



RESEARCH  
PROGRAM ON  
Roots, Tubers  
and Bananas



PERÚ

Ministerio  
de Agricultura y Riego



UNIVERSIDAD NACIONAL AGRARIA  
**LA MOLINA**

**“Viroma de la papa en el Perú y fortalecimiento de capacidades INIA y UNALM en el diagnóstico de patógenos con técnicas de última generación para enfrentar al riesgo de enfermedades emergentes por el calentamiento global”**  
**Programa Nacional de Innovación Agraria :**  
**029-2015-INIA-PNIA/UPMSI/IE**

# PRESENTACIÓN PÚBLICA DE RESULTADOS

**Jan Kreuze** (Coordinador General)

**Segundo Fuentes** (Coordinador Técnico - Investigador Principal)

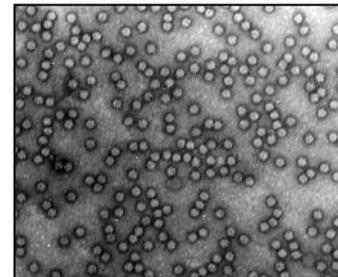
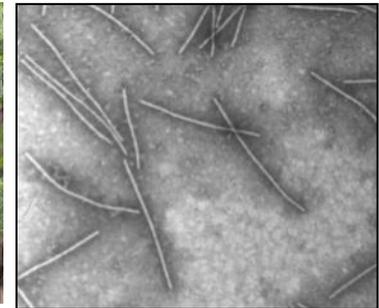
**Ana Pérez** (Coinvestigadora)

**Dina Gutierrez** (Representante del INIA)

**Carlos Cadenas** (Representante de la UNALM)

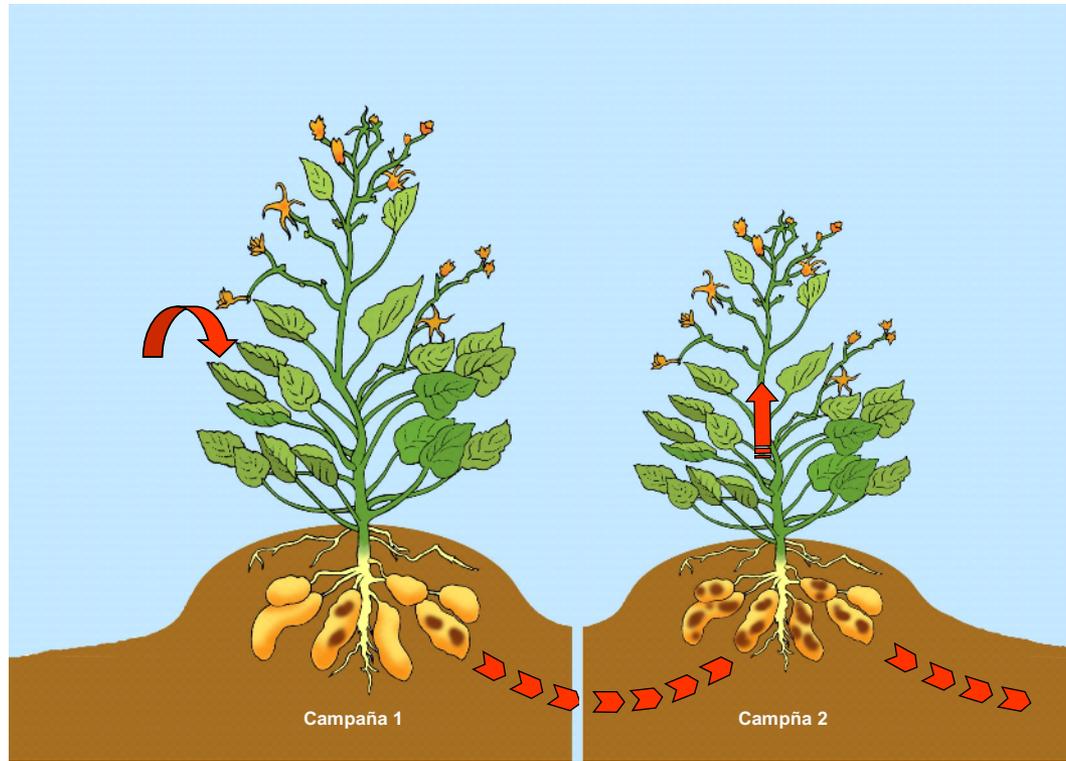
# Justificación del Proyecto

- Región Andina centro de la **diversidad de papa** → **co-evolución de virus**



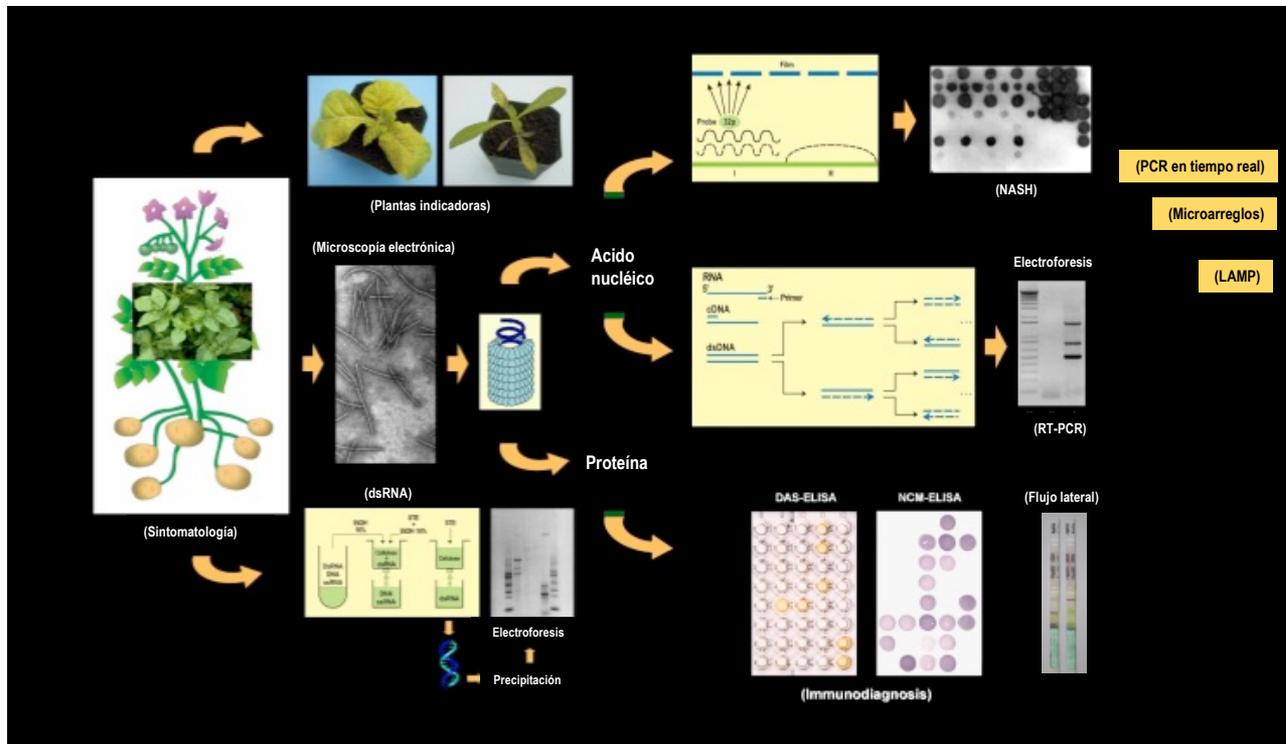
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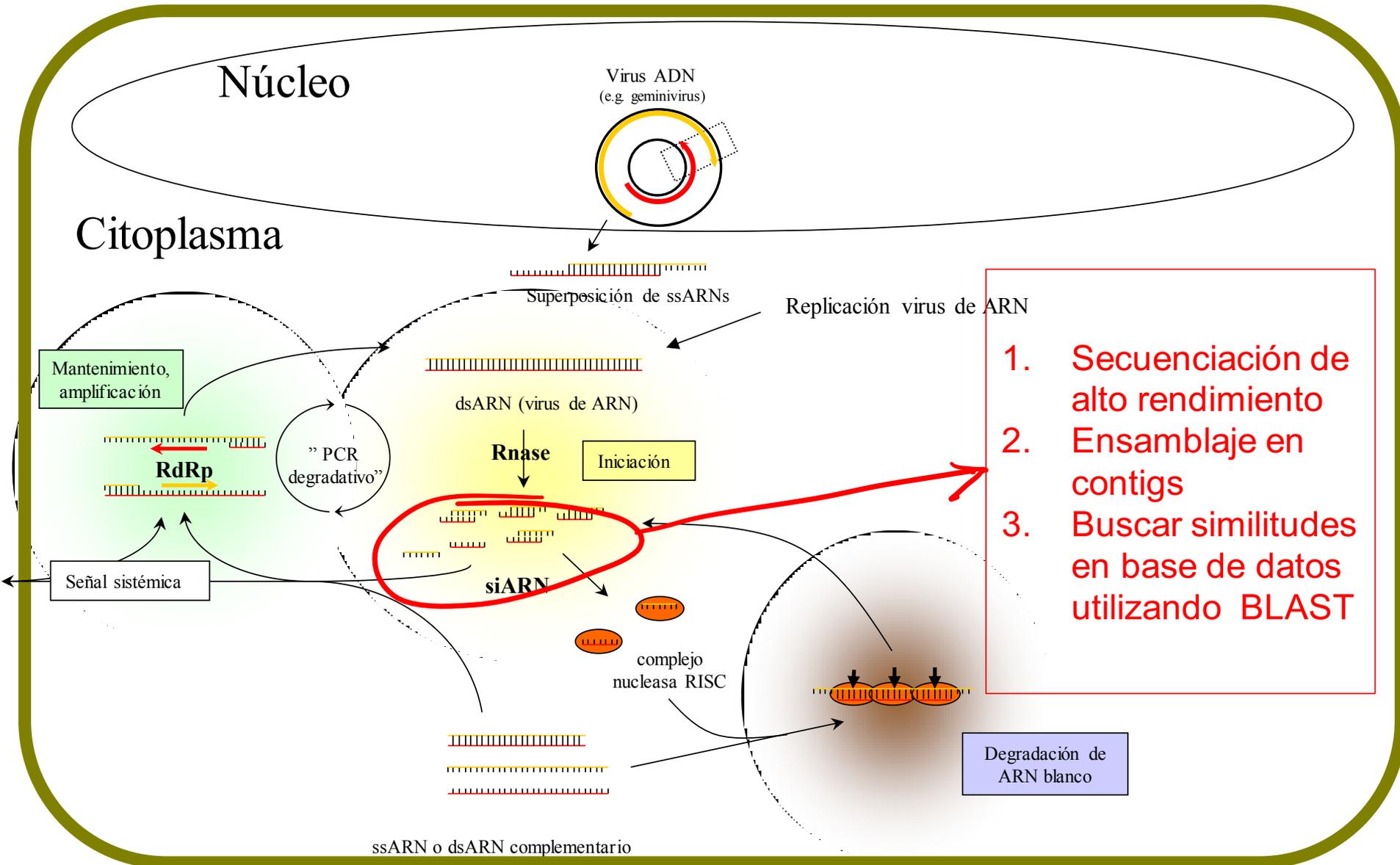
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# Virus – Silenciamiento del RNA – sRSA



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- **sRSA** puede **reconstituir** la **secuencia genómica** de los virus
- **Viroma** = datos moleculares de las secuencias virales
- **Carencia de información** detallada de la **variabilidad, distribución** y frecuencia de los virus en las diferentes áreas productoras en Perú

# COMPONENTES



Conocer la diversidad molecular de los virus (viroma), su distribución y su correlación con la producción de papa en el Perú

# Muestras colectadas

994 muestras de hojas georreferenciadas

(Cajamarca, Huánuco, Junín, Huancavelica, Apurímac, Cusco, Puno, Lima, Ica)

