Barley yellow dwarf virus (Tombusviridae, Luteovirus)	BYDV-PAV (Luteovirus pavhordei)	Rhopalosiphum padi, Sitobion avenae, Sitobion miscanthi, Sitobion fragariae,ª Metapolophium dirhodum, Schizaphis graminum	Bencharki et al. (2000), Creamer and Falk (1989), Farrell and Sward (1989), Guo et al. (1996), Papura et al. (2002), Parizoto et al. (2013), Quillec et al. (1995), Sadeghi, Dedryver, and Gauthier (1997), Schliephake et al. (2013), Yu et al. (2022)
	BYDV-MAV (Luteovirus mavhordei)	S. avenae, S. fragariae, <sup>a</sup> M. dirhodum, S. graminum <sup>b</sup>	Creamer and Falk (1989), Farrell and Sward (1989), Gray et al. (2002), Guo et al. (1997a), Halbert et al. (1992), Quillec et al. (1995), Schliephake et al. (2013)
	BYDV-PAS (Luteovirus pashordei)	Rhopalosiphum maidis, <sup>a</sup> R. padi, <sup>a</sup> S. avenae, <sup>a</sup> M. dirhodum <sup>a</sup>	Jarošová et al. (2013)
	BYDV-GAV	S. graminum, S. avenae	Du et al. (2007)
	BYDV-OYV	Vector not reported	Bisnieks et al. (2004), Sõmera et al. (2021)
	ker-II (Luteovirus kerbihordei)	R. padi <sup>a</sup>	Svanella-Dumas et al. (2013)
	ker-III (Luteovirus kertrihordei)	R. padi <sup>a</sup>	Svanella-Dumas et al. (2013)
Cereal yellow dwarf virus (Solemoviridae, Polerovirus)	CYDV-RPV	R. padi, S. graminum, S. avenae <sup>c</sup>	Creamer and Falk (1989), Gray et al. (2007), Guo et al. (1997a), Halbert et al. (1992), Schliephake et al. (2013), Tamborindeguy et al. (2013)
	CYDV-RPS	R. padi <sup>a</sup>	Minato et al. (2022)
Maize yellow dwarf virus (Solemoviridae, Polerovirus)	MYDV-RMV	R. maidis, R. padi, S. graminum	Gray et al. (2002), Halbert et al. (1992), Lucio- Zavaleta et al. (2001)
Wheat yellow dwarf virus (Solemoviridae, genus unassigned)	WYDV-GPV	R. padi, S. avenae, S. graminum	Du et al. (2007), Wang et al. (2015)
Unassigned (Solemoviridae)	SGV	S. graminum, R. padi, S. avenae, R. maidis $^{\rm c}$	Halbert et al. (1992), Johnson and Rochow (1972), Lei et al. (1995)
Barley virus G (Solemoviridae, Polerovirus)	BVG	R. maidis	Erickson et al. (2023)
Wheat leaf yellowing- associated virus (Solemoviridae, Polerovirus)	WLYaV	Vector not reported	Zhang et al. (2017)

<sup>a</sup>Transmission or infection reported but no efficiency data.

<sup>b</sup>Competent clones identified for some aphid biotypes.

<sup>c</sup>Reported to transmit some variants.

## 1.3 | An overview of virus epidemiology

It is believed that different virus species dominate in different regions, for example in mainland Europe, the United States, China, Algeria and Iran BYDV-PAV is thought to be the most abundant species infecting cereals and is therefore considered to be the most agriculturally important (Adhikari et al., 2020; Boubetra et al., 2023; Liu et al., 2019; Pakdel et al., 2010), whereas in the United Kingdom BYDV-MAV and BYDV-PAV occur at similar levels (Foster et al., 2004) and in Ireland BYDV-MAV is the dominant species (Kennedy & Connery, 2005). However, most monitoring surveys were only conducted over a relatively short time-period (up to three growing seasons) and more up-to-date information for some regions is lacking. Furthermore, YDV incidence is sporadic in nature and the prevalence and dominance of species can vary within regions (Dempster & Holmes, 1995; Henry et al., 1993; Liu et al., 2019), fluctuate between monitoring years (Bisnieks et al., 2006; Liu et al., 2019) and be further influenced by the divergence of new YDV species (Bisnieks et al., 2004; Sõmera et al., 2021). Shifts in the dominance of a given species within a region have also been reported, for example in China BYDV-GAV was the dominant strain for 9 years before BYDV-PAV became predominant (Liu et al., 2019). The dominance of a given species can also vary spatially within a region, for example in Australia, BYDV-PAV is dominant in Victoria but BYDV-MAV is dominant in New South Wales (Milgate et al., 2016; Nancarrow et al., 2018). This sporadic nature of YDV dominance, coupled with a lack of long-term epidemiological studies on YDV prevalence, makes it difficult to state with confidence which species dominates in any given region. Indeed, the lack of long-term YDV epidemiological studies is a significant knowledge gap that potentially restricts and limits the development of sustainable YDV management practices. There are also methodological constraints in virus monitoring that need to be considered. Some diagnostic methods are less sensitive than others, which can lead to an underestimation of risk. Transmission tests are thought to be less sensitive than ELISA (Torrance et al., 1986), which is in turn less sensitive than real-time PCR (Fabre, Kervarrec, et al., 2003). These methodological variations in diagnostic detection can restrict survey impact.

