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Proposal for a Uniform Nomenclature for Defective Interfering Viruses of Vesicular Stomatitis Virus

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Defective interfering particles of vesicular stomatitis virus have been named according to their parental derivation and to their genomic length and physical properties. This suggested uniform nomenclature can be adapted for other virus systems.

Defective interfering (DI) particles are found in every major animal virus family (10). Studies of them as deletion mutants are contributing to our understanding of the complex genetic rearrangements and essential sequences required for viral replication and packaging. Biologically, the heterogeneity in viral populations introduced by DI particles appears to affect virus-host interactions and thus, presumably, the outcome of viral diseases in intact animals. As more DI particles are isolated and characterized, it becomes necessary that their nomenclature be such that they can be readily identified and related one to the other.

A proposal for naming individual DI particles is made here. Examples are taken from the rhabdovirus vesicular stomatitis (VS) virus, from which many DI particles have been isolated and studied (23). The proposed principles for nomenclature are as follows.

(i) Name the parent virus and serotype according to the conventions established by the International Committee on Taxonomy of Viruses (2, 6); e.g., VS (Indiana) = VSI, and VS (New Jersey) = VSNJ.

(ii) Give the wild-type, temperature-sensitive (*ts*) mutant, or revertant designation, followed by the strain or isolate designation if known (4), e.g., VSI ts^+ ATCC and VSI *ts* G31.

(iii) Give the vernacular name of the DI particle which will be used in the text, and underline it. An example of a vernacular name is DI-T (11). The ideal name would be designated by a fractional number between 0 and 1.0 representing the known total length of the genome of the DI particle, e.g., VSI ts^+ ATCC DI 0.38 and VSI *ts* G31 DI 0.10.

(iv) Place other pertinent information within parentheses following this, such as: derivation from which end or from what part of the genome, percent self-annealing, and any other important phenotype or genotype, e.g., VSI ts^+ ATCC DI 0.38 (5′, 8%) and VSI *ts* G31 DI 0.10 (5′, 65%).

(v) Follow with a reference giving the original isolation and any other references giving the characteristics of the DI particle, e.g., VSI ts^+ ATCC DI 0.38 (5′, 8%) (13) and VSI *ts* G31 DI 0.10 (5′, 65%) (15, 17, 18).

For the sake of uniformity, we recommend that fractional DI particle genomes should be calculated, whenever possible, from the data shown in Table 1 and using the value of 4×10^6 as the molecular weight of virion RNA. Most of the data in Table 1 have been summarized previously (23).

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TABLE 1. *Physical properties of some DI particles of VS virus and of their RNA*

Isolate	Particle length (nm)	Particle width (nm)	Sedimentation coefficient (S)			Diffusion coefficient ($\times 10^{-8}$ cm^2/s)	Mol wt ($\times 10^{-6}$)			
			Particle	RNA in gradients	RNA in gels		Particle	RNA in gradients	RNA in gels	RNA in electron micrographs
Indiana wild types										
Ind C	62[a]	62[a]	330[a]							
Hu	65[b]	65[b]		25[c]	23[d,e]			1.3[c]	1.1[d,e]	
How	63[f]	66[f]		24[g]	26[d,e]			1.2[h]	1.4[d,e]	
PS	65[i]		344[j]		22[e,k]				1.1[e,k]	1.1[f]
ts$^+$ G	79[j]	72[j]	330[j]	14[g,m]	31[e,k,m]	3.28[n]	111[n]	0.4[h,m]	2.0[e,k,m]	
MS				19[o]	21[d,e]			0.8[h]	0.9[d,e]	0.8[o]
MS (011)				10[m,o]				0.2[h,m]		0.8[o]
PI	65[p]	65[p]		19[q]				0.8[h]		
Indiana mutants										
HR	100[i]		422[j]	30–32[i]	31[e,k]			1.7–2.0[i]	2.1[e,k]	
ts G11	98[f]	73[f]	410[f]	28[f,m]	29[e,k,r], 39[e,k,m]	2.85[n]	127[n]	1.7[h,m]	1.8[e,k,r], 3.4[e,k,m]	
ts G12		68[f]	280[f]							
ts G22	99[f]	69[f]	435[f]		36[e,k,m]				2.9[e,k,m]	
ts G31	50[f]	50[f]	150[f]	15[f]	14[d,e]	3.95[n]	42[n]	9.5[h]	0.4[d,e]	
Hol			470[s]	34[e,k,m]					2.4[e,k,m]	
New Jersey wild types										
Ogden short	82[t]	65[t]			20, 24[e,u,v]				0.9, 1.2[e,u,v]	
Ogden long					29, 31[e,u,v]				1.8, 2.0[e,u,v]	
Missouri short	98[w]	74[w]	393[w]		20[e,u]	3.46[w]	163[w]		0.9[e,u]	
Missouri long	135[w]	71.5[w]	523[w]		27, 32[e,u,v]	2.97[w]	252[w]		1.6, 2.3[e,u,v]	
Indiana wild-type virion (G)	172[f]	68[f]	610[f]	43[g]	42[e,k]	2.32[n]	290[n]	4.2[h]	4.1[e,k]	

[a] Reference 1.
[b] Reference 5.
[c] Reference 12.
[d] Reference 7.
[e] Estimated by a comparison with BHK-21 rRNA markers.
[f] Reference 16.
[g] J. A. Lesnaw, R. N. Leamnson, J. T. Unger, and M. E. Reichmann, unpublished data.
[h] Calculated by means of the Spirin equation, $M = 1550S^{2.1}$.
[i] Reference 19.
[j] Calculated from sucrose gradient profiles of reference 19, assuming 610S for the virion marker.
[k] Reference 21.
[l] Reference 20.
[m] Aberrant values because of secondary structure in the molecule.
[n] Reference 24.
[o] Reference 14.
[p] Reference 5.
[q] Reference 3.
[r] RNAs electrophoresed in 4% polyacrylamide gels and 99% formamide.
[s] Reference 9.
[t] Reference 7.
[u] Reference 22.
[v] Two RNA components separated on gels.
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