2016-2018



Campo



Planta



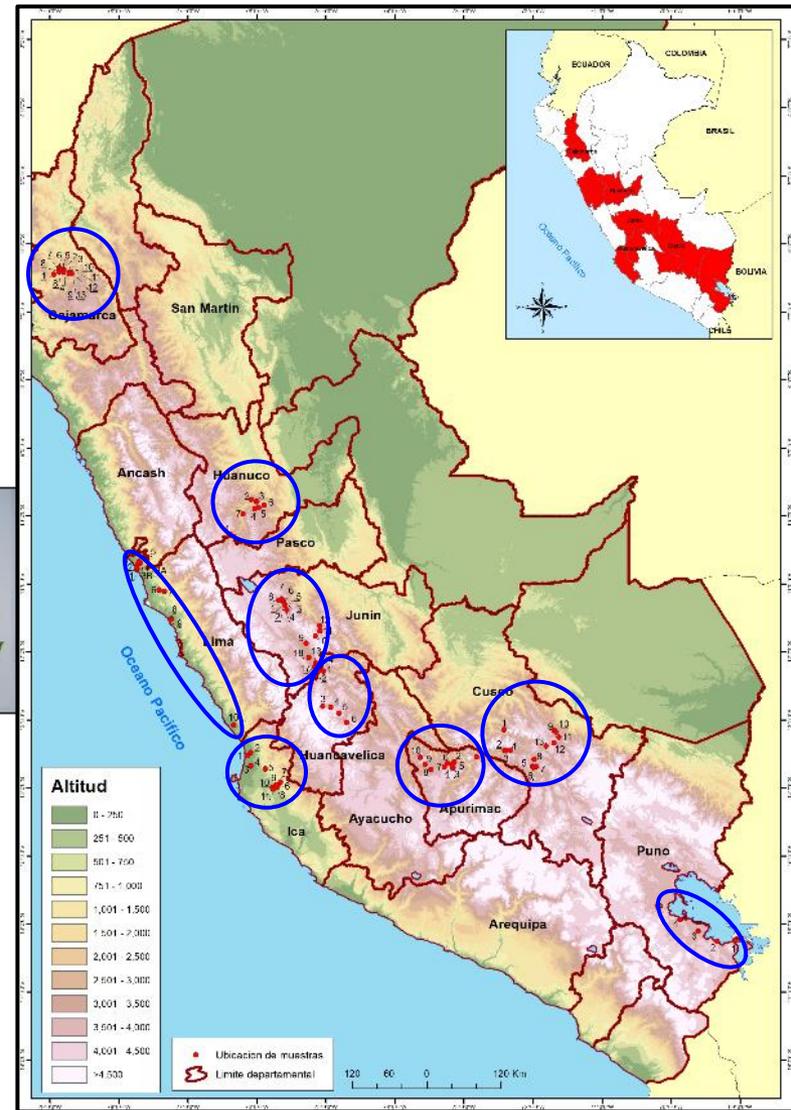
Hojas



Deshidratación

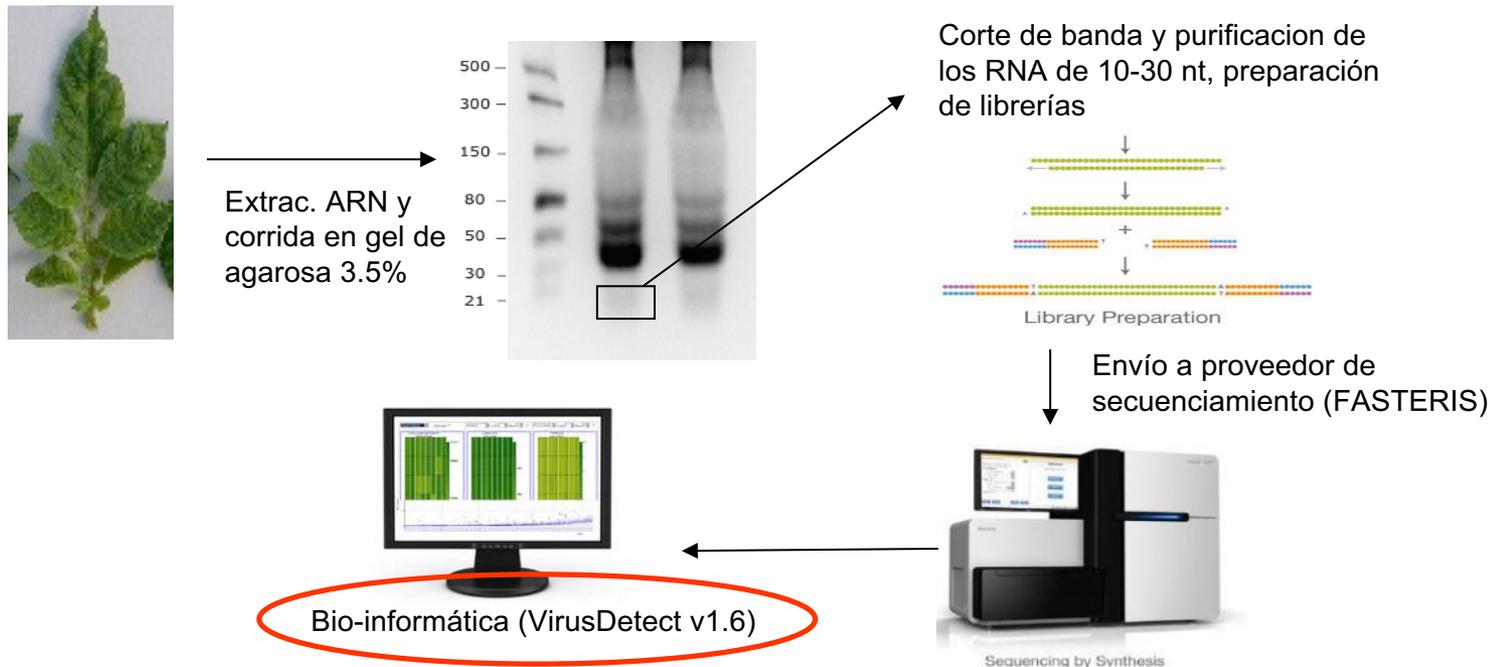


Procesamiento



# Procesamiento de muestras por sRSA

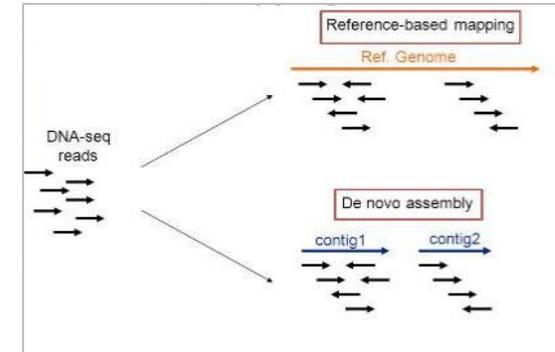
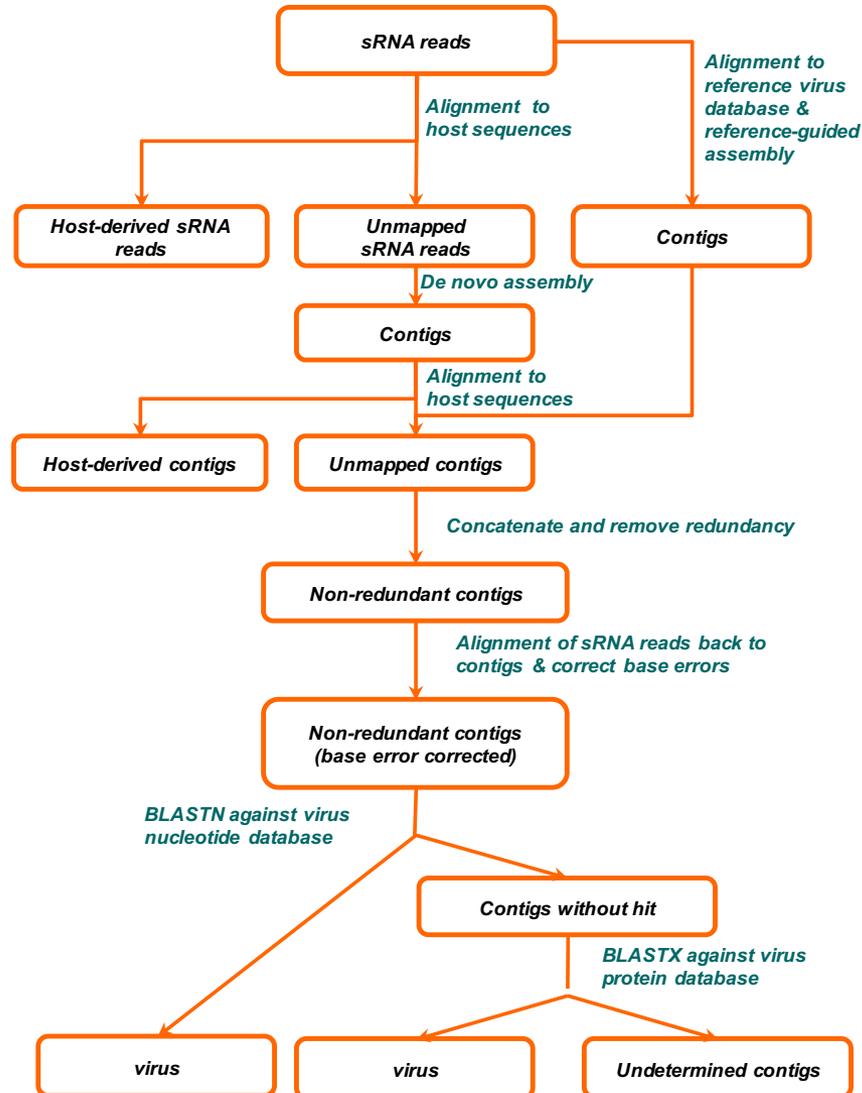
Extrac. de ARN y prep. librerías / secuenciamiento / análisis bioinformático



Grupo de 48 muestras "codificadas" por carril en Illumina HiSeq 4000: 260-350 millones de "reads"

# Flujo de trabajo automatizado: VirusDetect\_v1.6

[http://virusdetect.feilab.net/cgi-bin/virusdetect/vd\\_download.cgi](http://virusdetect.feilab.net/cgi-bin/virusdetect/vd_download.cgi)



**Identificación de virus**

# Identificación automatizada – visualización de resultados

Reference	Length	Coverage (%)	#contig	Depth	Depth	%Identity	%Iden	%Iden	Genus	Description
AF493951	949	418 (44)	7	40.9						
KX656671	4527	4009 (88.6)	13	28.1						
KX656670	7148	2134 (29.9)	35	27.0						
KJ534601	6445	6445 (100)	9	481.0						
M72416	7568	1745 (23.1)	25	52.2						

Genomic map showing contigs KJ534601, CONTIG33, CONTIG63, CONTIG86, CONTIG15, CONTIG17, CONTIG76, CONTIG36, CONTIG83, and CONTIG104 along a 6k scale.

Order	Query ID	Query Start	Query End	Subjct Start	Subjct End	Identity	E value	Strand
1	CONTIG15	3	49	3340	3386	44/47(93%)	1e-12	1

Alignment:

```

Query: 3  aacttccgagaattcttaacaagaaggacattggggacgtcctctt 49
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 3340 aacttccgtgagttcctaacaagaaggacattggggacgtcctctt 3386
    
```

2	CONTIG17	1	74	4261	4334	69/75(92%)	1e-22	1
---	----------	---	----	------	------	------------	-------	---

Alignment:

```

Query: 1  gccgaagctaagggtgaactgaagaaatgccaagactcctatgaaatcga-tctgagta 59
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 4261 gccgaagcaaaggagaattgaagaaatgccaagactcctatgaaatcgayt-tgagta 4319

Query: 60  tgcgtatgaccacaa 74
          ||| ||| ||| ||| |||
Sbjct: 4320 tgcgtatgaycaciaa 4334
    
```

# Análisis de datos generados por VirusDetect v1.6

Sustration potato genome with VirusDetect v1.6 and vrl_Plants_217_U95																					
Library PNIA-2017-06 (muestras colectadas en Junín y Cuzco)																					
Library code	Sample code	FASTQC	reads	Parameters utilized	Reference	Length	Coverage(%)	#contig	Depth	Depth (Norm)	%identit y	%iden Max	%iden Min	Genus	Description	Final conclusion: Viruses identified					
1	Jin-134	good siRNA peak, 21-<24, 32	4682527		M84483	2265	1786 (78.9)	2	183.3	39.1	83.32	95.65	83.01	comovirus	Andean potato mottle virus RNA-dependent RNA polymerase.	PVX, PVY					
					M72416	7568	7568 (100)	16	590.2	126	93.43	98.72	79.8	potexvirus	Potato virus X complete genome.	APMoV (new strain)					
					KJ534601	6445	6445 (100)	22	698.2	149.1	94.81	98.78	88.06	potexvirus	Potato virus X isolate SA-CIP, complete genome.	New Comovirus					
					KM659859	6487	6439 (99.3)	16	600	128.1	92.27	98.51	79.77	potexvirus	Potato virus X isolate PVX-Gooseberry, complete genome.	New Comovirus					
					KJ620840	620	620 (100)	3	470.9	100.6	95.63	97.06	91.18	potexvirus	Potato virus X strain NSX002 coat protein (cp) gene, partial cds.	New Ophiovirus					
					HQ396166	548	491 (89.6)	3	419.6	89.6	92.85	93.69	89.02	potexvirus	Potato virus X isolate Pasto-cubijan coat protein (CP) gene, partial cds.						
					AF172259	6435	2278 (35.4)	24	482.6	103.1	92.51	98.11	86.57	potexvirus	Potato virus X complete genome.						
					Z23256	6433	1675 (26)	18	476.5	101.8	90.42	97.59	87.27	potexvirus	Potato virus X coat protein RNA and 3 ORF's, complete CDS's.						
					KR270797	9726	2228 (22.9)	37	27.1	5.8	99.37	100	93.75	potyvirus	Potato virus Y isolate mar7, complete genome.						
					AAA42421.1	997	997 (100)	2	406.4	86.8	72.37	75.43	70.76	comovirus	Andean potato mottle virus polyprotein encoding small and large coat proteins and						
					AKL83120.1	1856	1222 (65.8)	2	447.1	95.5	37.28	38.27	32.9	comovirus	Bean rugose mosaic virus isolate Parana segment RNA1 polyprotein gene, complete cds.						
					AIF28243.1	515	454 (88.2)	1	325.7	69.6	36.66	36.66	36.66	ophiovirus	Blueberry mosaic associated virus segment RNA2, complete sequence.						
					AAF00018.1	439	253 (57.6)	3	124.6	26.6	40.93	46.81	39.42	ophiovirus	Citrus ringspot virus coat protein gene, complete cds.						
					AJR35881.1	401	117 (29.2)	2	115.7	24.7	45.3	56	42.39	ophiovirus	Blueberry mosaic associated virus isolate New Jersey10 nucleocapsid protein gene,						
					2	Jin-135	good siRNA peak, 21-<24, 26, 32	3703328		M72416	7568	6614 (87.4)	47	6	1.6	97.62	100	93.88	potexvirus	Potato virus X complete genome.	PVX
KM659859	6487	5421 (83.6)	43	6.1						1.7	96.14	100	93.1	potexvirus	Potato virus X isolate PVX-Gooseberry, complete genome.						
KJ534601	6445	5363 (83.2)	37	5.9						1.6	98.69	100	95.52	potexvirus	Potato virus X isolate SA-CIP, complete genome						
Z23256	6433	720 (11.2)	10	5.1						1.2	94.88	100	91.92	potexvirus	Potato virus X coat protein RNA and 3 ORF's, complete CDS's.						
3	Jin-136	good siRNA peak, 21-<24, 26, 32	4255748		M72416	7568	6209 (82)	47	5.3	1.2	97.93	100	91.78	potexvirus	Potato virus X complete genome.						
					KJ534601	6445	5845 (90.7)	39	6.7	1.6	98.26	100	91.26	potexvirus	Potato virus X isolate SA-CIP, complete genome.						
					KM659859	6487	4975 (76.7)	45	5.3	1.2	96.49	100	92.94	potexvirus	Potato virus X isolate PVX-Gooseberry, complete genome.						
					HQ433258	4408	1388 (31.5)	13	6.3	1.5	97.35	98.99	93.75	potexvirus	Potato virus X RNA-dependent RNA polymerase-like gene, complete sequence						
					D13953	5882	5789 (98.4)	15	197.3	38.7	97.08	98.82	89.21	polerovirus	Potato leaf roll virus (Australian isolate) genomic RNA, complete sequence.	PLRV, PVX, PVY?					
					Z23256	6433	983 (15.3)	10	471.1	92.4	91.77	96.08	89.44	potexvirus	Potato virus X coat protein RNA and 3 ORF's, complete CDS's.	APMoV (new strain)					
					M72416	7568	7562 (99.9)	14	1026.5	201.3	96.38	98.56	87.9	potexvirus	Potato virus X complete genome.	New Comovirus (BLASTX)					
					X88788	711	711 (100)	4	980.1	192.2	96.37	98.73	93.29	potexvirus	Potato virus X coat protein gene, XS strain.						
					KJ534601	6445	5635 (87.4)	39	226.4	44.4	95.58	100	89.24	potexvirus	Potato virus X isolate SA-CIP, complete genome.						
					AF172259	6435	2548 (39.6)	29	234.7	46	94.94	100	89.04	potexvirus	Potato virus X complete genome.						
					KR270797	9726	1359 (14)	24	8.6	1.7	98.97	100	95.24	potyvirus	Potato virus Y isolate mar7, complete genome						
					AAA42421.1	997	979 (98.2)	3	772.8	151.6	72.7	78.84	70.92	comovirus	Andean potato mottle virus polyprotein encoding small and large coat proteins and						
					AAA42422.1	729	729 (100)	1	709.1	139.1	94.24	94.24	94.24	comovirus	Andean potato mottle virus RNA polymerase mRNA, 3' end.						
					5	Jin-138	good siRNA peak, 21-<24, 32	4319033		KJ534601	6445	5699 (88.4)	33	21.4	5	98.37	100	91.3	potexvirus	Potato virus X isolate SA-CIP, complete genome.	PVX
										AF172259	6435	2227 (34.6)	32	6.6	1.5	97.58	100	91.23	potexvirus	Potato virus X complete genome.	
AAA47167.1	1456	617 (42.4)	9	6						1.4	99.51	100	97.18	potexvirus	Potato virus X complete genome						
M84986	2303	1746 (75.8)	7	214.2						57.1	93.93	95.35	81.13	comovirus	Andean potato mottle virus RNA polymerase mRNA, 3' end.	PVX					
6	Jin-139	good siRNA peak, 21-<24, 26, 32	3751276		M72416	7568	7567 (100)	17	498.2	132.8	96.05	97.5	88.76	potexvirus	Potato virus X complete genome.	APMoV (new strain)					
					HQ433258	4408	587 (13.3)	5	250.1	66.7	92.19	97.5	90.24	potexvirus	Potato virus X RNA-dependent RNA polymerase-like gene, complete sequence.	New Comovirus					
					KJ534601	6445	5174 (80.3)	38	107.6	28.7	96.06	100	89.74	potexvirus	Potato virus X isolate SA-CIP, complete genome.	New Fabavirus?					
					AF172259	6435	1912 (29.7)	26	124.5	33.2	95.24	100	91.84	potexvirus	Potato virus X complete genome.						
					Z23256	6433	1064 (16.5)	16	137.4	36.6	92.49	95.45	88.89	potexvirus	Potato virus X coat protein RNA and 3 ORF's, complete CDS's						
					AAA42421.1	997	973 (97.6)	6	344.7	91.9	72.64	83.33	66.05	comovirus	Andean potato mottle virus polyprotein encoding small and large coat proteins and						
					AKL83120.1	1856	1065 (57.4)	3	384.8	102.6	35.29	48.57	32.46	comovirus	Bean rugose mosaic virus isolate Parana segment RNA1 polyprotein gene, complete cds.						
					7	Jin-140	good siRNA peak, 21-<24, 26, 32	4063652		M84483	2265	1840 (81.2)	7	169.2	41.6	84.78	92.06	82.77	comovirus	Andean potato mottle virus RNA-dependent RNA polymerase.	PVX, PVY?
										M72416	7568	7568 (100)	19	333.3	82	94.94	98.85	80.72	potexvirus	Potato virus X complete genome.	APMoV (new strain)
KM659859	6487	6431 (99.1)	18	339.4						83.5	94.01	98.97	79.52	potexvirus	Potato virus X isolate PVX-Gooseberry, complete genome.	PVX (new strain)					
KJ534601	6445	6379 (99)	50	316.7						77.9	89.47	98.18	80.8	potexvirus	Potato virus X isolate SA-CIP, complete genome.	New Comovirus					
AF172259	6435	5248 (81.6)	49	348.8						85.8	87.87	100	81.25	potexvirus	Potato virus X complete genome.						
HQ433258	4408	503 (11.4)	3	755.7						186	84.82	96.15	81.33	potexvirus	Potato virus X RNA-dependent RNA polymerase-like gene, complete sequence.						
Z23256	6433	4383 (68.1)	31	360.7						88.8	86.62	100	82.91	potexvirus	Potato virus X coat protein RNA and 3 ORF's, complete CDS's.						
KR270797	9726	1165 (12)	22	5.8						1.4	98.88	100	95.83	potyvirus	Potato virus Y isolate mar7, complete genome.						
AAA42421.1	997	987 (99)	2	316.5						77.9	72.89	73.26	72.86	comovirus	Andean potato mottle virus polyprotein encoding small and large coat proteins and						
CAA46104.1	1864	843 (45.2)	3	417.9						102.8	39.09	44.38	27.53	comovirus	Red Clover Mottle Virus genomic RNA sequence for bottom component RNA.						
AJA37613.1	1858	771 (41.5)	3	335.2						82.5	38.19	44.97	26.04	comovirus	Squash mosaic virus segment RNA-1, complete sequence.						
AKL83120.1	1856	412 (22.2)	2	435.6						107.2	30.25	32.46	26.67	comovirus	Bean rugose mosaic virus isolate Parana segment RNA1 polyprotein gene, complete cds.						
AAA42422.1	729	126 (17.3)	4	109.3						26.9	90.77	93.75	88.57	comovirus	Andean potato mottle virus RNA polymerase mRNA, 3' end						

