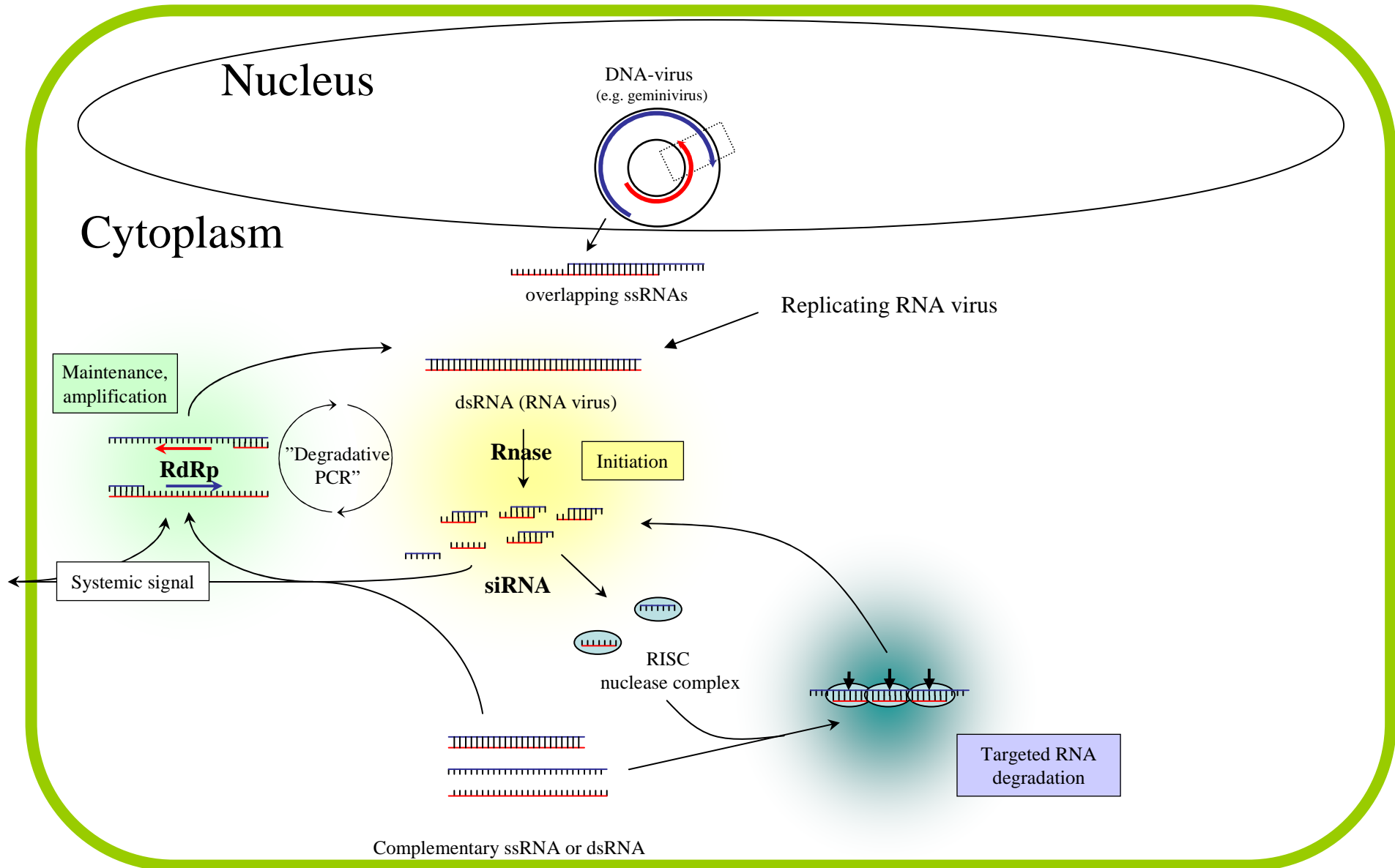


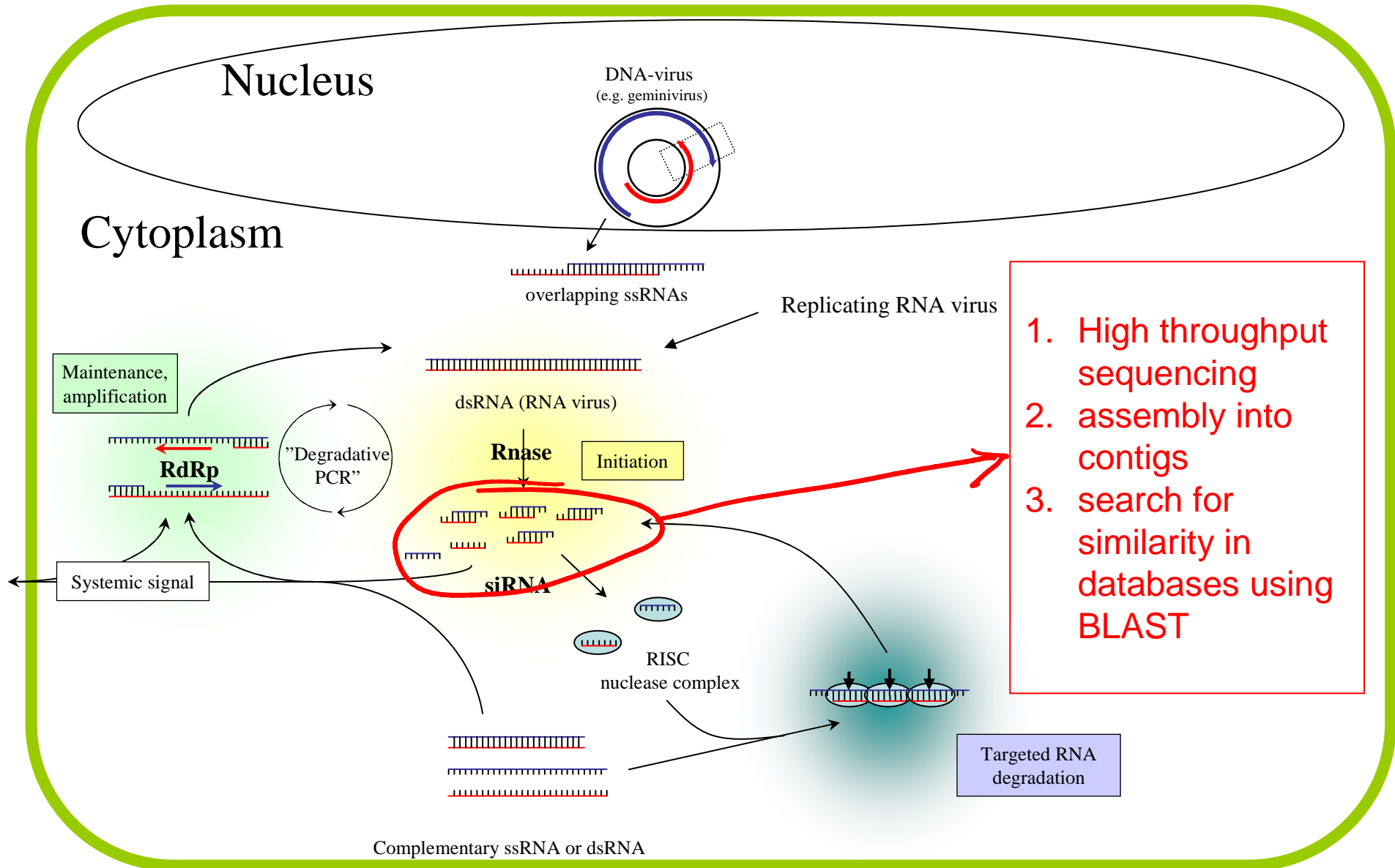
Sequencing by siRNA: a novel generic tool for virus discovery

Kreuze et al. (2009) Complete viral genome sequence and discovery of novel viruses by deep sequencing of small RNAs: a generic method for diagnosis, discovery and sequencing of viruses. *Virology* 388: 1-7



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- De novo assembly of short reads (35-55 bp) using VCAKE and Velvet
- Hundreds of contigs 50-3150
- Blast against database (virus sequences):

Number of contigs assembled by Velvet using 21–24 nt sRNA, or only 22 nt sRNA sequences, with virus specific hits as identified using Translated Nucleotide Blast (Blastx).