There are multiple factors that could explain the observed variation in species dominance between different regions, including the host-range and prevalence of the main aphid vector, variation in agricultural practices between regions, and the presence (Dempster & Holmes, 1995) and composition (Kendall et al., 1996) of common grassland species within the landscape, especially *Poa* species. An increased proportion of grassland in the landscape can act as a YDV source for migrating aphids (Holland et al., 2021) and increase the risk of YDV infection during the growing season (Rashidi et al., 2020).

## 2 | BIOLOGICAL DIVERSITY WITHIN A VECTOR SPECIES CAN INFLUENCE TRANSMISSION EFFICIENCY

Variation in transmission efficiency for a given YDV species has been identified between competent vector species. Vector species have been ranked in terms of transmission efficiency (Halbert & Pike, 1985; Power et al., 1991), with *R. padi* often classified as the most efficient vector (Halbert & Pike, 1985). This highlights the importance of addressing the composition of the aphid community present within the field when devising YDV management plans, as the local aphid population (or species of aphid that migrates into the field) could greatly influence the YDV risk of a given crop.

There is also evidence that biological diversity within a given vector species can significantly impact virus transmission efficiency. Several studies have reported variation in virus transmission efficiency between clones, genotypes or biotypes of a given aphid vector species (Guo et al., 1997a; Kern et al., 2022; Lucio-Zavaleta et al., 2001). This includes variation in transmission efficiency for BYDV-PAV, BYDV-MAV and CYDV-RPV among *R. padi* and *S. avenae* clones (Guo et al., 1997a). Further variation in transmission efficiency between aphid clones has also been reported for *R. padi* (Bencharki et al., 2000; Guo et al., 1997a; Kern et al., 2022; Sadeghi, Dedryver, & Gauthier, 1997), *S. graminum* (Gray et al., 2007; Tamborindeguy et al., 2013), *Rhopalosiphum maidis* (Lucio-Zavaleta et al., 2001) and *S. avenae* (Bencharki et al., 2000; Guo et al., 1997a). Table 3 provides an overview of the studies that describe variable transmission efficiency between aphid clones or genotypes of a

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given species. Interestingly, intraspecies diversity appears to also influence the success of incompetent vector-virus interactions. For example, *R. padi* is supposedly an inefficient, or incompetent, vector of BYDV-GAV. However, a study examining transmission efficiencies in multiple *R. padi* populations found one clone with high transmission efficiency (52%) and three clones with moderate transmission efficiency (18%–33%) for BYDV-GAV, with 15 additional *R. padi* genotypes unable to transmit BYDV-GAV (Du et al., 2007).

It is unclear what biological factors drive this variation in transmission efficiency. From a biological perspective, variation in transmission efficiency is likely related to either inefficient uptake of the virus by the aphid vector and limited transport across the gut barrier, inefficient transport of virions into the salivary glands, or ineffective transmission of virus particles from the aphid vector into the plant.

## 3 | POTENTIAL MECHANISMS BEHIND VARIABLE VIRUS TRANSMISSION EFFICIENCY

There is significant variation in YDV transmission efficiency between clonal populations for the main YDV vectors (Table 3). Variation in transmission efficiency was identified for different populations for *R. maidis* (5 studies), *R. padi* (15 studies), *S. avenae* (12 studies), *S. miscanthi* (1 study) and *S. graminum* (10 studies). Vectoring efficiency has rarely been examined for *M. dirhodum* or *S. fragariae*, and these two species, alongside *S. miscanthi*, are significantly understudied when compared with the other vectors. Some virus species are also more widely studied than others; both BVG and WLYaV are significantly understudied when comparative transmission studies were found for BVG or WLYaV.