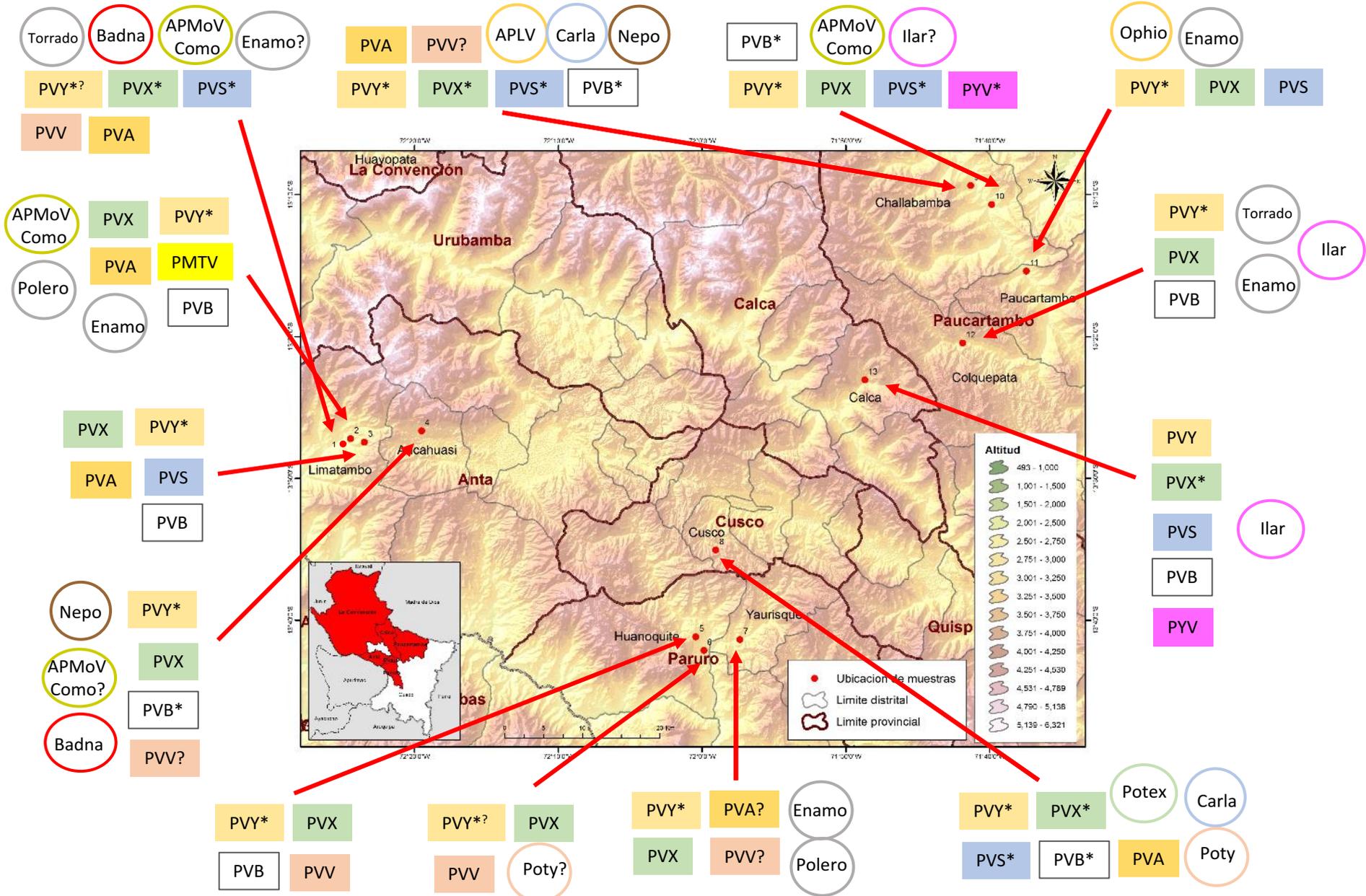
## Virus detectados por sRSA - VirusDetect

Departamento	Muestras analizadas	PVX	PVY	PVV	PVA	PVS	PLRV	PYV	APLV	APMMV	APMoV	PMTV	PVB	PBRV	PVT	AVB	Variantes y virus nuevos
Cajamarca	153	87	17	33	*	77	20	1	3		1	3	12				72
Huanuco	79	46	15	8	*	9	4	3	3	*	1	3	4				64
Junin	176	121	63	1		8	6	3			2	11	24				113
Huancavelica	65	53	6	25	5	3		7	1	14	4		39	1			135
Apurimac	102	23	27	90	75	1		2	5			10	44				86
Cusco	144	77	140	17	18	10		3	*		*	1	20				109
Puno	44	35	34	18	26	6		1		1	4	1	25		1	5	104
Lima	110	56	39			7	5	1			3	9	8				92
Ica	121	47				13	2	2			8		1				65
<b>TOTAL</b>	994	<b>545</b>	<b>341</b>	<b>192</b>	<b>124</b>	<b>134</b>	37	23	12	15	23	38	<b>177</b>	1	1	5	<b>839</b>

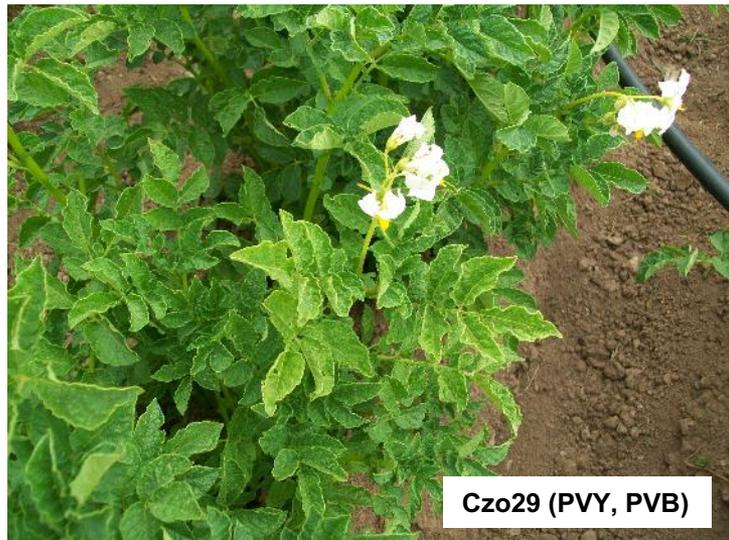
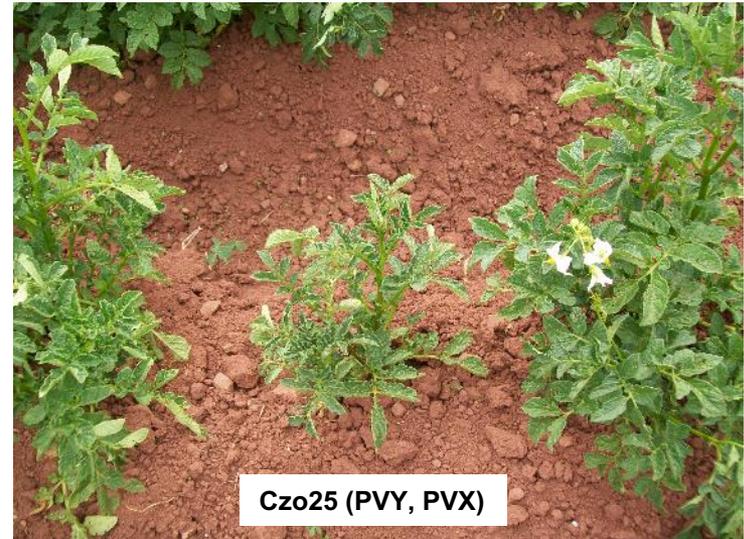
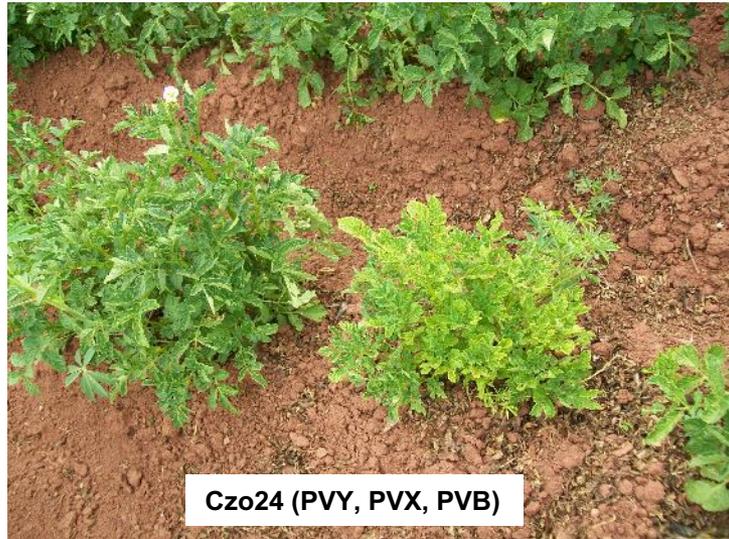
## Variantes /especies virales nuevas detectados por sRSA - VirusDetect

Department	PVX / PAMV / Potexvirus	PVA / PW / PVY / Potyvirus	PVB / PBRV / Nepovirus	APMoV / Comovirus	APLV / Tymovirus	PVS / Carlavirus	APMMV	PYV / Iarvirus	Badnavirus	Torradovirus	Enamovirus	Ophiovirus	Polerovirus	Fabavirus	Tobravirus	Pomovirus	PVT / Tepovirus	AVB / Cheravirus	TOTAL
Cajamarca	34 0 0	1 18 0 1	0 0 3	3 3	1 0	4 0									3	1			72
Huánuco	14 0 0	7 7 3 1	1 0 8	5 5	2 1	2 0	1	2 1	1	2		1							64
Junín	31 0 0		1 0 5	24 26		4 0		3 2	1	7	1	1		7					113
Huancavelica	24 0 0	1 2 0 0	3 1 19	4 4	1 0	2 2	11	7 6	23	3	1	9		8			0 4		135
Apurímac	6 1 1	17 18 0 7	14 0 3		5 0			2? 2	8			3		1					88
Cusco	9 0 1	0 0 38 2	4 0 2	6 6	1 0	8 3		3 3	2	12	6	1	2						109
Puno	25 0 2	0 0 13 1	4 0 4	6 6		5 2		1? 1	23	1							2 0	7 1	104
Lima	18 0 0	0 0 6 0	1 0 13	13 13		6 3		1? 1	2	11				3	2				93
Ica	14 0 0		0 0 10	11 11		3 0		2 2		12									65
<b>TOTAL</b>	<b>180</b>	<b>143</b>	96	<b>146</b>	11	44	12	39	60	48	8	15	2	19	5	1	6	8	<b>843</b>