Plant infected with	siRNAs sequenced	Contigs identified	Contigs with Blastx hits 21–24 nt sRNA $k = 15$, cov = 30 ^a	Contig sizes 21–24 nt sRNA $k = 15$, cov = 30 ^a	Contigs with Blastx hits 21–24 nt sRNA $k = 15$, cov = 3 ^b	Contigs with Blastx hits only 22 nt sRNA $k = 15$, cov = 3 ^b
SPFMV	1,275,673	Total contigs	239		1633	431
		SPFMV	25	(≤949)	71	78
		SPCSV	0	-	0	0
		Badnavirus	38	(≤256)	62	55
		Mastrevirus	5	(≤210)	6	5
SPCSV	1,271,382	Total contigs	283		1675	285
		SPFMV	0	-	0	0
		SPCSV	10	(≤70)	64	12
		Badnavirus	44	(≤181)	63	44
		Mastrevirus	8	(≤260)	10	6
SPFMV + SPCSV	1,067,577	Total contigs	221		1363	581
		SPFMV	20	(≤1600)	43	51
		SPCSV	2	(≤81)	41	12
		Badnavirus	38	(≤266)	63	51
		Mastrevirus	5	(≤210)	8	5

Sequencing by siRNA: complete nucleotide sequence of SPFMV-Piu3 and ~50% of genome of three novel viruses