For the cereal aphid species that have been studied in more detail (*R. padi, R. maidis, S. avenae* and *S. graminum*), substantial variation in YDV transmission efficiency between populations within each aphid species was identified. This included variation in transmission efficiency for competent (e.g., *R. padi* and BYDV-PAV; 50%–100%; Du et al., 2007) and incompetent (e.g., *R. padi* and BYDV-GAV; 0%–53%; Du et al., 2007) vector-virus combinations. Below, three mechanisms that potentially drive this variation in transmission efficiency between aphid clones within a given aphid species are proposed (Figure 1).

## 3.1 | Mechanism 1: Nonessential endosymbionts alter vector feeding behaviour to indirectly increase virus transmission

Aphids can form facultative (nonessential) relationships with a range of bacterial endosymbionts that confer a diverse range of traits to the aphid (Zytynska et al., 2021). Multiple facultative endosymbionts have been described to associate with aphids, and eight of these endosymbiont species have been detected in cereal aphids: *Fukatsuia symbiotica*, *Hamiltonella defensa*, *Regiella insecticola*,

TABLE 3 Overv	Overview of the variation in transmission efficiency between clones of a given aphid species.	n efficiency betwe	en clones of	a given aphid s	oecies.		
Aphid species	Study	Aphid morph	Plant species	YDV species	Number of clones examined	The range of transmission efficiencies (%)	Notes
Rhopalosiphum maidis	Saksena et al. (1964)	Apterous	Oat	Not specified	4	28-87	Used one genotype/clone to examine vector transmission efficiency for multiple virus variants in more detail
	Brumfield et al. (1992)	Not specified	Oat	MYDV-RMV	5	19-77	Compared four virus variants
				CYDV-RPV	4	0	
				BYDV-MAV	4	0-2	
				BYDV-PAV	4	0	
				SGV	4	0	
	Rochow and Eastop (1966)	Mixed	Oat	BYDV-MAV	2	0	
				CYDV-RPV		0	
				MYDV-RMV		83-100	
				BYDV-PAV		0-2	
	Gill (1972)	Apterous	Oat	Not specified	ო	3-18	Compared two virus variants
		Nymph				38-58	
	Lucio-Zavaleta et al. (2001)	Nymph	Oat	MYDV-RMV	7	0-95	Compared 10 virus variants
Rhopalosiphum	Rochow and Eastop (1966)	Mixed	Oat	BYDV-MAV	2	0	
padi				CYDV-RPV		48-62	
				MYDV-RMV		2-21	
				BYDV-PAV		69-73	
	Guo et al. (1996)	Apterous	Barley	BYDV-PAV	6	11-96	Compared three variants
		Alate				9-76	
	Price et al. (1971)	Not specified	Oat	BYDV-MAV	6	0-10	
				BYDV-PAV		100	
				CYDV-RPV		100	
	Guo et al. (1997a)	Apterous	Barley	BYDV-PAV	2	35-87	Competent combination
		Apterous		BYDV-MAV		0-10	Incompetent combination
		Apterous		CYDV-RPV		32-62	Competent combination
	Guo et al. (1997b)	Apterous	Barley	BYDV-PAV	21	26-93	Examined transmission efficiency in 20 <i>R. padi</i> clones collected from France and one clone collected from China

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	Notes	48h acquisition; 6h inoculation	48h acquisition; 120h inoculation	6h acquisition; 6h inoculation.	6h acquisition; 24h inoculation	6h acquisition; 120h inoculation	Compared two variants	Examined the impact infection with the aphid	virus, Rhopalosiphum padi virus (RhPV)	assessed how aphid abundance affected	transmission efficiency. Data presented in the table represent the range across RhPV- uninfected aphids									Used the most and least efficient clones to examine how acquisition access period affects transmission efficiency	Compared efficiencies over a temperature range: 5°C	Compared efficiencies over a temperature range: 10°C	Compared efficiencies over a temperature range: 15°C	Compared 10 virus variants	(Continues)
	The range of transmission efficiencies (%)	45-80	80-100	0-10	0-40	50-85	6–58	75-100	0	0	50-100	99-100	99-100	10-73	0-2	0	100	80-100	0-100	20-38	39-61	62-80	80-86	0-29	
	Number of clones examined	20					5	2				2					6			10	7			4	
	YDV species	BYDV-PAV					BYDV-MAV	CYDV-RPV	MYDV-RMV	BYDV-MAV	BYDV-PAV	BYDV-PAV	CYDV-RPV	MYDV-RMV	BYDV-MAV	SGV	BYDV-PAV	CYDV-RPV	Mixed BYDV- MAV/ PAV	BYDV-PAV	BYDV-PAV			MYDV-RMV	
	Plant species	Barley					Barley	Oat				Oat					Barley			Oat	Wheat			Oat	
	Aphid morph	Apterous					Nymph	Not specified				Mixed					Not stated			Not stated	Apterous			Nymph	
	Study	Sadeghi, Dedryver, and	Gauthier ( <mark>1997</mark> )				Sadeghi, Dedryver, Riault, et al. (1997)	Gildow and D'Arcy (1988)				Gray et al. (1998)					Habekuss et al. (1999)			Bencharki et al. (2000)	Smyrnioudis et al. (2001)			Lucio-Zavaleta et al. (2001)	
	Aphid species																								