# Virus detectados en Cusco – en muestras colectadas en noviembre 2016

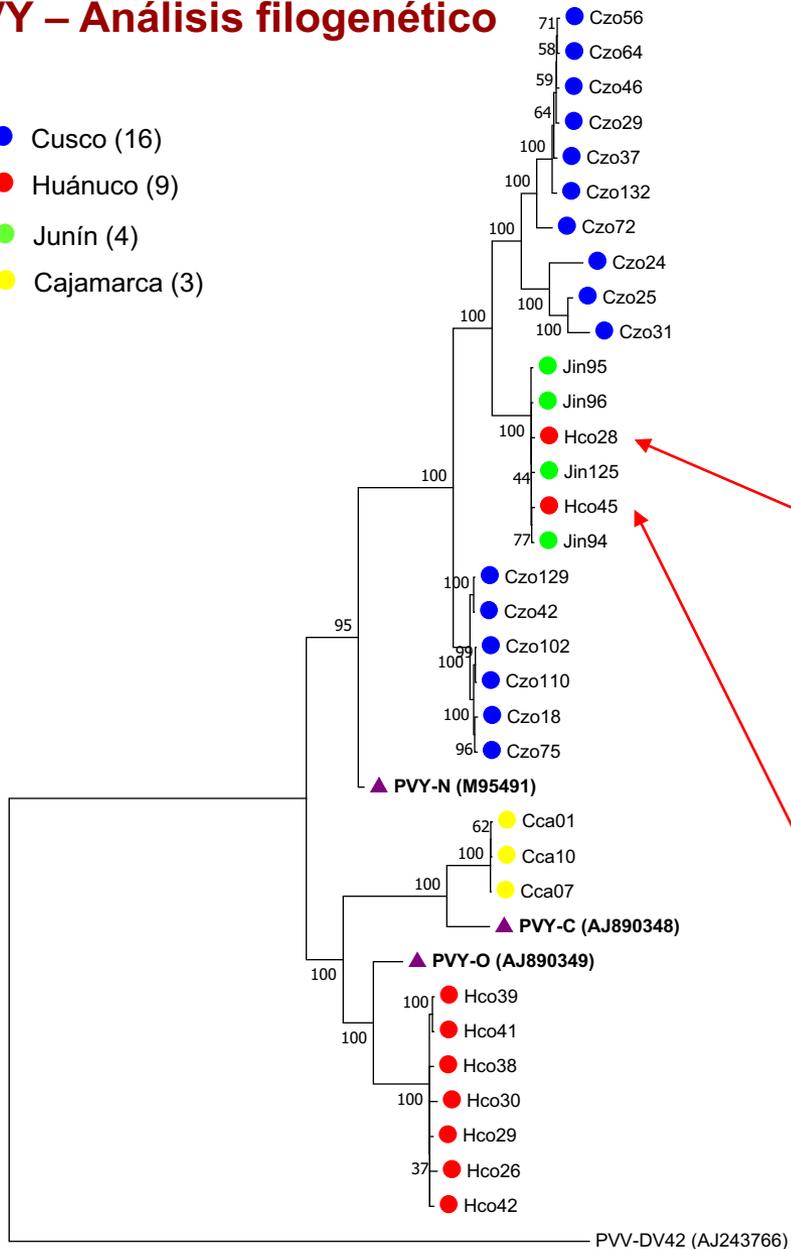


## Plantas de papa “Cica” infectada con virus – Cusco (2016)



# PVY – Análisis filogenético

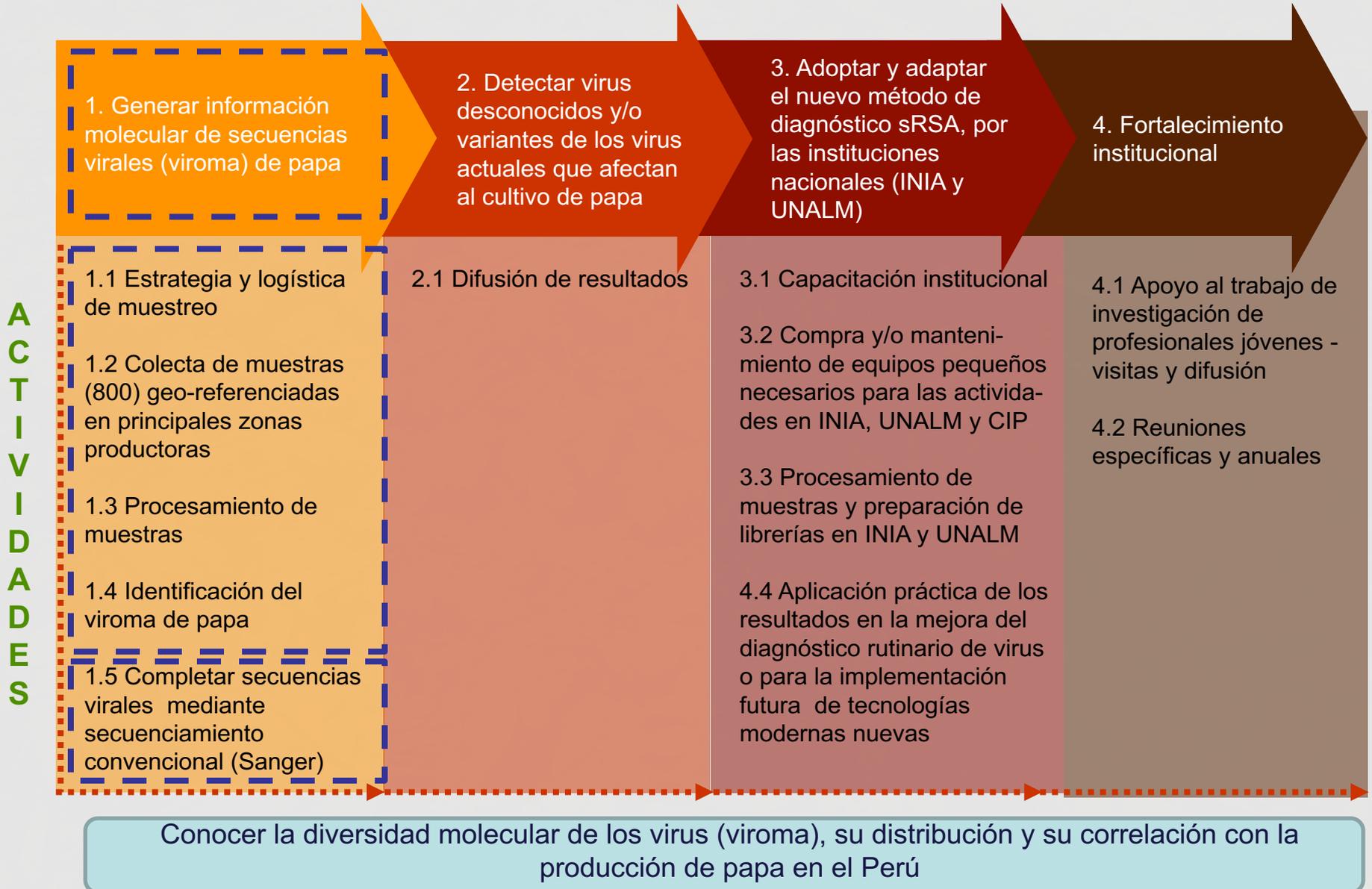
- Cusco (16)
- Huánuco (9)
- Junín (4)
- Cajamarca (3)



## Recombinación (RDP4)

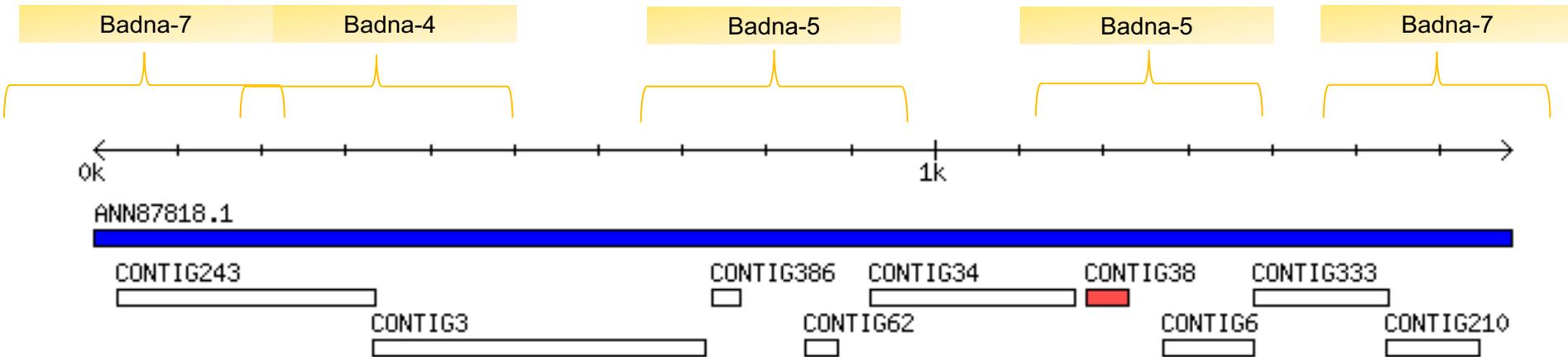


# COMPONENTES



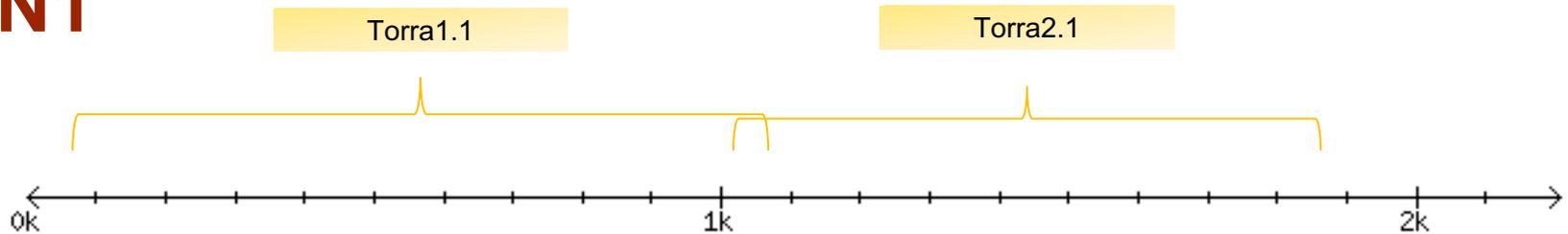
# Badnavirus – nueva especie viral

## ADN

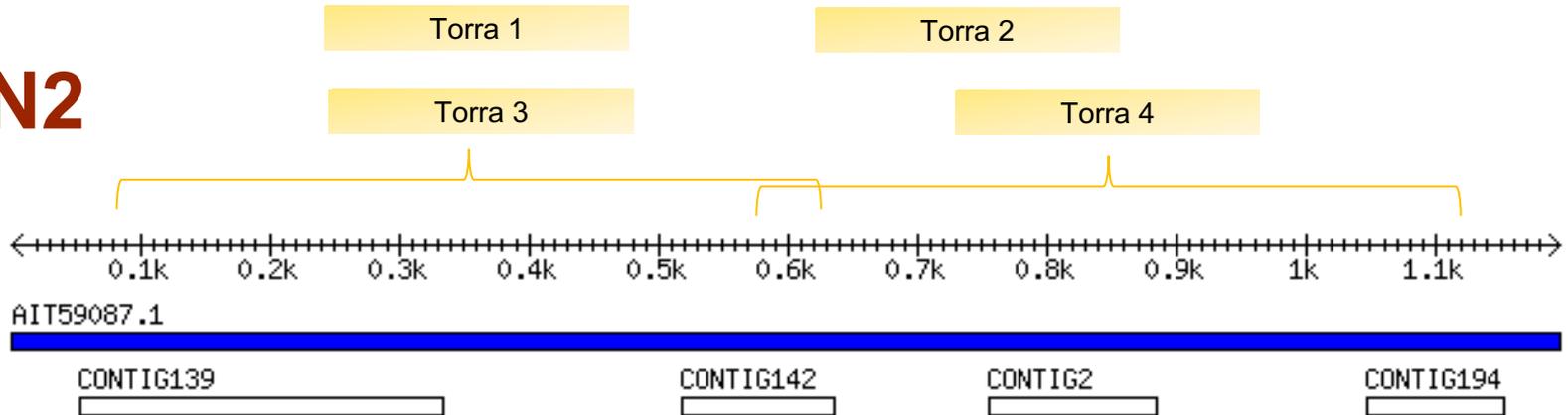


# Torradovirus – nueva especie viral

## ARN1



## ARN2



# COMPONENTES



Conocer la diversidad molecular de los virus (viroma), su distribución y su correlación con la producción de papa en el Perú

## Capacitaciones



**CIP (8 personas)**

## Equipamiento



**UNALM (Lab. de Virología)**



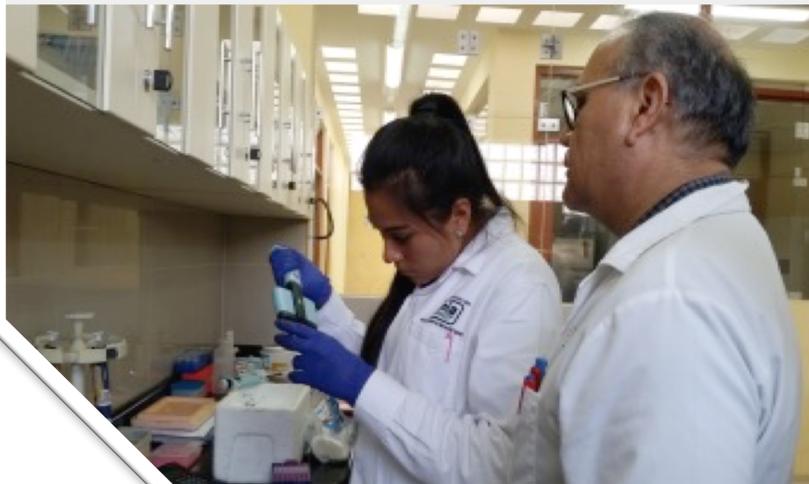
**INIA (6 personas)  
UNALM (2 personas)**



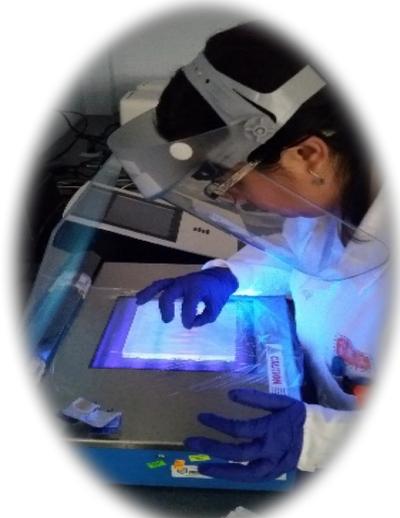
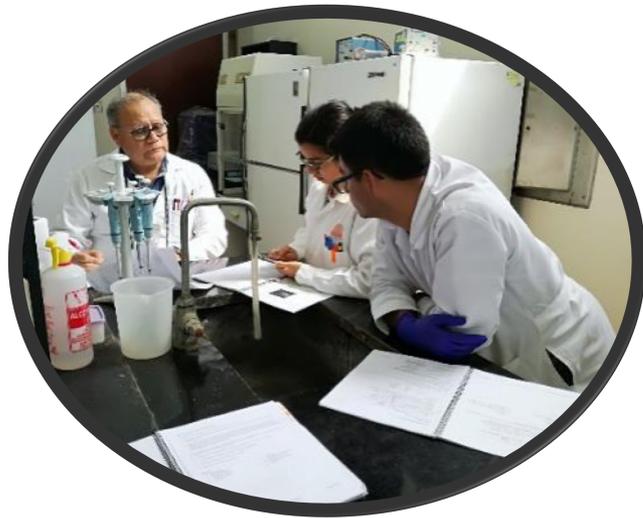
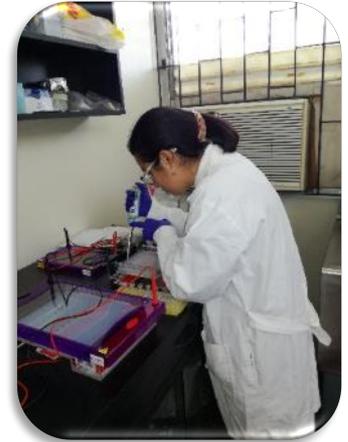
**Mantenimiento  
de equipos**

