

Supporting Information

Luque *et al.* 10.1073/pnas.0808498106

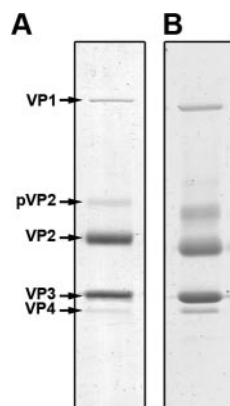


Fig. S1. Analysis by SDS/PAGE and autoradiography (A) or Coomassie blue stain (B) of E5 population virions. Protein profiles for E2, E3, E4, and E6 populations are similar. Bands corresponding to proteins VP1, pVP2, VP2, VP3, and VP4 are indicated.

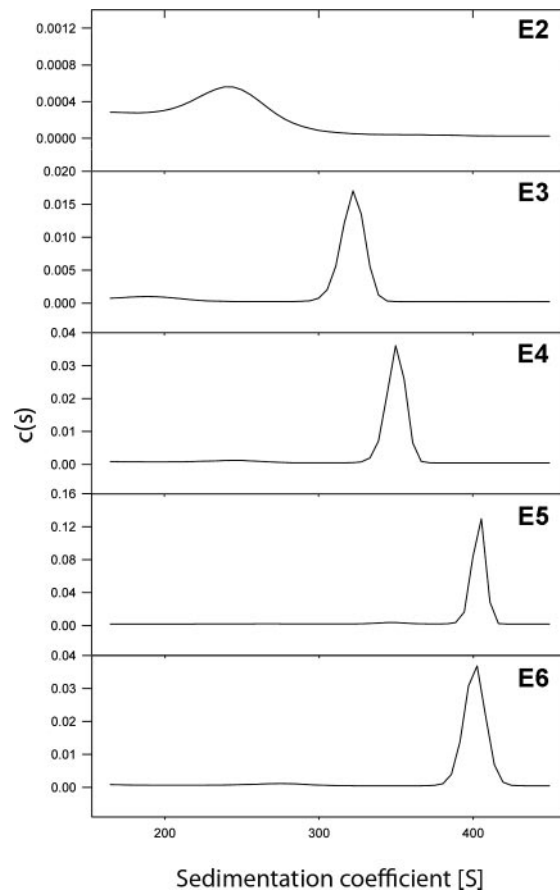


Fig. S2. Sedimentation velocity analysis of IBDV populations. Apparent sedimentation coefficient distribution, $c(s)$, of E2-E6 IBDV particles obtained from sedimentation velocity taken at $8,000 \times g$ and 20°C .