TABLE 3 (Continued)

BYDV-PAV BYDV-GAV WYDV-GPV
BYDV-PAV
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сүри-кри МҮDV-RMV
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BYDV-MAV
CYDV-RPV
BYDV-PAV
BYDV-PAV

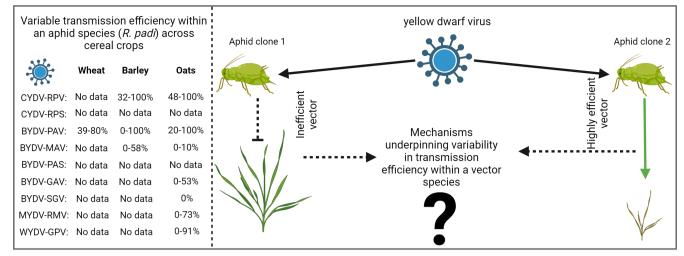
TABLE 3 (Continued)

ΞΥI	BOURNE										Pla	nt P	atho	log	y men	national Journal sh Boolety for M			-V	<b>V</b> 11	LE`	Y  (se
	Notes	Produced $F_1$ clones by selfing a clone with poor transmission efficiency; used a subset of clones to examine transmission efficiency of other PAV variants	Used a subset of clones to also examine transmission efficiency of other PAV variants; developed $F_1$ progeny by crossing aphids with contrasting BYDV transmission phenotypes	Used one genotype/clone to examine vector transmission efficiency for multiple virus variants in more detail	Compared two variants	Compared different acquisition and inoculation periods. Also speculated on the potential role of endosymbionts in transmission success	Compared two variants. Examined effect removing endosymbionts had on the inhibition of virus transmission										Examined transmission efficiency in wild grass-	adapted and agricultural crop-adapted	Diotypes			(Continues)
	The range of transmission efficiencies (%)	0-88	3-92	11-68 50-100 0-57	23-66	8- O	2-61	0	33-38	0-8	8-12	3–36	3-37	16	0-1	388	2-85	0-57	0-38	8-72	0-87	
	Number of clones examined	39	44	12 12 12	14	4	7	2				2					6					
	YDV species	BYDV-PAV	BYDV-PAV	BYDV-PAV BYDV-GAV WYDV-GPV	BYDV-PAV	BYDV-PAV	BYDV-PAV	BYDV-MAV	CYDV-RPV	MYDV-RMV	BYDV-PAV	BYDV-PAV	CYDV-RPV	MYDV-RMV	BYDV-MAV	SGV	SGV	BYDV-PAV	BYDV-MAV	MYDV-RMV	CYDV-RPV	
	Plant species	Barley	Barley	Oat	Wheat	Wheat	Wheat	Oat				Oat					Oat					
	Aphid morph	hqmyN	hqmyN	Not stated	Nymph	Apterous	Nymph	Mixed				Nymph					Adult					
	Study	Papura et al. (2002)	Dedryver et al. (2005)	Du et al. (2007)	Yu et al. (2013)	Alkhedir et al. (2015)	Yu et al. (2022)	Rochow and Eastop (1966)				Gray et al. (1998)					Gray et al. (2002)					
	Aphid species						Sitobion miscanthi	Schizaphis	graminum													

TABLE 3 (Continued)