**INIA (Lab. de Biología Molecular y Genómica)**

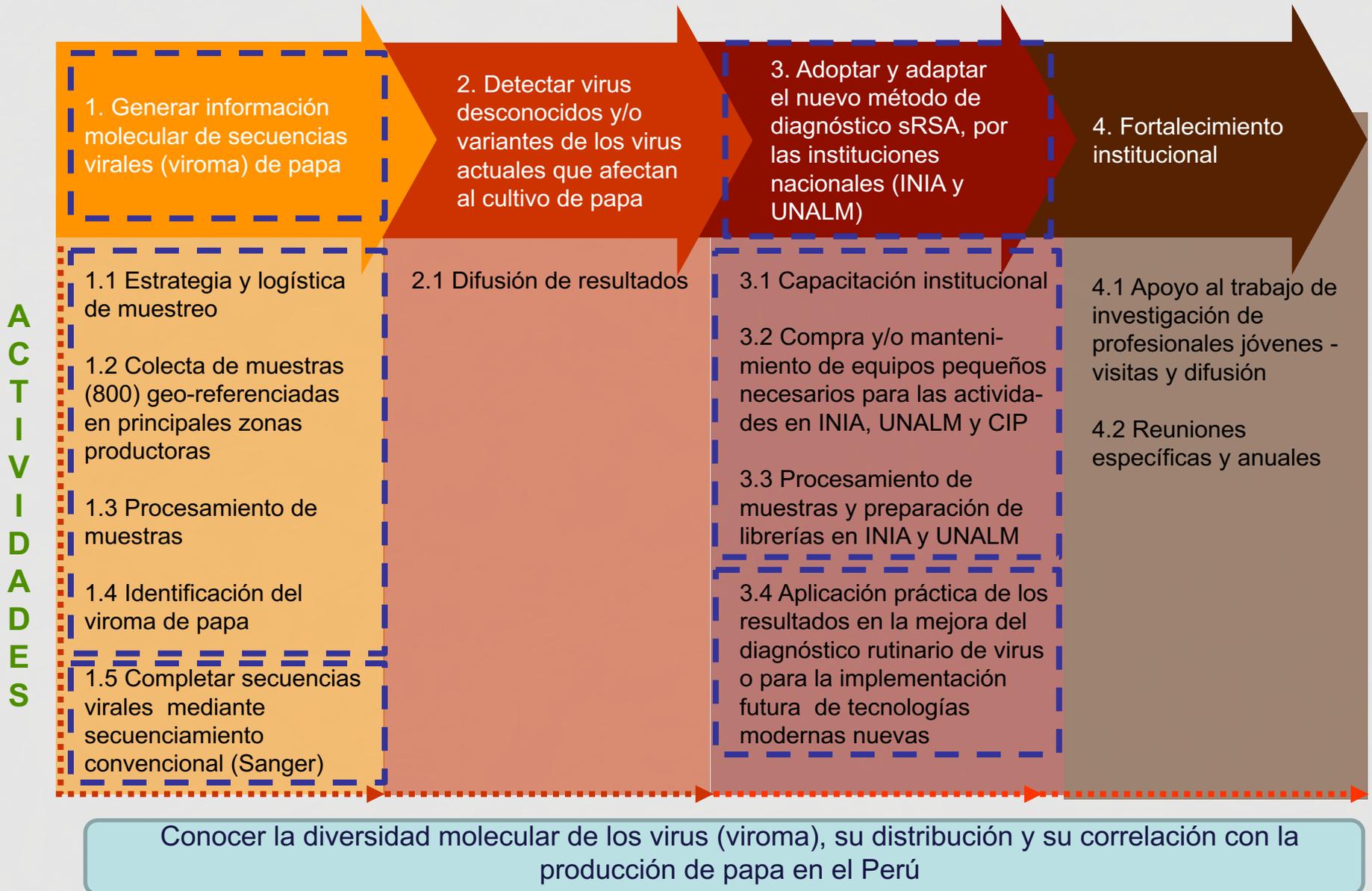
# *Procesamiento de muestras (INIA) - junio 2017*



# *Procesamiento de muestras (UNALM) – octubre 2017*

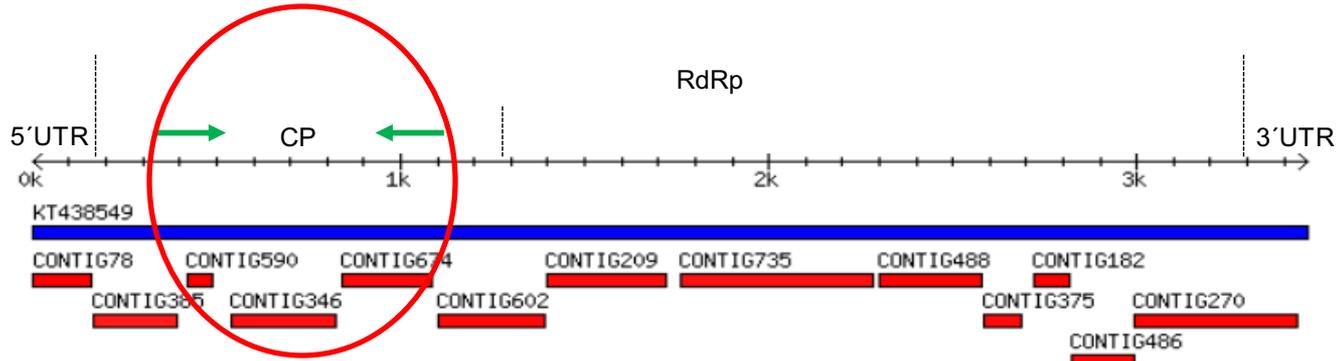


# COMPONENTES

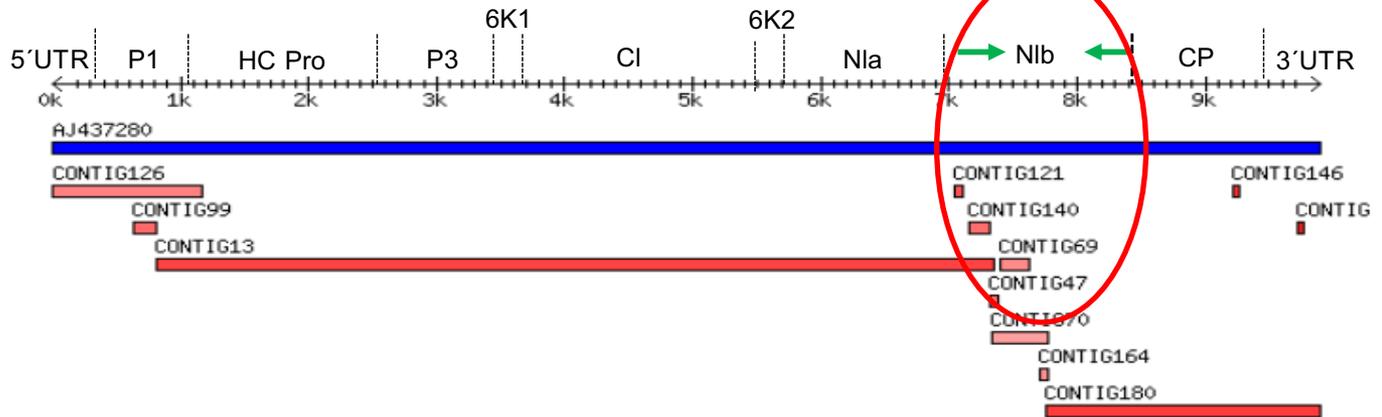


# Diagnóstico de virus en tomate y ají

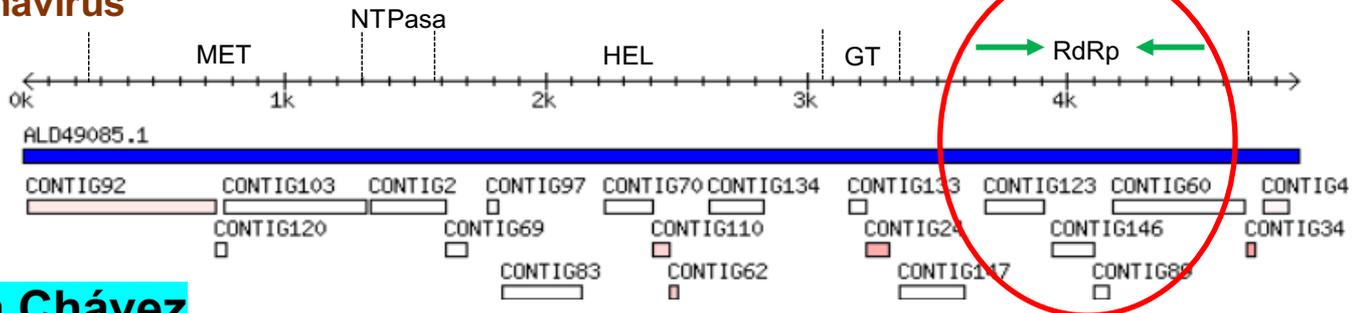
STV



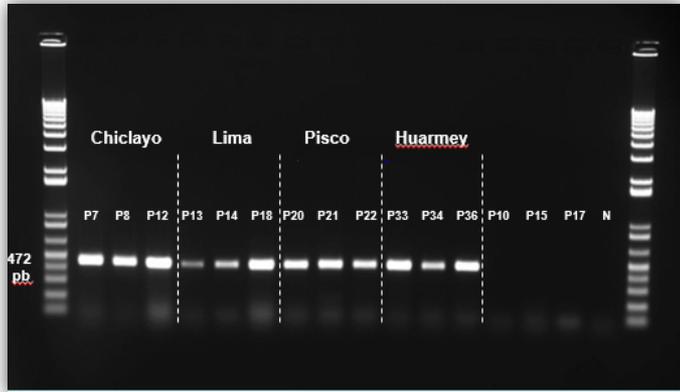
PTMV



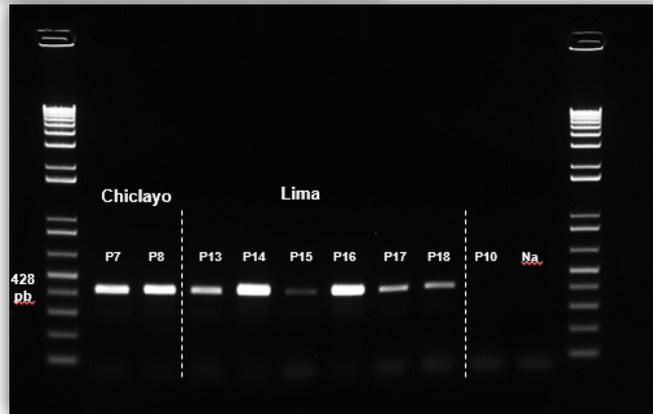
Alphaendornavirus



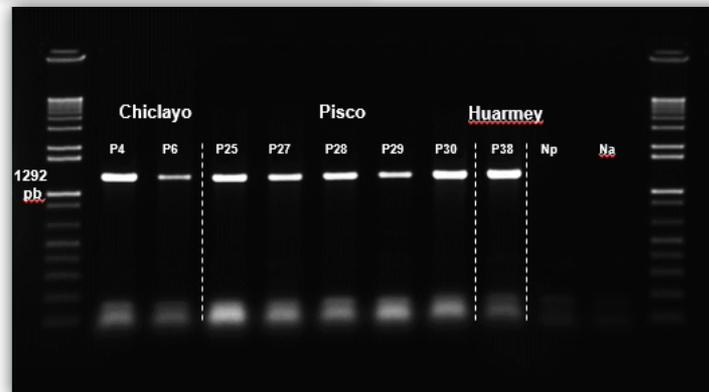
# Diagnóstico de virus en tomate y ají



STV



PTMV



Alfaendornavirus

# Detección de virus de papa mediante LAMP

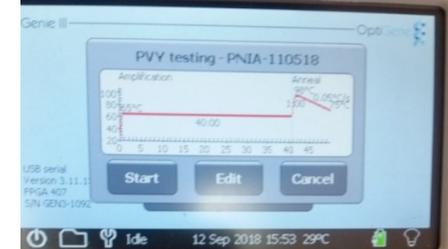
## Diagnóstico en campo



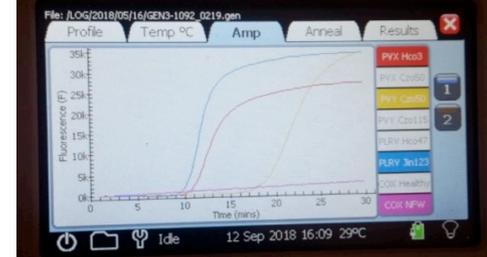
Detección de virus que en papa (e.g. PVY, PVX, PLRV)

- Extracción de savia
- Reacción en el aparato (Genie)
- Monitoreo de la curva de amplificación de las reacciones en la pantalla

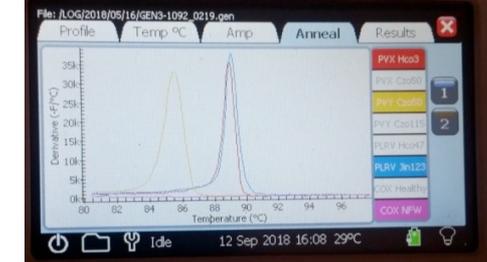
1. Ajuste de las cond. func.



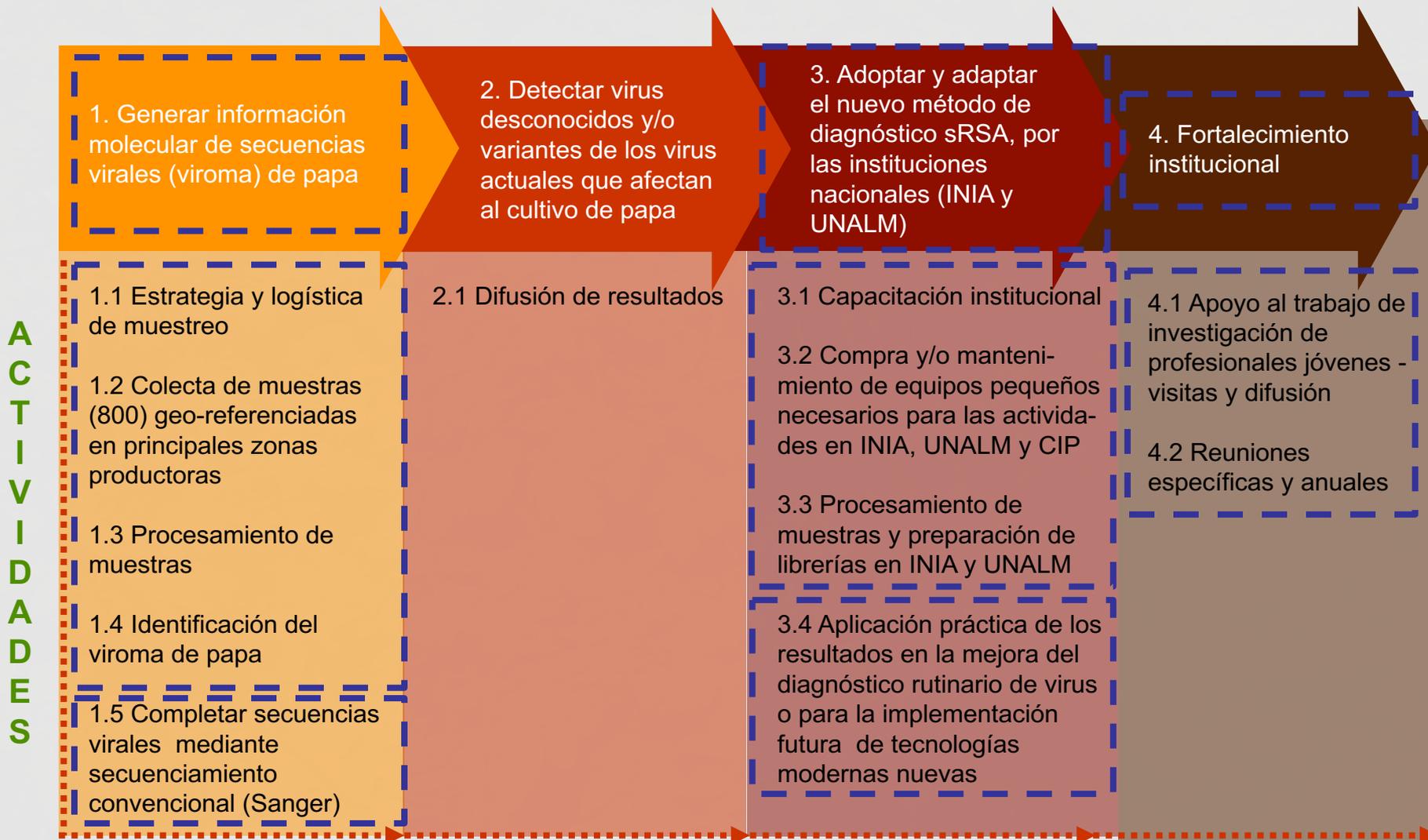
2. Monitoreo de la curva de amplif.



