































## Overview of comoviruses

There are 15 „good“ species and one not yet included (TuRSV) in the Virus taxonomy, release 9 (July 2010). The comovirus type virus cowpea mosaic virus (CPMV) has been described almost 90 years ago (1924), but three species only have been described in the last 30 years (UVC, GMV, TuRSV). This is very strange in comparison with continuously growing amount of new potyviruses that used very similar expression strategy. More probably, the lack of simple molecular method like „universal primers“ known for potyviruses is the main problem for discovering new comoviruses.

We suppose that complete sequence data help us to design such diagnostic tools. There is no reason for searching *Fabaceae* family for comovirus only. It is the most frequent host family of comoviruses till now, but by far different families could be also hosts of this viruses! Insufficiently characterized isolates, e.g. with electron microscopy only, could be good candidates for new species searching!

## Recent species of the genus

species		description	hosts	complete sequence
Andean potato mottle v	APMoV	1977	 <i>Solanaceae</i>	 partial RNA1
Bean pod mottle v	BPMV	1948	 <i>Fabaceae</i>	
Bean rugose mosaic v	BRMV	1972		 partial RNA1, RNA2
Broad bean stain v	BBSV	1965		
Broad bean true mosaic v	BBTMV	1953		
Cowpea mosaic v	CPMV	1924		
Cowpea severe mosaic v	CPSMV	1949		
Glycine mosaic v	GMV	1980		
Pea mild mosaic v	PMiMV	1972		
Quail pea mosaic v	QPMV	1973		
Radish mosaic v	RaMV	1939	 <i>Brassicaceae</i>	
Red clover mottle v	RCMV	1960		
Squash mosaic v	SqMV	1941	 <i>Cucurbitaceae</i>	
Turnip ringspot v	TuRSV	2006		
Ullucus C v	UVC	1982	 <i>Baselaceae</i>	

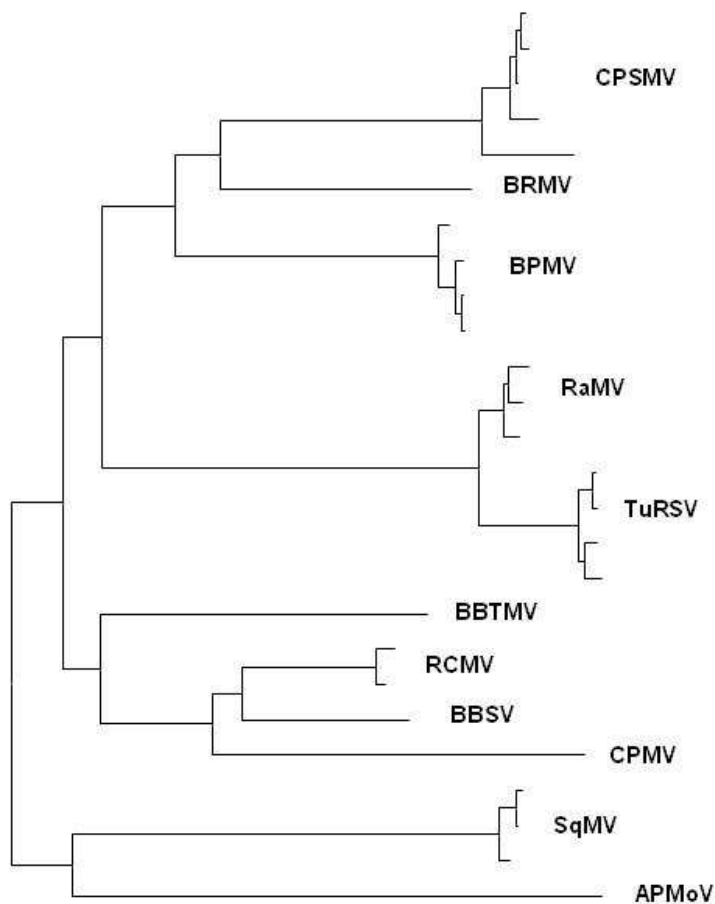
+ Pea green mottle virus PGMV (Valenta et al., 1969, *Acta Virol.* 13: 422-434)

### Variability, phylogeny e.t.c.

Up to now, the intraspecies identity of the CP-L protein calculated for 5 comovirus species is about 97% and that for combined CP-L + CP-S proteins is about 95% (Petrzik and Koloniuk, 2010, *Virus Genes* 40: 290-292).

We propose to use both capsid protein genes for comparison and discrimination of species with analogy to criteria accepted for the proposed family *Secoviridae*.

### Topology of the phylogenetic tree based on the longest available overlapping protein segment of small capsid protein



## Looking for isolates and cooperation

There are several isolates that could be interesting for the phylogenetic study. Most of them were partially characterized but often nonsequenced or only partially sequenced.