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	Notes	Compared transmission efficiencies between a competent clone, an incompetent clone, and subsequent progeny generated by crossing these clones ( $F_1$ and $F_2$ ). Identified barriers preventing transmission in incompetent parent and nonvector progeny	Produced 89 F <sub>1</sub> S. graminum genotypes from parents with contrasting transmission efficiency to correlate genetic diversity with virus transmission efficiency	Used one genotype/clone to examine vector transmission efficiency for multiple virus variants in more detail	Identified proteins associated with transmission success in competent aphid clones	Identified barriers to CYDV transmission in incompetent clones	Identified a vectoring allele associated with high transmission efficiency
	The range of transmission efficiencies (%)	0-80+ 0-80+	2-35 7-63	0-36 41-84 62-100	0-88	0-100	0-75
	Number of clones examined	Multiple Multiple	2	7	ω	10	11
	YDV species	CYDV-RPV SGV	BYDV-PAV CYDV-RPV	BYDV-PAV BYDV-GAV WYDV-GPV	CYDV-RPV	CYDV-RPV	CYDV-RPV
	Plant species	Oat	Wheat Wheat	Oat	Barley	Barley	Oat
	Aphid morph	Adult	Nymph Nymph	Not stated	Not stated	Not stated	Not stated
nued)	Study	Burrows et al. (2006, 2007)	Gray et al. (2007)	Du et al. (2007)	Yang et al. (2008)	Cilia, Tamborindeguy, et al. (2011)	Tamborindeguy et al. (2013)
TABLE 3 (Continued)	Aphid species						



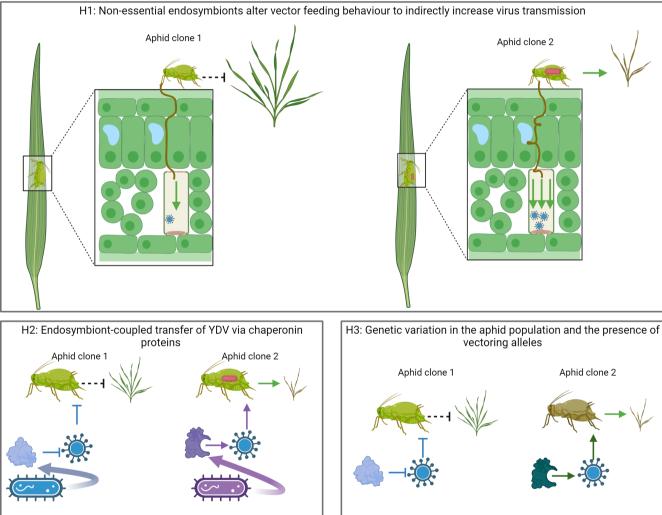


FIGURE 1 Graphical representation of the three proposed mechanisms (hypotheses) underpinning variability in virus transmission efficiency. H1: Nonessential (facultative) endosymbionts alter vector feeding behaviour to indirectly increase virus transmission. Uninfected aphids display routine interactions with the host plant whereas aphids infected with a facultative endosymbiont show a greater number of cellular punctures and an increase in phloem ingestion (Leybourne, Valentine, et al., 2020). H2: Endosymbiont-coupled transfer of YDV via chaperonin proteins. H3: Genetic variation in the aphid population and the presence of vectoring alleles. Image was created in bioRender (biorender.com).

Rickettsia spp., Ricketsiella spp., Aresnophonus spp., Serratia symbiotica and Spiroplasma spp. (Guo et al., 2019; Leybourne et al., 2023; Leybourne, Bos, et al., 2020; Zytynska et al., 2023). In cereal aphids these endosymbionts can occur individually or co-occur alongside other endosymbionts in a range of multi-infections (Leybourne et al., 2023; Zytynska et al., 2023). Infection frequencies of these nonessential endosymbionts are highly variable and generally range from 0% to 80%, depending on the endosymbiont and aphid species (Guo et al., 2019; Henry et al., 2015; Leybourne et al., 2023; Leybourne, Bos, et al., 2020; Zytynska et al., 2023). When present, facultative endosymbionts can have a significant impact on aphid phenology, providing beneficial traits that include protection against parasitism (Leybourne, Bos, et al., 2020). Facultative endosymbionts occasionally confer fitness consequences to the host aphid, including lower fecundity (Zytynska et al., 2021) and reduced growth (Leybourne, Bos, et al., 2020).

Facultative endosymbionts can also modulate the probing and feeding behaviour of cereal aphids (Leybourne, Valentine, et al., 2020), with potential consequences for virus acquisition and transmission. Previous research using the electrical penetration graph (EPG) technique to monitor aphid probing and feeding behaviour has shown that the presence of a facultative endosymbiont, H. defensa, in R. padi can alter aphid feeding behaviour (Leybourne, Valentine, et al., 2020). This included altering behavioural traits that are involved in virus transmission, such as phloem contact. These behaviours could increase the vectoring capacity of endosymbiontinfected aphids by making them more efficient at acquiring and transmitting the virus (Figure 1).