3. Visualización del anal. de disoc.



# COMPONENTES



Conocer la diversidad molecular de los virus (viroma), su distribución y su correlación con la producción de papa en el Perú

# Tesis de posgrado

## Tesis de Maestría – Fitopatología

 UNIVERSIDAD NACIONAL AGRARIA LA MOLINA  
ESCUELA DE POSGRADO  
"Año del Buen Servicio al Ciudadano"  


**RESOLUCIÓN EPG N° 041/2017**  
La Molina, 17 de enero de 2017

**CONSIDERANDO:**

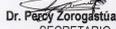
1. Que, para optar el grado de *Magister Scientiae* y/o *Doctoris Philosophiae* el alumno debe sustentar y aprobar una tesis de naturaleza original basada en una investigación, que realiza bajo la dirección de un Profesor Patrocinador y con el apoyo de dos miembros de su Comité Consejero.
2. Que, los alumnos que se mencionan a continuación han presentado a la EPG los respectivos

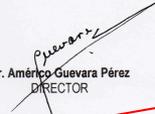
**FITOPATOLOGÍA**

**TÍTULO:** POTYVIRUS EN TOMATE (*Solanum lycopersicum*) Y AJÍ (*Capsicum spp.*) MEDIANTE EL SECUENCIAMIENTO Y ENSAMBLADO DE PEQUEÑOS FRAGMENTOS DE ARNs (sgRNA).

**ALUMNA:** **Chávez Infante, Pamela Alejandra**  
**PATROCINADOR:** Mg.Sc. Carlos Cadenas Giraldo  
**CO-PATROCINADOR:** Mg.Sc. Segundo Fuentes Delgado  
**MIEMBRO:** Mg.Sc. César Fribourg Solís  
**MIEMBRO:** Mg.Sc. Liliana Aragón Caballero

**SE RESUELVE:**  
Aprobar los siguientes proyectos de tesis presentados a la Escuela de Posgrado:  
Regístrese, comuníquese y archívese.

 Dr. Percy Zorogástua Cruz  
SECRETARIO

 Dr. Américo Guevara Pérez  
DIRECTOR



**PROYECTO DE TESIS APROBADO**

ENE (Pág. 6 de 6)

Av. La Molina 1207, La Molina, Lima – Perú | 511-7600 anexos 209 – 200 / 614 7142  
escuela@lamolina.edu.pe | www.lamolina.edu.pe/posgrado



**Pamela Alejandra Chávez Infante**

“Detección de secuencias virales en *Solanum lycopersicum* y *Capsicum spp.* mediante el secuenciamiento y ensamblado de ARN pequeños (siRNA)”

# Tesis de posgrado

## Tesis de Maestría – Biología Molecular



UNIVERSIDAD NACIONAL MAYOR DE SAN MARCOS  
Oficinas de la Facultad de Ciencias Biológicas

FACULTAD DE CIENCIAS BIOLÓGICAS

VICEDECANATO DE INVESTIGACIÓN Y POSGRADO  
UNIDAD DE POSGRADO

DICTAMEN N° 214-UPG-VDIPG-FCB-17

Lima, 17 de noviembre de 2017. — VISTO: La solicitud que presenta la Señorita Bachiller **MELODY AMAO PEÑA** con Código de Matrícula N° 14107016, de la Maestría en Biología Molecular, de la Unidad de Posgrado de la Facultad de Ciencias Biológicas de la UNMSM pidiendo el nombramiento de Asesor e inscripción de su Trabajo de Tesis intitulada: **Identificación y obtención del genoma completo de virus nuevos de papa mediante secuenciamiento profundo de ARN de interferencia extraídas de plantaciones provenientes de Cusco - Perú**. — CONSIDERANDO: — Que, dicha solicitud cuenta con la aceptación del Dr. Pablo Sergio Ramírez Roca, como Asesor del Trabajo de Tesis arriba mencionado y la aprobación del Comité Coordinador de la Maestría en Biología Molecular. — Que, la Dirección de la Unidad de Posgrado, previo examen de la documentación presentada por la recurrente y en uso de las atribuciones que la Ley y el Estatuto de la Universidad confiere a la Directora de la Unidad de Posgrado, Dictamina:

1. Inscribir el Trabajo de Tesis presentado por la Señorita Bachiller **MELODY AMAO PEÑA** con Código de Matrícula N° 14107016 de la Maestría en Biología Molecular de esta Unidad Académica.
2. Nombrar al Profesor **DR. PABLO SERGIO RAMÍREZ ROCA** como asesor de la solicitante para el mencionado Proyecto de Tesis.

Regístrese, comuníquese, publíquese y archívese.

*Rina Lastenia Ramírez Mesías*

DRA. RINA LASTENIA RAMÍREZ MESÍAS  
Directora de la Unidad de Posgrado  
Vicedecana de Investigación y Posgrado

**PROYECTO DE TESIS APROBADO**

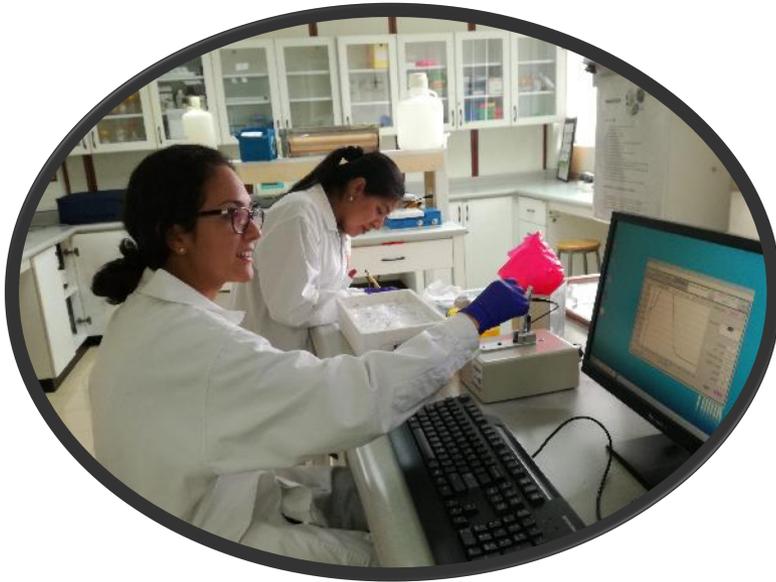


**Melody Amao Peña**

“Identificación y obtención del genoma completo de nuevos virus de papa mediante secuenciamiento profundo de ARN de interferencia extraídas de plantaciones provenientes de Cusco-Perú”

# Estancias de Investigación

Universidad de Bonn – Alemania



**Carina Fernández**  
(enero 2018)

USDA-APHIS, MD, USA



**Marco Gálvez**  
(enero 2019)

UNALM



**Angie Burgos**  
(enero 2019)

## *Reuniones interinstitucionales*



# COMPONENTES



Conocer la diversidad molecular de los virus (viroma), su distribución y su correlación con la producción de papa en el Perú

# Participación en Eventos Científicos



10th World Potato Congress  
XXVIII CONGRESO DE LA ASOCIACIÓN LATINOAMERICANA DE LA PAPA

WPC | ALAP | CUSCO, PERU | 2018

## PERUVIAN POTATO VIROME: WHY WE NEED TO KNOW MORE

**Segundo Fuentes, Ana Perez, Jan F. Kreuze**

International Potato Center (CIP), Crop and Systems Sciences Division  
• Av. La Molina 1895. La Molina, Lima 12, Perú  
Corresponding author's email: s.fuentes@cigar.org



Logos: INIA, CIP, LA MOLINA, prom-peru, Organización de las Naciones Unidas para la Alimentación y la Agricultura



CUSCO-PERU | MAY 27-31, 2018  
10th World Potato Congress  
XXVIII CONGRESO DE LA ASOCIACIÓN LATINOAMERICANA DE LA PAPA  
BIODIVERSITY, FOOD SECURITY, AND BUSINESS



*“Peruvian potato virome: why we need to know more”*

# Participación en Eventos Científicos



**Peruvian Potato Virome: mapping virus diversity to understand current and future threats under a changing climate**

Jan F. Kreuze, Segundo S. Fuentes, Ana L. Pérez

International Potato Center (CIP), Av. La Molina 1895, Lima 12, Lima, Peru.

Corresponding author: [j.kreuz@cgiar.org](mailto:j.kreuz@cgiar.org)

**Abstract**

The Andean Region, which includes Peru, is the center of potato diversity and therefore likely also of potato viruses. Under global warming, the emergence of new viral diseases can be expected due to changes in the population of virus and their vectors as affected by temperature. Here we report the viruses detected in potato samples collected in five areas in Peru by using small RNA sequencing and assembling approach. The viruses detected with the highest incidence were PVX, PVY, PVS, PVV, and PVB. Other viruses detected with lower incidence were PLRV, PVA, PMTV, PVV, APLV, APMoV, and PBRSV. New strains corresponding to the viruses PVX, PVY, PVV, PVA, PVB, PBRSV, APMoV, APLV, PVS, APMMV, and PVV were identified; as well as of several novel viruses in the genera Potexvirus, Potyvirus, Nepovirus, Comovirus, Tymovirus, Carlavirus, Ilarvirus, Badnavirus, Torradovirus, Enamovirus, Ophiovirus, Pterovirus, Fabavirus, Tobravirus, and Pomovirus. Viruses PVB, PVA and a torrado-like virus (coded as SB26/SB29) were found more widespread than expected. This variability gives a snapshot of the viral diversity in potato in its center of domestication and was higher in Cusco and Junin than in Cajamarca, Huánuco, and Iquitos. This could be the result of higher variability of domesticated and wild potato species in these regions, but may also imply that there is a greater risk for potato cultivation in Cusco and Junin, considering that greater variation means a greater possibility that new variant viruses could emerge as a result of a changing climate.

Keywords: Potato, *Solanum tuberosum*, virus detection, small RNA, high-throughput sequencing

# Participación en reuniones diversas (abril 2018)

**Universidad Tecnológica de los Andes**  
FACULTAD DE INGENIERÍA  
ESCUELA PROFESIONAL DE AGRONOMÍA  
Comprometidos con la acreditación

  
"Año del Diálogo y la Reconciliación Nacional"

Andahuaylas, 02 de abril del 2018.

**OFICIO No.008-2018-UTEA-FA-EPA/SD.**

**Señor:**  
**M.Sc. Segundo Saúl Fuentes Delgado**  
**Investigador Asociado Senior en la Unidad**  
**de Viología del Centro Internacional de la**  
**Papa (CIP).**

**LIMA -**

**ASUNTO:** SOLICITA APOYO EN PONECIA SOBRE EL TRABAJO QUE REALIZA EN EL VIROMA DE LA PAPA.

Tengo el agrado de dirigirme a usted para saludarlo cordialmente y a la vez invitarlo a poder apoyarnos con una ponencia el día martes 03 de abril a las 6:00 pm, en el Auditorio principal de nuestra casa de estudios, sobre el trabajo que realiza en el viroma de la papa; Ponencia que servirá de mucho en la formación de nuestros estudiantes de la escuela profesional de agronomía de la Universidad Tecnológica de los Andes filial Andahuaylas.

Seguro de contar con su gentil atención hago la ocasión para manifestarle los sentimientos de mi consideración y estima.

Atentamente,

  
Ing. Jorge Luis Veloz Casas  
Director de la UTEA-Andahuaylas

  
Ing. Wladimir Vozquez  
Sub director de la E.P. Agronomía



CC  
HU  
Archivo.

UNIVERSIDAD TECNOLÓGICA DE LOS ANDES  
Ciudad: Andahuaylas Av. 700, N° 700, Alameda, Corral Teñido s/n 02 - (084) 521550  
Hidalgo: Arequipa, Of. 16 - Teléfono: 084 291566  
Sub. Soc. Andahuaylas: Av. Juan Antonio Irigoin 2° y la calle 3800, 421762  
www.utea.uni.pe



**Viroma de la papa en Perú**

**Segundo Fuentes**  
(s.fuentes@cigar.org)

Andahuaylas, 05 Abril de 2018

CENTRO INTERNACIONAL DE LA PAPA  
CIP



# Participación en reuniones diversas (octubre 2018)

**INTERNATIONAL PHYTOSANITARY AWARENESS WEEK**  
22-26 OCTUBRE / OCTOBER  
LIMA HARARE KILIMAKI YANGON MAPUTO

**CIP**  
INTERNATIONAL POTATO CENTER  
A CGIAR RESEARCH CENTER

Segundo Fuentes  
s.fuentes@cigar.org

**The Peruvian potato virome and pathogen diversity database: what can we expect in the future under a changing climate**  
October 26, 2018

Genebank Platform  
CGIAR

AfricaRice  
Bioversity International  
World Agroforestry Centre  
ICARDA  
Accession for Better Livelihoods in Dry Areas  
CIP  
INTERNATIONAL POTATO CENTER  
A CGIAR RESEARCH CENTER

CROP TRUST  
ILRI  
INTERNATIONAL LIVESTOCK RESEARCH INSTITUTE  
IITA  
Transforming African Agriculture  
IRRI

ICRISAT  
INTERNATIONAL CROPS RESEARCH INSTITUTE FOR THE SEMI-ARID TROPICS  
CIAT  
Centro Internacional de Agricultura Tropical  
Desde 1967. Ciencia para cultivar el mundo.  
CIMMYT  
International Maize and Wheat Improvement Center

**GERMPLASM HEALTH UNITS: SECURING THE PATH TO FOOD SECURITY**

Health Quarantine Unit

# Artículo Científico enviado a Revista Internacional

## Potato virus Y; the Andean connection

Segundo Fuentes<sup>1</sup>, Roger A.C. Jones<sup>2</sup>, Hiroki Matsuoka<sup>3</sup>, Kazusato Ohshima<sup>3</sup>, Jan Kreuze<sup>1</sup>, and Adrian J. Gibbs<sup>4\*</sup>

<sup>1</sup> Crop and System Sciences Division, International Potato Center (CIP), Apartado 1558, Lima 12, Peru; <sup>2</sup> Institute of Agriculture, University of Western Australia, 35 Stirling Highway, Crawley, WA 6009, Australia, and Department of Primary Industries and Regional Development, 3 Baron-Hay Court, South Perth, WA 6151; Australia. <sup>3</sup>Laboratory of Plant Virology, Department of Applied Biological Sciences, Faculty of Agriculture, Saga University, 1-banchi, Honjo-machi, Saga 840-8502, Japan; <sup>4\*</sup> Emeritus Faculty, Australian National University, ACT 2601, Australia.

\*Corresponding author: E-mail: adrian\_j\_gibbs@hotmail.com.

Key words: potato virus Y, phylogenetics, dating, history, Colombian exchange.