Here there are some of them:

RaMV – isolate from Morocco, published by Koenig and Fischer, (1981), *Pl.Disease* 65: 758-760, nonsequenced

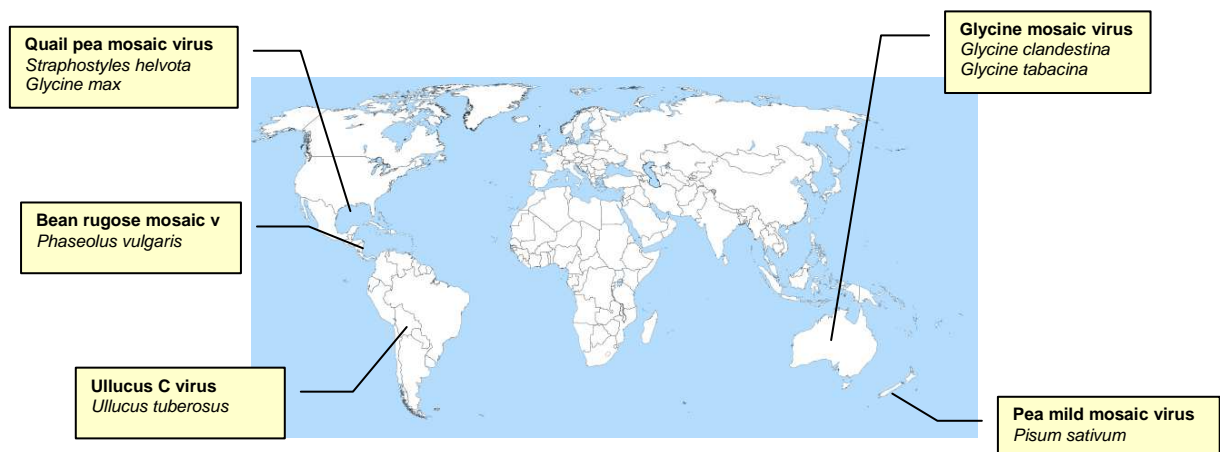
RaMV – isolate from Iran

RCMV – O isolate from Sweden, CP-L and CP-S protein sequence published only

But, some species still missing: **we are looking** for isolates of previously described viruses from Australia and New Zealand (GMV, PMMV), Middle and South America (QPMV, BRMV, UCV) to perform partial (et least) or whole genome sequencing of these viruses. Providing isolates and any further cooperation is welcome!

**Contact:** [petrzik@umbr.cas.cz](mailto:petrzik@umbr.cas.cz)

## Home regions and hosts of nonsequenced viruses



## Alignment of putative cleavage sites of the polyproteins encoded by RNA1 and RNA2 genome segments

### Alignment of the putative cleavage sites of the polyproteins encoded by comovirus genome segments

virus	Co-Pro/Hel	Hel/VPg	VPg/Pro	Pro/RdRp
BBSV	* * * * * ↓ *	* * * * * ↓ *	* * * * * ↓ *	* * * * * ↓ *
BBTMV	K I T T A Q ↓ G	S A A E A Q ↓ S	N W A T A Q ↓ M	P I A Q A Q ↓ G
BPMV	E E I K G Q ↓ F	S V L E A Q ↓ S	A W V E G Q ↓ M	P V V Q A Q ↓ S
BRMV	* * * * * ↓ *	* * * * * ↓ *	* * * * * ↓ *	* * * * * ↓ *
CPMV	E K D N A Q ↓ S	F S A E P Q ↓ S	V W A D A Q ↓ M	P I A Q A Q ↓ G
CPSMV	V S A E S Q ↓ S	Q A V V A Q ↓ S	N W A E G Q ↓ M	I P V Q A Q ↓ A
RCMV	K K V N A Q ↓ G	S T A E A Q ↓ S	S W G N A Q ↓ M	P C A Q A Q ↓ G
RaMV	C V A V L Q ↓ G	A R A T A Q ↓ S	K R A W A Q ↓ G	K K V Q A Q ↓ H
TuRSV	A V V A F Q ↓ G	D I A V A Q ↓ S	K R A W A Q ↓ G	R K A Q A Q ↓ H
SqMV	P Q T I L Q ↓ D	T N A V A Q ↓ S	Q W A D A Q ↓ M	Q A A D A Q ↓ C
APMoV	* * * * * ↓ *	* * * * * ↓ *	* * * * * ↓ *	P K A Q A Q ↓ S

virus	MP/CP-L	CP-L/CP-S
BBSV	V Y A N P Q ↓ M	A I A T P Q ↓ N
BBTMV	C H T F A Q ↓ T	L G A K A Q ↓ G
BPMV	N E V Q A Q ↓ M	L G T I P Q ↓ S
BRMV	* * * * * ↓ *	G S V Q A Q ↓ G
CPMV	N V A F P Q ↓ M	L G A I A Q ↓ G
CPSMV	T H A T L Q ↓ S	L G A V A Q ↓ S
RCMV	V F A N P Q ↓ T	M Q A E A Q ↓ G
RaMV	R R A F G Q ↓ T	L P A S P Q ↓ G
TuRSV	Q R A F G Q ↓ A	L A V S P Q ↓ G
SqMV	T K A Y G Q ↓ N	L G I S G Q ↓ S
APMoV	V V A Q A Q ↓ M	L L A W P Q ↓ F