Due to this observation, the impact of endosymbiont infection on virus acquisition, retention and transmission of YDV should be a key area of future research. However, to date there has been limited examination of the influence facultative endosymbionts have on aphid-virus interactions; only three studies have examined how endosymbionts influence aphid-YDV interactions (Alkhedir et al., 2015; Chirgwin et al., 2024; Yu et al., 2022). Yu et al. (2022) provide anecdotal evidence that suggests the endosymbiont Rickettsia spp. is important for efficient BYDV-PAV transmission in Sitobion miscanthi. By selectively removing facultative endosymbionts, including Rickettsia spp., from aphid clones through antibiotic treatment, Yu et al. (2022) showed that the vectoring capacity of two S. miscanthi populations was reduced. Alkhedir et al. (2015) examined BYDV-PAV transmission efficiency in four S. avenae clones with differing levels of genetic and endosymbiotic diversity, and Chirgwin et al. (2024) show that R. padi harbouring Rickettsiella viridis have a higher BYDV-PAV density than aphids that lack R. viridis. However, in these studies, the authors were unable to disentangle vector genotype effects from facultative endosymbiont effects, and no study examined the potential role endosymbiont presence had on aphid feeding behaviour and the impact of this on BYDV transmission. Therefore, the proposed first mechanism remains purely hypothetical and requires experimental examination. Studies have examined endosymbiont-aphid-virus interactions in other aphidvirus systems (Angelella et al., 2018; Sanches et al., 2023), including

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for another persistent plant virus, the pea enation mosaic virus, where facultative endosymbionts were implemented in the modulation of plant-aphid-virus interactions including increased virus transmission in H. defensa-infected aphids (Sanches et al., 2023).

#### Mechanism 2: Endosymbiont-coupled 3.2 transfer of YDV via chaperonin proteins

All aphids form an essential relationship with the obligate endosymbiont Buchnera aphidicola. B. aphidicola is retained in specialized cells, bacteriocytes, within the aphid tissue (Braendle et al., 2003). The obligate nature of the aphid-B. aphidicola relationship stems from the provision of essential amino acids, particularly those often lacking in the phloem sap, to the aphid from B. aphidicola (Wilson et al., 2010). Several studies have suggested that B. aphidicola plays a pivotal role in virus-vector interactions. Specifically, it has been suggested that B. aphidicola facilitates the retention of Tombusviridae (previously classified as Luteoviridae) within vector populations via coupling of virus particles to the B. aphidicola-derived chaperonin proteins GroEL (van den Heuvel et al., 1997) or SymL (Filichkin et al., 1997). This coupling between B. aphidicola chaperonins and plant viruses has been reported for several viruses previously classified as Luteoviridae, including BYDV-PAV (Filichkin et al., 1997), pea enation mosaic virus (Solemoviridae, Enamovirus), beet western yellows virus (Solemoviridae, Polerovirus; van den Heuvel et al., 1997), and potato leafroll virus (Solemoviridae, Polerovirus; van den Heuvel et al., 1994). Therefore, variation in YDV transmission efficiency between aphid clones within a given aphid species could be associated with variability in *B. aphidicola* titre between the aphid clones, with a greater B. aphidicola titre resulting in greater chaperonin production that increases the acquisition, and indirectly the transmission, efficiency of the vector.

However, evidence of the potential role B. aphidicola-derived chaperonins play in YDV transmission is not consistent. Experiments using immunoblotting and immunocytochemistry in R. padi have found no direct evidence of binding or other potential interactions between YDV and B. aphidicola-derived GroEL (Bouvaine et al., 2011) and BYDV-MAV did not bind to GroEL homologues identified in S. avenae (Li et al., 2001). This is in contrast with earlier observations of GroEL-virus interactions with other viruses (Filichkin et al., 1997; van den Heuvel et al., 1997). Li et al. (2001) identified alternative non-GroEL proteins of B. aphidicola that play an important role in binding BYDV-MAV in S. avenae, and Cilia, Tamborindeguy, et al. (2011) identified other B. aphidicola-derived factors that potentially influence transmission efficiency of CYDV-RPV in S. graminum. Therefore, genetic variation within B. aphidicola strains could alter the binding capacity of these factors and influence YDV acquisition and transmission efficiency, although this needs to be examined.