### Abstract

*Potato virus Y* (PVY) causes disease in potatoes and other solanaceous crops. The appearance of its necrogenic strains in the 1980s made it the most economically important virus of potatoes. PVY originated in the Andean region of South America which is where potatoes were first domesticated. We report the isolation and genomic sequences of 32 Peruvian isolates of PVY which, together with 428 published genomic sequences, gave an alignment of 460 sequences. Of these 190 (41%) were non-recombinant, and 162 of them provided a dated phylogeny. The phylogeny, its dates and the likely history of PVY correspond well. The current PVY population originated around 156 CE. It was probably first taken from South America to Europe in the 16<sup>th</sup> century in tubers. The most basal divergences of the O and N phylogroups occurred before this, but most present PVY diversity probably emerged after the mid 19<sup>th</sup> century, when the *Phytophthora infestans* epidemics of the mid-19<sup>th</sup> century destroyed the European crop and stimulated potato breeding. Imported breeding lines were shared, and there was no quarantine. The O and C phylogroup populations probably established first in the European crop, and were joined later by N phylogroup isolates generating the R1 and R2 populations of damaging necrogenic strains. Our dating study has confirmed that human activity has probably dominated the phylodynamics of PVY for the last two millennia.

### Introduction

The potato is now the third most important food crop globally (Devaux et al. 2014, and virus diseases are a major factor constraining its production, especially in developing countries (Jones 2014; Kreuze et al. 2019). *Potato virus Y* (PVY; genus *Potyvirus*) causes disease in potato and a wide range of other solanaceous species, including the important crop species tobacco, tomato,

## Potato virus Y; the Andean connection

Journal:	Virus Evolution
Manuscript ID:	VEVOLL-2019-015
Manuscript Type:	Research Article
Date Submitted by the Author:	12-Feb-2019
Complete List of Authors:	Fuentes, Segundo; Centro Internacional de la Papa, Crop and Systems Science Jones, Roger; University of Western Australia, Institute of Agriculture Ohshima, Kazusato; Saga University, Department of Applied Biological Sciences Kreuz, Jan; Centro Internacional de la Papa, Crop and System Sciences Gibbs, Adrian; Australian National University, ANU Emeritus Faculty
Keywords:	potato virus Y, phylogenetics, dating, history, Colombian exchange

### Acknowledgements

This research was part of the CGIAR Research Program on Roots, Tubers and Bananas (RTB). Funding support was provided by Programa Nacional de Innovación Agraria (PNIA, contract 029-2015-INA-PNIA-UPMSI/IE) from Peru. We are very grateful for technical support at C.I.P. by Ana Perez and Pamela Chavez

### Legends

Figure 1. Map of potato sample collection sites in the Andean Highlands of Peru showing where PVY was detected (red spots). The numbers clustered around each collection site indicate where each individual infected sample came from (Table 1). The names marked on the map are those of the countries regional departments (red lines are departmental boundaries). Inset shows an outline map of the entire country and neighboring regions of the five countries with land borders.

PYV, Badnavirus, Torradovirus,....

# Plataforma Web (acceso público) – datos del viroma Peruano de la papa

<http://potpathodiv.org/>

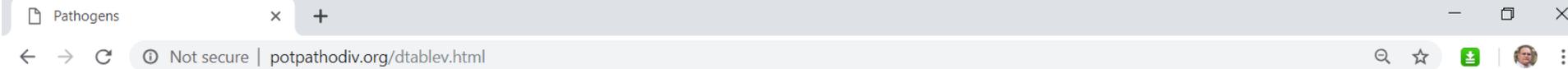
Database of the main pathogens detected, identified and characterized in the potato crop in Peru

P. INFESTANS R. SOLANACEARUM VIROME

CIP-PNIA

7:16 AM 10/26/2018

# Viroma Peruano de la papa – Plataforma Web



- Home
- Map**
- R. solanacearum
- P. Infestans
- Virome
- Data
- Admin
- Tutorial

## Virome data

- Field List**
- Samples**

Show 10 entries

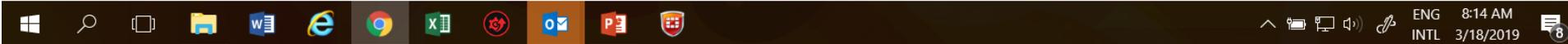
Search:

Country	Field ID	Department	Province	District	Latitude	Longitude	Altitude
Peru	Cus	Cusco	Anta	Ancahuasi	-13.44399	-72.32522	3592
Peru	Cus	Cusco	Anta	Limatambo	-13.46131	-72.41885	2871
Peru	Cus	Cusco	Calca	Pisac	-13.38435	-71.81136	3518
Peru	Cus	Cusco	Cusco	Santiago	-13.58426	-71.98408	3844
Peru	Cus	Cusco	Paruro	Huanoquite	-13.68634	-72.00740	3432
Peru	Cus	Cusco	Paruro	Yaurisque	-13.68939	-71.95618	3106
Peru	Cus	Cusco	Paucartambo	Challabamba	-13.15574	-71.68884	2956
Peru	Cus	Cusco	Paucartambo	Colquepata	-13.34083	-71.69811	3381
Peru	Hua	Huancavelica	Angaraes	Lircay	-13.04094	-74.69817	3494
Peru	Hua	Huancavelica	Huancavelica	Chuñuranra	-12.80568	-75.04839	3804

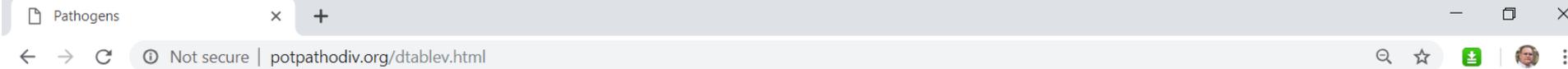
Showing 11 to 20 of 64 entries

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## Virome data

- Field List**
- Samples**

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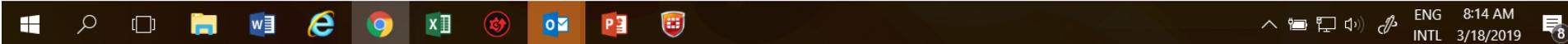
Search:

Country	Field ID	Department	Province	District	Latitude	Longitude	Altitude
Peru	Cus	Cusco	Anta	Ancahuasi	-13.44399	-72.32522	3592
Peru	Cus	Cusco	Anta	Limatambo	-13.46131	-72.41885	2871
Peru	Cus	Cusco	Calca	Pisac	-13.38435	-71.81136	3518
Peru	Cus	Cusco	Cusco	Santiago	-13.58426	-71.98408	3844
Peru	Cus	Cusco	Paruro	Huanoquite	-13.68634	-72.00740	3432
Peru	Cus	Cusco	Paruro	Yaurisque	-13.68939	-71.95618	3106
Peru	Cus	Cusco	Paucartambo	Challabamba	-13.15574	-71.68884	2956
Peru	Cus	Cusco	Paucartambo	Colquepata	-13.34083	-71.69811	3381
Peru	Hua	Huancavelica	Angaraes	Lircay	-13.04094	-74.69817	3494
Peru	Hua	Huancavelica	Huancavelica	Chuñurana	-12.80568	-75.04839	3804

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## Field (Cus) information

Field ID:	Cus
Country:	Peru
Department:	Cusco
Province:	Paucartambo
District:	Challabamba
Locality:	
Latitude:	-13.15574°
Longitude:	-71.68884°
Altitude:	2956 m

## Field Map



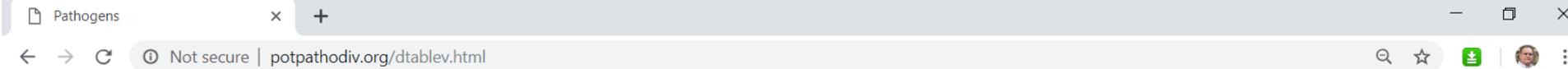
## Samples in field Cus

Show 10 entries

Search:

Sample	Date	Pathogen Host	Cultivar	Sequenced
Cus-081	2016	Potato	Macclillo	1
Cus-082	2016	Potato	Macclillo	1
Cus-083	2016	Potato	Macclillo	1
Cus-084	2016	Potato	Amarillis	1
Cus-085	2016	Potato	Amarillis	1
Cus-086	2016	Potato	Amarillis	1

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Field List

Samples

Show 10 entries

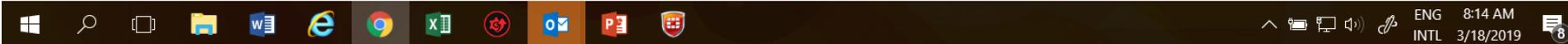
Search:

Country	Field ID	Department	Province	District	Latitude	Longitude	Altitude
Peru	Cus	Cusco	Anta	Ancahuasi	-13.44399	-72.32522	3592
Peru	Cus	Cusco	Anta	Limatambo	-13.46131	-72.41885	2871
Peru	Cus	Cusco	Calca	Pisac	-13.38435	-71.81136	3518
Peru	Cus	Cusco	Cusco	Santiago	-13.58426	-71.98408	3844
Peru	Cus	Cusco	Paruro	Huanoquite	-13.68634	-72.00740	3432
Peru	Cus	Cusco	Paruro	Yaurisque	-13.68939	-71.95618	3106
Peru	Cus	Cusco	Paucartambo	Challabamba	-13.15574	-71.68884	2956
Peru	Cus	Cusco	Paucartambo	Colquepata	-13.34083	-71.69811	3381
Peru	Hua	Huancavelica	Angaraes	Lircay	-13.04094	-74.69817	3494
Peru	Hua	Huancavelica	Huancavelica	Chuñuranra	-12.80568	-75.04839	3804

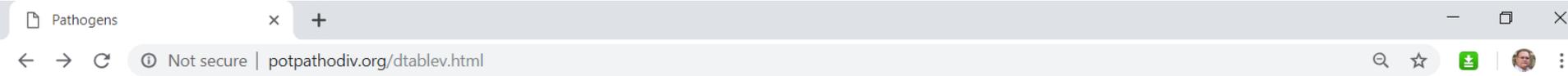
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Field List Samples

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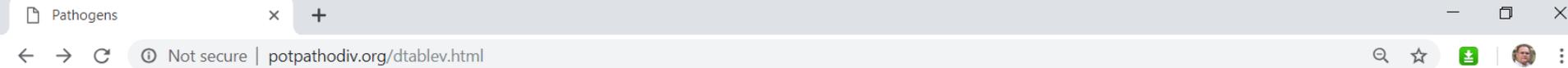
Search:

Sample	Field	Year	Pathogen host	Cultivar/Specie	Cultivar age (months)	Phenologic state	Intercultivar	Field number	Field size	Field picture	Plant picture	Leaf picture	Seed Origin	Management system	Pesticides	Common Virus	New Viru
Cus-093	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	<a href="#">Ver</a>	<a href="#">Ver</a>	<a href="#">Ver</a>	Cusco			PVY	APM
Cus-094	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	<a href="#">Ver</a>	<a href="#">Ver</a>	<a href="#">Ver</a>	Cusco			PVY	PVY
Cus-095	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	<a href="#">Ver</a>	<a href="#">Ver</a>	<a href="#">Ver</a>	Cusco			PVY, PVB	
Cus-096	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	<a href="#">Ver</a>	<a href="#">Ver</a>	<a href="#">Ver</a>	Cusco			PVY, PVB, PVY, PVV	PVY
Cus-097	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	<a href="#">Ver</a>	<a href="#">Ver</a>	<a href="#">Ver</a>	Cusco			PVY, PVB, PVY, PVV	PVY
Cus-098	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	<a href="#">Ver</a>	<a href="#">Ver</a>	<a href="#">Ver</a>	Cusco			PVY, PVV, PVX?	
Cus-099	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	<a href="#">Ver</a>	<a href="#">Ver</a>	<a href="#">Ver</a>	Cusco			PVY, PVV, PVY	PVY
Cus-100	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	<a href="#">Ver</a>	<a href="#">Ver</a>	<a href="#">Ver</a>	Cusco			PVX, PVY	
Cus-100B	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	<a href="#">Ver</a>	<a href="#">Ver</a>	<a href="#">Ver</a>	Cusco			PVX, PVY	PVS APM
Cus-101	Cus	2016	Potato	Cica	4	Floración		11	1500	<a href="#">Ver</a>	<a href="#">Ver</a>	<a href="#">Ver</a>	Mercado Cusco			PVX, PVY	

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Field List Samples

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Search:

thogen st	Cultivar/Especie	Cultivar age (months)	Phenologic state	Intercultivar	Field number	Field size	Field picture	Plant picture	Leaf picture	Seed Origin	Management system	Pesticides	Common Virus	New Virus	Novel Virus	Symptoms
tato	Canchan	2	Vegetativo		10	3000	Ver	Ver	Ver	Cusco			PVY	APMoV	Comovirus	
tato	Canchan	2	Vegetativo		10	3000	Ver	Ver	Ver	Cusco			PVY	PVY		
tato	Canchan	2	Vegetativo		10	3000	Ver	Ver	Ver	Cusco			PVY, PVB, PVY, PVV	PVY	Varicosavirus	
tato	Canchan	2	Vegetativo		10	3000	Ver	Ver	Ver	Cusco			PVY, PVB, PVY, PVV	PVY	Iilarvirus	
tato	Canchan	2	Vegetativo		10	3000	Ver	Ver	Ver	Cusco			PVY, PVV, PVX?			
tato	Canchan	2	Vegetativo		10	3000	Ver	Ver	Ver	Cusco			PVY, PVV, PVY	PVY		
tato	Canchan	2	Vegetativo		10	3000	Ver	Ver	Ver	Cusco			PVX, PVY			
tato	Canchan	2	Vegetativo		10	3000	Ver	Ver	Ver	Cusco			PVX, PVY	PVS, PVY, APMoV	Comovirus	
tato	Cica	4	Fioración		11	1500	Ver	Ver	Ver	Mercado Cusco			PVX, PVY			

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Pathogens

Evento Proyecto\_PPT\_2019 - One

Evento Proyecto\_PPT\_2019 - One

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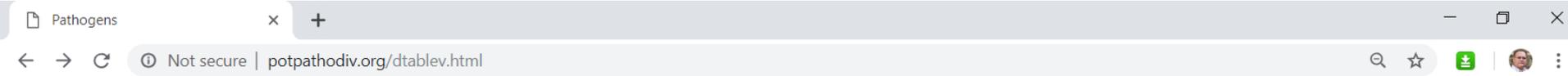
Tutorial

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Pesticides	Common Virus	New Viru
	PVY	APV
	PVY	PVY
	PVY, PVB	
	PVY, PVB PVY, PVW	PVY
	PVY, PVB PVY, PVW	PVY
	PVY, PVW PVX?	
	PVY, PVW PVY	PVY
	PVX, PVY	PVY APV
	PVX, PVY	

ENG 11:35 AM  
INTL 3/18/2019

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## Virome data

Field List Samples

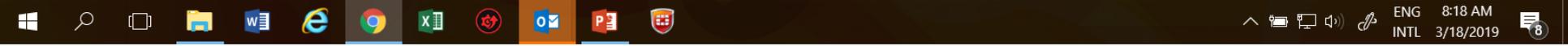
Show 10 entries

Search:

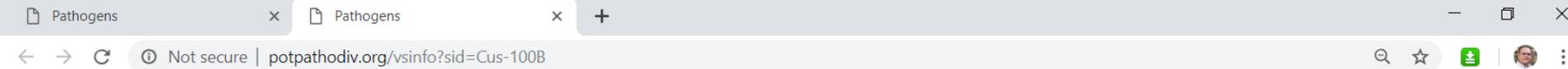
Sample	Field	Year	Pathogen host	Cultivar/Specie	Cultivar age (months)	Phenologic state	Intercultivar	Field number	Field size	Field picture	Plant picture	Leaf picture	Seed Origin	Management system	Pesticides	Common Virus	New Viru
Cus-093	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	Ver	Ver	Ver	Cusco			PVY	APM
Cus-094	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	Ver	Ver	Ver	Cusco			PVY	PVY
Cus-095	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	Ver	Ver	Ver	Cusco			PVY, PVB	
Cus-096	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	Ver	Ver	Ver	Cusco			PVY, PVB, PVY, PVV	PVY
Cus-097	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	Ver	Ver	Ver	Cusco			PVY, PVB, PVY, PVV	PVY
Cus-098	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	Ver	Ver	Ver	Cusco			PVY, PVV, PVX?	
Cus-099	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	Ver	Ver	Ver	Cusco			PVY, PVV, PVY	PVY
Cus-100	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	Ver	Ver	Ver	Cusco			PVX, PVY	
Cus-100B	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	Ver	Ver	Ver	Cusco			PVX, PVY	PVS APM
Cus-101	Cus	2016	Potato	Cica	4	Floración		11	1500	Ver	Ver	Ver	Mercado Cusco			PVX, PVY	

