Supporting Information

Biodistribution of Filamentous Plant Virus Nanoparticles: Pepino Mosaic Virus versus Potato Virus X

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The sequences of PepMV vs. PVX. The first 20 aa corona sequences are highlighted in red; these sequences were further analyzed, see Figure S1 and Table S1.

PepMV

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        10         20         30         40         50         60
MPDTTPVAAT SSAPPTAKDA GAKAPSDFSN PNTAPSLSDL KKVKYVSTVT SVATPAEIEA

        70         80         90        100        110        120
LGKIFTAMGL AANETGPAMW DLARAYADVQ SSKSAQLIGA TPSNPALSRR ALAAQFDRIN

       130        140        150        160        170        180
ITPRQFCMYF AKVVWNILLD SNIPPANWAK LGYQEDTKFA AFDFFDGVTN PASLQPADGL

       190        200        210        220        230
IRQPNEKELA AHSVAKYGAL ARQKISTGNY ITTLGEVTRG HMGGANTMYA IDAPPEL
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PVX

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        10         20         30         40         50         60
MSAPASTTQA TGSTTSTTTK TAGATPATAS GLFTIPDGDF FSTARAVVAS DAVATNEDLS

        70         80         90        100        110        120
EIEAVWKDMK VPTDTMAQAA WDLVRHCADV GSSAQTEMID TGPYSNGISR ARLAAAIKEV

       130        140        150        160        170        180
CTLRQFCMKY APVVWNWMLT NNSPPANWQA QGFKPEHKFA AFDFFNGVTN PAAIMPKEGL

       190        200        210        220        230
IRPPSEAEMN AAQTAAFVKI TKARAQSNDF ASLDAAVTRG RITGTTTAEA VVTLPPP
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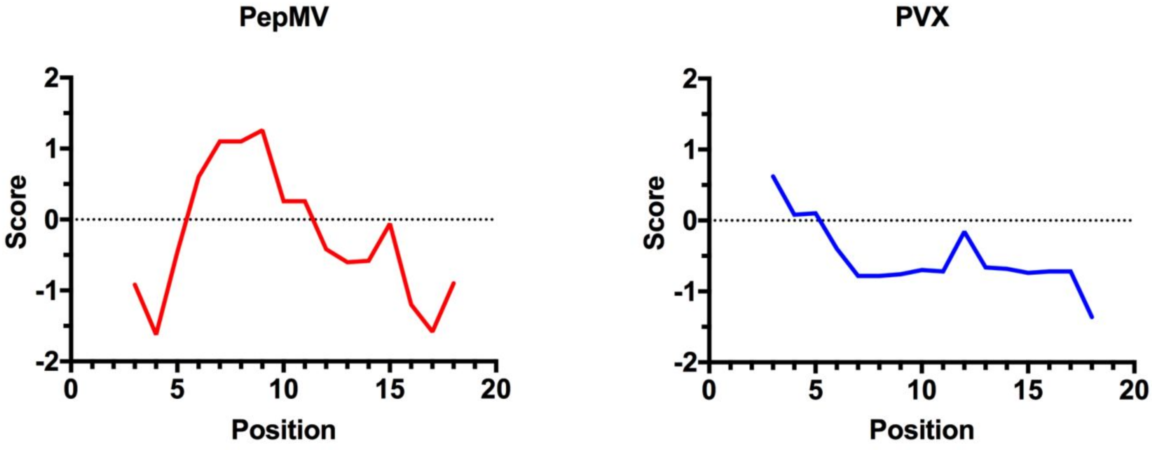

Figure S1. Hydropathy plots, based on the Kyte-Doolittle scale, of the first 20 amino acid sequences in PepMV and PVX CP illustrating the hydrophobicity distribution from each residue. The window size was set at 5.

Table S1. Summary of 20-mer peptide tails (Calculated by Protein Calculator tool and EXPASY)

	PepMV	**PVX**
pI	4.47	8.88
Estimated charge at pH 7.4	-1.2	0.8
% acidic residues	10 %	0%
% basic residues	5%	5%
% hydrophobic residues	55%	25%
% neutral residues	30%	70%
Grand average of hydropathicity (GRAVY)	-0.330	-0.545

GRAVY: a value for a protein or a peptide is calculated by adding the hydropathy values (Kyte, J. and Doolittle, R.F., 1982) of each amino acid residues and dividing by the number of residues in the sequence or length of the sequence. A positive GRAVY value indicates that the protein is hydrophobic and a negative value indicates that it is hydrophilic. The score is calculated based on the Kyte-Doolittle scale.