One other potential symbiont-derived mechanism, which complements the mechanism proposed above, is the potential role of nonessential (facultative) endosymbionts and chaperonin proteins derived from these endosymbionts. There is evidence for this in

other plant virus vectors (Rana et al., 2012; Su et al., 2013) and this has been proposed for YDV vectors (Bouvaine et al., 2011) but not directly explored. Bouvaine et al. (2011) proposed an alternative GroEL mechanism whereby differential interactions between BYDV and bacterial GroEL derived from facultative endosymbionts, not the essential endosymbiont B. aphidicola. Facultative endosymbionts can contribute toward virus transmission in other virus vectors (Pinheiro et al., 2015), including transmission of tomato yellow leaf curl virus (Geminiviridae, Begomovirus) and cotton leaf curl virus (Geminiviridae, Begomovirus) in the whitefly Bemisia tabaci (Rana et al., 2012; Su et al., 2013). This could be an endosymbiont-derived mechanism that increases transmission efficiency via a combination of (a) increased likelihood of YDV acquisition and transmission in facultative endosymbiont-infected vectors through heightened interactions with the plant phloem by the aphid vector, and (b) greater uptake of YDV virions into the salivary gland in facultative endosymbiontinfected vectors via the chaperonins of facultative endosymbionts (Figure 1). However, this requires further investigation.

#### Mechanism 3: Genetic variation in aphid 3.3 populations and the role of vectoring alleles

An observation made in S. avenae found that transmission efficiency (BYDV-PAV; 3%-92%) varied between aphid genotypes, with the high transmission phenotype found to have a high level of heritability (Dedryver et al., 2005). The molecular mechanisms underpinning this genotype-driven variation in transmission efficiency are unclear; however, significant insight into potential genetic traits that influence YDV transmission efficiency has been gained in S. graminum (Burrows et al., 2006, 2007; Gray et al., 2007; Tamborindeguy et al., 2013; Yang et al., 2008). This has primarily been achieved by crossing low (incompetent) and highly efficient (competent) parents to generate  $F_1$  and  $F_2$  populations (Gray et al., 2007; Tamborindeguy et al., 2013) and supplementing these observations with comparative quantitative proteomics to identify key biological drivers determining YDV transmission efficiency (Cilia, Tamborindeguy, et al., 2011; Yang et al., 2008).

A "vectoring" allele of the cyclophilin gene has been identified as a key genetic trait driving variable YDV transmission in S. graminum (Tamborindeguy et al., 2013). Cyclophilin proteins are involved in multiple cellular and biological processes, including cell signalling, immune response and protein trafficking. Cyclophilin proteins also play an important, and diverse, role in virus-host and virus-vector interactions. Cyclophilin A was shown to directly interact with CYDV-RPV (Tamborindeguy et al., 2013; Yang et al., 2008). Although the direct role of cyclophilin A is unknown, Tamborindeguy et al. (2013) proposed that the protein facilitates CYDV-RPV transport across the aphid hindgut. Allelic variation in the cyclophilin gene could underpin variable YDV transmission between aphid clones in other vector species; however, this would require direct examination for each vector species. Similar interactions between vector-derived cyclophilin proteins and plant viruses have been described in other

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plant virus vectors, including the western flower thrips, Frankliniella occidentalis, where cyclophilin interacts with a structural glycoprotein of tomato spotted wilt virus (Bunyaviridae, Orthotospovirus; Badillo-Vargas et al., 2019). This glycoprotein is thought to facilitate virus entry into vector cells, including interaction with the thrips gut (Montero-Astúa et al., 2014; Whitfield et al., 2007). Badillo-Vargas et al. (2019) proposed that F. occidentalis cyclophilin facilitates ribonucleoprotein packing into tomato spotted wilt virus particles. It should be noted that tomato spotted wilt virus is capable of propagating within the host, whereas YDVs cannot; therefore, the exact interactions between the virus and the vector could differ.