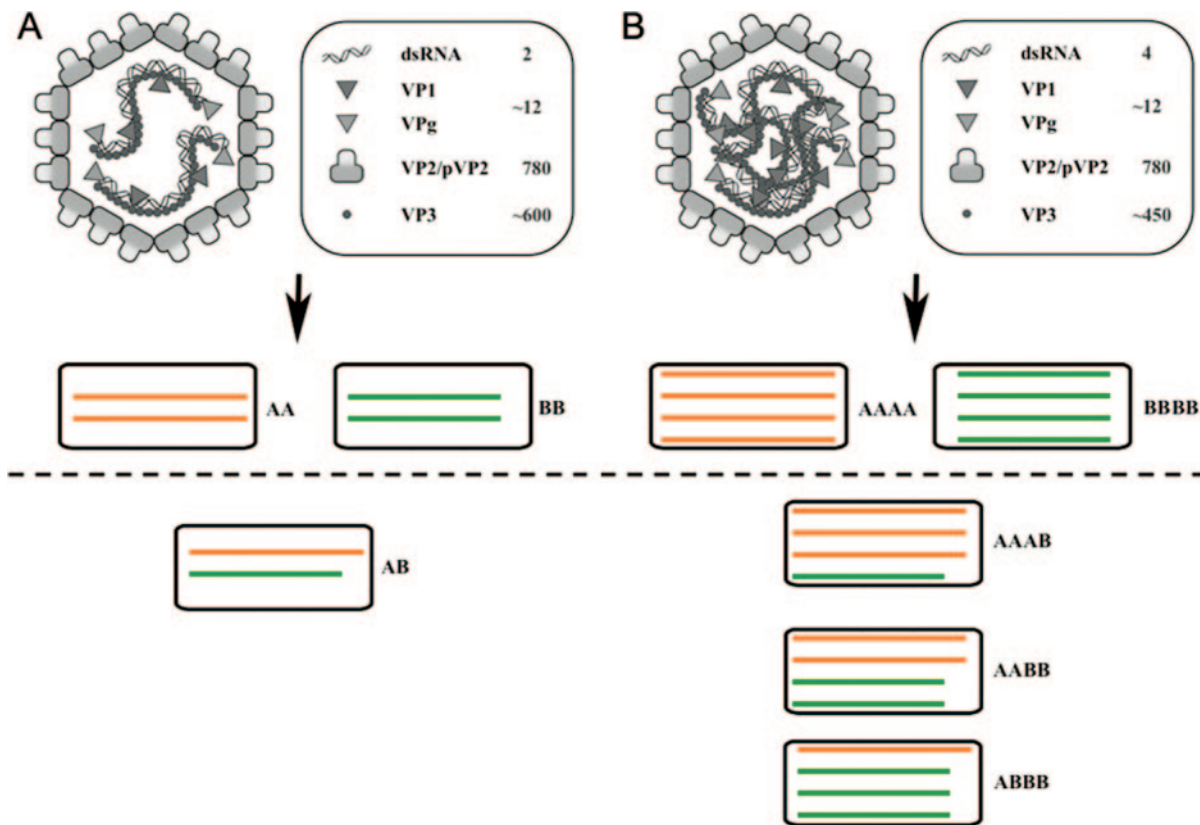


Fig. S3. Haploidy versus polyploidy in IBDV. (A) Scheme representing the standard IBDV model with its estimated stoichiometry for the structural components (Right). Note that the virion is haploid (2 dsRNA segments, 1 copy each of A and B, inside the capsid). If all progeny virion particles contain 2 dsRNA segments (i.e., E3 particles), a random packaging mechanism implies that 66% of the viral progeny is noninfectious (particles AA and BB, Upper). Only particles containing a copy of segment A and one of segment B are infectious (particles AB, Lower). The particle-to-infectivity ratio is relatively low ($\text{pfu/pp} = 0.33$). (B) Scheme showing the new IBDV model with its associated stoichiometry (Right), as deduced from this and other studies. A polyplloid virion with four packaged dsRNA segments is shown as E5 and E6 IBDV particles. In this scenario, only particles AAAA and BBBB (Upper), accounting for 40% of the viral progeny, are defective. All other combinations result in infectious particles (Lower), and generation of an infectious particle is three times more likely. A similar calculation can be made for E4 particles, which package three dsRNA segments (50% are non-infectious, i.e., AAA and BBB particles; the other 50% are infectious, i.e., AAB and BBA particles). Note that the larger the number of segments packaged, the greater the chance of a full genome complement, hence more infectious particles.

Table S1. Genome packaging densities in dsRNA viruses^a

Virus family	dsRNA features					Inner capsid features					dsRNA density, bp/100 nm ³
	No. of segments	Size ^d , kbp	MW ^e , MDa	Length ^f , μm	Packed dsRNA spacing, nm ^g	T	RdRPs copy no.	φ ^h , nm	r ⁱ (nm)	V ⁱ , nm ³	
HSV	1	≈152	103.7	51.4	2.6	—		≈60	43.0	333.000	46
Reoviridae											
Orthoreovirus	10	≈23.5	16	7.0	2.6	2	12	≈60	24.5	61,600	38
Rotavirus	11	≈18.5	12.6	5.6	2.5–3.0	2	12	≈52	23.5	54,400	34
Orbivirus	10	≈19.2	13.1	5.8	3.0	2	12	≈52	22.0	44,600	43
Aquareovirus	11	≈23.6	16.0	7.1		2	12	≈60	23.0	51,000	46
Phytoreovirus	12	≈25.7	17.5	7.7		2	12	≈57	26.0	73,600	35
Cypovirus	10	≈31.4	21.4	9.5	2.5	2	12	≈58	24.0	57,900	54
Cystoviridae, phage φ6	3	≈13.4	9.1	3.4		2	12	≈50	20.0	33,500	40
Totiviridae, L-A	1	≈4.6	3.1	1.3	3.6–4.0	2	1	≈43	17.0	20,600	22
Chrysoviridae, PcV	1 (4) ^c	≈3.2 (12.6)	2.2 (8.6)	0.9 (3.5)	4.0*	1	1/2	≈40	16.0	17,150	19
Patitviridae, PsV-S	1 (2)	≈1.7 (3.3)	1.2 (2.2)	0.5 (0.9)		2	1	≈35	12.0	7,240	23
Birnaviridae											
IBDV, T = 13 capsid						NP ^b	12	≈65	26.5	77,900	
1 genome	2	≈6.0	4.1	1.8	6.1*						10
2 genomes	4	≈12.0	8.2	3.6	4.3*						20
IBDV, T = 7 capsid	2	≈6.0	4.1	1.8	2.9*			≈55	18.1	24,400	31

^aData reviewed in Castón *et al.* [Castón JR, *et al.* (2003) Three-dimensional structure of *Penicillium chrysogenum* virus: A double-stranded RNA virus with a genuine T=1 capsid. *J Mol Biol* 331:417–431].

^bNP, not present.

^cPcV dsRNA features: the genome is formed by 4 dsRNA molecules, but an average value was calculated for each column since there is a dsRNA molecule/particle.

^dData taken from Virus taxonomy: classification and nomenclature of viruses. Seventh Report of the International Committee on Taxonomy of Viruses.

^eMW were calculated assuming a mass of 682 Da/bp.

^fLength were calculated assuming 3 Å axial rise per bp for members of the family *Reoviridae*, 2.56 Å for phage φ6, and 2.81 Å for L-A and PcV dsRNAs. HSV dsDNA is assumed to have a B-form structure (3.38 Å/bp).

^gMeasurements were mostly obtained from cryo-EM and 3DR studies and represent average Bragg spacings. An * denotes estimated values. The corresponding interstrand spacings are calculated by introducing the factor (2/√3), if strands exhibit a quasi-hexagonal packing.

^hOuter diameter.

ⁱInner radius.

^jVolume when a perfect sphere is assumed and any other internal components are ignored.

Table S2. Infectivity of E1-E6 IBDV populations

IBDV population	%, wt/wt ^a	[pp/pfu] ^b	[pfu/totalpp] ^c	[pfu/totalpfu] ^d
E1	3	7000	0,0004	0,004
E2	5	7000	0,0007	0,006
E3	12	100	0,1200	1,080
E4	16	50	0,3200	2,881
E5	48	6	8,0000	72,021
E6	16	6	2,6667	24,007

^aFraction (wt/wt) of each population: [physical particle/total physical particle] ([pp/totalpp]).

^b[pp/pfu] ratios deducted by titration of IBDV populations.

^c[pfu/totalpp] = [pp/totalpp]/[pp/pfu]; Σ (E1-E6) [pfu/totalpp] = [totalpfu/totalpp] = 11,1078.

^d[pfu/totalpfu] = [pfu/totalpp]/[totalpfu/totalpp]; Σ (E1-E6) [pfu/totalpfu] = 100.