Vector-derived proteins can also restrict virus binding with vector tissue and influence virus transmission efficiency (Cilia, Tamborindeguy, et al., 2011). Several proteins have been identified that are thought to interact with YDV virions, including CoA ligase, a cuticle protein and Troponin-T (Cilia, Tamborindeguy, et al., 2011). Several of these proteins have been predicted to interact with the aphid hindgut or accessory salivary gland (Cilia, Tamborindeguy, et al., 2011), with binding of these proteins to the hindgut proposed to act as a barrier against virus acquisition and binding to the aphid accessory salivary gland acting as a barrier against virus transmission (Burrows et al., 2006; Cilia, Tamborindeguy, et al., 2011). Similar proteins were identified to interact with WYDV-GPV in R. padi (Wang et al., 2015), and putative cuticle proteins were identified as differentially abundant in viruliferous and nonviruliferous aphids in R. padi and S. graminum (Cilia, Tamborindeguy, et al., 2011; Wang et al., 2015). Differential regulation and abundance of putative cuticular proteins in YDV-carrying aphids (Cilia, Tamborindeguy, et al., 2011; Wang et al., 2015) suggests that these proteins are potentially involved in facilitating virus interactions with vector tissue, as proposed by Wang et al. (2015). Additional molecular drivers include several proteins detected to be differentially regulated between competent and incompetent clones, including putative proteins present in the gut and the accessory salivary gland (Cilia, Tamborindeguy, et al., 2011). Similar work using an  $F_1$  population in S. avenae highlighted analogous proteins potentially involved in variable transmission efficiency of BYDV-PAV (Papura et al., 2002). Therefore, structural changes to these proteins (potentially via allelic variation within these genes, as reported for cyclophilin) could interfere with vector-virus interactions and influence virus uptake into vector tissue (Figure 1).

Genetic diversity within vector populations could significantly contribute toward YDV transmission efficiency. These insights primarily derive from one vector species, S. graminum, with supporting evidence in R. padi (Wang et al., 2015) and S. avenae (Papura et al., 2002). Further exploration of the underlying genetic factors that drive variable YDV transmission efficiency in other vector-virus combinations is required. However, the work in S. graminum has produced important insights that can be further explored in other vector-virus combinations, including (a) the presence of genetic loci and alleles that influence and determine transmission efficiencies, including cyclophilin vectoring alleles (Gray et al., 2007; Tamborindeguy et al., 2013; Yang et al., 2008) and (b) the impact barriers at the aphid

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hindgut and accessory salivary gland have on the uptake of YDV virions and the role they play in transmission efficiency, especially in restricting virus acquisition and transmission in incompetent clones (Burrows et al., 2006, 2007; Cilia, Tamborindeguy, et al., 2011).

## 4 | CONCLUSIONS

Understanding how biological variation in vector populations influences virus transmission efficiency can help to identify biological traits that underpin successful virus transmission in competent vector populations. Here, the available literature on YDV transmission efficiency is synthesized and significant variation in YDV transmission efficiency is detected in different populations for several vector species, including R. padi, R. maidis, S. avenae and S. graminum. Other vector species including M. dirhodum, S. miscanthi and S. fragariae are, comparatively, understudied and under-represented when compared with the other vector species. There are also significant knowledge gaps for transmission efficiency for each vector-virus combination across the main crop species (Table 3), as visualized for R. padi in Figure 1. Aphid endosymbionts and genetic traits within vector populations are potential drivers behind this biological variation in transmission efficiency, and recent modelling studies have attempted to disentangle these complex relationships (Enders & Hefley, 2023). Three biological mechanisms are proposed that potentially drive these variations in virus transmission efficiency within these vector populations, and it is recommended that these are investigated in future studies: (a) nonessential endosymbionts alter vector feeding behaviour to indirectly increase virus transmission, (b) endosymbiont-coupled transfer of YDV via chaperonin proteins. and (c) genetic variation in aphid populations and the role of vectoring alleles.

## 5 | LITERATURE SEARCH METHOD

The keywords "Barley OR Cereal" and "Yellow dwarf virus" and "Transmission" were used to search for BYDV and CYDV studies; the keywords "Maize" and "Yellow dwarf virus" and "Transmission" were used to search for MYDV studies; "Wheat" and "Yellow dwarf virus" and "Transmission" were used to search for WYDV studies; the search term for BVG comprised "Barley Virus G" and "Transmission"; and WLYV studies were searched for using the terms "Wheat leaf yellow virus" and "Transmission". The Web of Science and Scopus databases were used to conduct the literature search, with review articles and book chapters excluded. Duplicates were identified and removed by screening article titles and doi's in R (v. 4.3.0) using the R package revtools (v. 0.4.1) (Westgate, 2019). This filtered dataset was checked manually and any further duplicates were removed. This process yielded 392 articles. Of these articles, 278 described a YDV study with 81 reporting on YDV transmission. This database was used to compile information on variation in YDV transmission efficiencies between clones, genotypes or biotypes of a given vector

species that was used to screen articles for inclusion in Table 3. A full list of studies is provided in Table S1.

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## CONFLICT OF INTEREST STATEMENT

The author declares that he has no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

## DATA AVAILABILITY STATEMENT

Data sharing is not applicable to this article as no datasets were generated or analysed during the current study.

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## SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

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