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  - Data
- Virome
  - Data
- Admin
  - P. Infestans* complete set
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  - Logout
- Tutorial

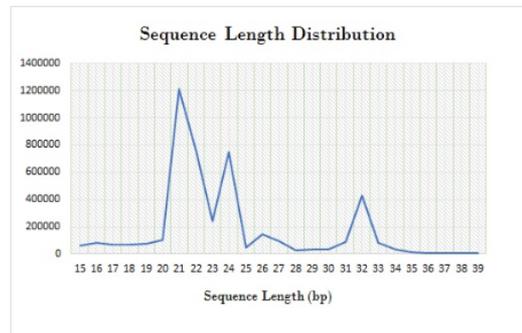
## Sample Cus-100B analyzing results

### Sample Cleaning

sample ID	Total Reads	Reads to be cleaned	% to be cleaned	Final Clean Reads	% Final Clean Reads
Cus-100B	8378743	3882636	46.34	4496107	53.66

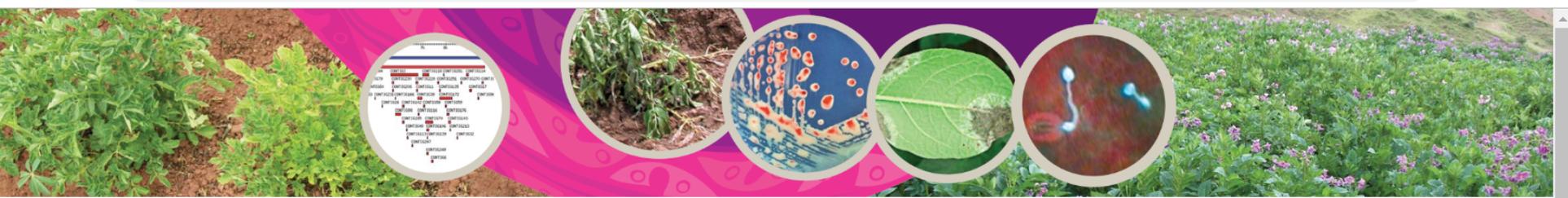
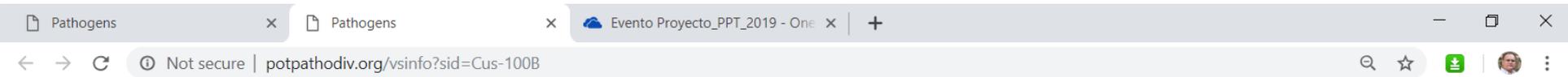
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### Length Distribution



Virus Identified by nucleotide similarity (BLASTN)

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## Sample Cus-100B analyzing results

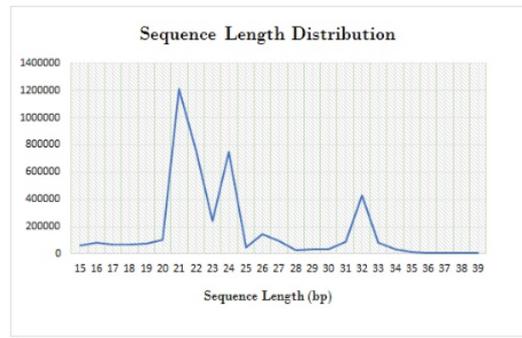
### Sample Cleaning

Number of reads that do not contain the adaptor sequence (unmatch), reads containing empty adaptors (Null), reads containing undetermined base (N) and reads that are short

sample ID	Total Reads	<a href="#">Reads to be cleaned</a>	% to be cleaned	Final Clean Reads	% Final Clean Reads
Cus-100B	8378743	3882636	46.34	4496107	53.66

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### Length Distribution



Virus Identified by nucleotide similarity (BLASTN)

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Pathogens x Pathogens x +  
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- Data
- Virome <
- Data
- Admin <
- P. Infestans complete set
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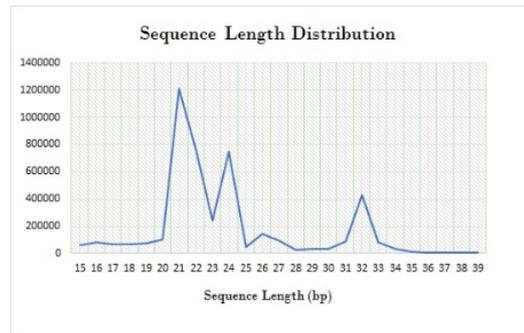
## Sample Cus-100B analyzing results

### Sample Cleaning

sample ID	Total Reads	Reads to be cleaned	% to be cleaned	Final Clean Reads	% Final Clean Reads
Cus-100B	8378743	3882636	46.34	4496107	53.66

Download Clean Reads

### Length Distribution



Virus Identified by nucleotide similarity (BLASTN)

Virus Identified by translated protein similarity (BLASTX)

FastQC



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## Virus Identified by nucleotide similarity (BLASTN)

Data interpretation Download Virus Contigs (BLASTN)

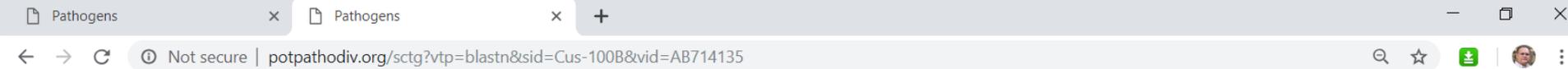
Reference	Length	Coverage (%)	#contig	Depth	Depth (Norm)	%identity	%iden Max	%iden Min	Genus	Description
AF493951	949	522 (55)	6	102.2	22.7	90.93	98.72	86.51	carlavirus	Potato virus S strain Andean coat protein mRNA, complete cds.
JQ847830	8482	4127 (48.7)	49	100.9	22.4	89.90	100	82.10	carlavirus	Potato virus S isolate BB-AND, complete genome.
JX883388	8117	3770 (46.4)	48	100.2	22.3	88.96	100	82.72	carlavirus	Potato virus S isolate RL5 RNA-dependent RNA polymerase gene, partial cds; and 12K protein, 7K protein, coat protein, and 11K protein genes, complete cds.
AJ863510	8494	3247 (38.4)	37	127.6	28.4	89.55	100	81.46	carlavirus	Potato virus S complete genome, isolate Vitava.
LN851194	8482	2754 (32.5)	31	139.5	31.0	88.46	100	79.75	carlavirus	Potato virus S complete genome, isolate Ewa.
KC430335	8488	2471 (29.1)	27	146.2	32.5	88.54	100	80.23	carlavirus	Potato virus S isolate Yunnan YN, complete genome.
HF571059	8485	2419 (28.5)	28	151.9	33.8	88.72	100	82.02	carlavirus	Potato virus S complete genome, isolate 89.249.
D00461	3552	2389 (67.3)	30	91.5	20.3	90.36	100	83.74	carlavirus	Potato virus S gene for Replicase, 25K protein, 12K protein, 42K protein, 7K protein, coat protein, 11K protein, complete and partial cds, 3'-terminal region.
KP089978	8498	2298 (27)	27	156.3	34.8	89.15	100	81.01	carlavirus	Potato virus S isolate SW-14, complete genome.
LN851190	8485	2273 (26.8)	26	154.0	34.2	89.63	100	84.07	carlavirus	Potato virus S complete genome, isolate Bonita.
FJ813512	8485	2280 (26.6)	27	147.9	32.9	89.65	100	80.57	carlavirus	Potato virus S isolate WaDef-US, complete genome.
JX419379	8507	2045 (24)	25	176.9	39.3	89.70	100	84.05	carlavirus	Potato virus S strain RVC Andean, complete genome.
M84483	2285	1583 (69.9)	7	297.8	66.2	84.29	96.83	80.52	comovirus	Andean potato mottle virus RNA-dependent RNA polymerase.
M72416	7588	6844 (90.4)	43	14.5	3.2	97.77	100	91.53	potexvirus	Potato virus X complete genome.
KM659859	6487	5501 (84.8)	41	11.0	2.4	95.14	100	89.80	potexvirus	Potato virus X isolate PVX-Gooseberry, complete genome.
KJ534601	6445	3458 (53.7)	42	12.7	2.8	97.86	100	93.75	potexvirus	Potato virus X isolate SA-CIP, complete genome.
KJ634024	9724	9724 (100)	49	2122.6	472.1	96.02	100	85.99	potyvirus	Potato virus Y isolate ShX14, complete genome.
JQ971975	9714	9714 (100)	59	2100.5	467.2	96.51	100	90.20	potyvirus	Potato virus Y isolate ME162, complete genome.
AB714135	9703	9703 (100)	52	2136.5	475.2	95.85	100	90.48	potyvirus	Potato virus Y genomic RNA, complete genome, isolate: T13.
KR270797	9726	9700 (99.7)	44	2164.0	481.3	94.48	100	87.88	potyvirus	Potato virus Y isolate mar7, complete genome.
AJ890348	9703	8985 (92.6)	17	2228.2	495.6	88.01	98.92	85.18	potyvirus	Potato virus Y strain C gene for polyprotein, genomic RNA, isolate Adgen.
EU482183	9691	8899 (91.5)	14	2230.0	496.0	84.94	97.85	84.23	potyvirus	Potato virus Y isolate Foggia, complete genome.
JN938418	9479	8713 (91.9)	57	2078.5	462.3	97.78	100	89.23	potyvirus	Potato virus Y isolate DD103A_164 polyprotein gene, partial cds.
AJ439545	9700	8557 (88.2)	14	2228.0	495.5	84.35	98.92	83.55	potyvirus	Potato virus Y gene for polyprotein, genomic RNA, isolate LYE84.2.
EU563512	9699	8419 (86.8)	18	2200.3	489.4	85.18	98.92	84.27	potyvirus	Potato virus Y strain C isolate PRI-509, complete genome.
JN938423	9383	8212 (87.7)	50	2109.0	469.1	96.57	100	87.69	potyvirus	Potato virus Y isolate NN300_80 polyprotein gene, partial cds.
JN938439	8801	7100 (80.7)	35	2171.3	482.9	95.83	100	86.54	potyvirus	Potato virus Y isolate Z001 polyprotein gene, partial cds.
KC296436	9703	4022 (41.5)	50	1775.3	394.9	96.64	100	86.54	potyvirus	Potato virus Y strain 1104, complete genome.



## Virus Identified by translated protein similarity (BLASTX)

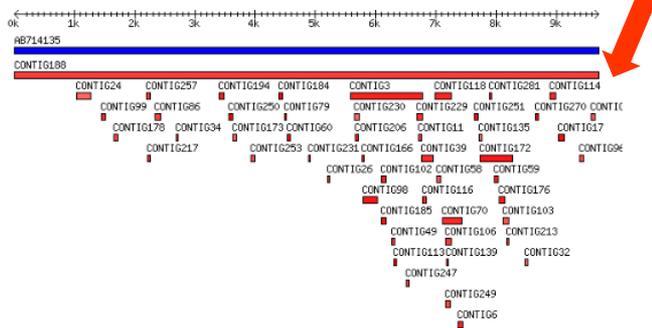
### FastQC

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Identification of virus AB714135 from sample Cus-100B



Order	Query ID	Query Start	Query End	Subject Start	Subject End	Identity	E value	Strand
1	CONTIG3	1	1189	5589	6777	1159/1189(97%)	0.0	-1

Alignment:

```
Query: 1 tccaactagacatccatcagctgtactactactgtaatccacaatgccatcattgt 60
      |||
Sbjct: 6777 tccaaccagacatccatcagctgtactactactgtaatccacaatgccatcattgt 6718

Query: 61 ttcaatccaatgcttccaaaagtgtcccggtacattgatgtactgctttctgt 120
      |||
Sbjct: 6717 ttcaatccaatgcttccaaaagtgtcccggtacattgatgtactgctttctgt 6658

Query: 121 gatgattgatgatcatgtttttctgaaaattagttccaaccaacaatccttcatt 180
      |||
Sbjct: 6657 gatgattgatgatcatgtttttctgaaaattagttccaaccaacaatccttcatt 6598

Query: 181 ctgcactggaagctcggaaatgcagtttttgggaaaacagggaaatcctttggcattct 240
      |||
```

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Pathogens x Pathogens x +

Not secure | potpathodiv.org/sctg?vtp=blastn&sid=Cus-100B&vid=AB714135#CONTIG188

36 CONTIG188 1 0700 1 0703 9276/9727(95%) 0.0 1

Alignment:

```
Query: 1 aaattaaaacaactcaatacaataagaanaatcaacgcaaaaacactcacaaaagcttt 60
      |||
Sbjct: 1 aaattaaaacaactcaatacaataagaanaatcaacgcaaaaacactcacaaaagcttt 60

Query: 61 caacttaattcaacaatttggtaagtttcaa-ttctgcttcatcaacaattc-t 118
      |||
Sbjct: 61 caattcaactcaagcaatttggtaagtttcaacttt-aatcttctctgtacaaa-cggt 118

Query: 119 ttcaa-ttccagtgtaagctatctgtaattcagtaag-ttattcaaaactctgtaaattg 176
      |||
Sbjct: 119 ttcaactt-cagtgtaagttctgtaactcaat-agttattcaaaactctcttatatag 176

Query: 177 caga-agatcatccatggcaacttacatcaacaatccagtttggttccattgaatgca 235
      |||
Sbjct: 177 ca-acataccagccatggcaacttacatgcaacgattcaattcagttccattgaatgca 235

Query: 236 gacttccatactaccctctctttggctagttgag-gggaaacgagaagtttcaacc 294
      |||
Sbjct: 236 aacttccatactaccctctctttggctagttgagggaa-cgagaagtttcaacc 294

Query: 295 accactgaccccttgcgaagttggagatgcagcttagtgcgcttaccgaagcaagag 354
      |||
Sbjct: 295 atcactgaccccttgcgaagttggagatgcagcttagtgcgcttaccgaagcaagag 354

Query: 355 ttgcaactattgaacatccaagaatgacttgcctgtatcgatacaagactgatgct 414
      |||
Sbjct: 355 ttgcaactattgaacatccaagaatgacttgcctgtatcgatacaagactgatgct 414

Query: 415 cagattgcgctcattcaaaagaagcgcgagaagaagaagaagaagaataatttccaa 474
      |||
Sbjct: 415 cagattgcgctcattcaaaagaagcgcgagaagaagaagaagaagaacaacttccaa 474

Query: 475 atggctgctcaagttgtgtcgaagatcactattgctgtggagagccaccttcaaaa 534
      |||
Sbjct: 475 atggctgctcaagttgtgtcgaagatcactattgctgtggagagccaccttcaaaa 534

Query: 535 cttgaatcacaagtgccgaggggtgtcatccacacaactccaagatgcccacagcaaaa 594
      |||
Sbjct: 535 cttgaatcacaagtgccgaggggtgtcatccacacaactccaagatgcccacagcaaaa 594

Query: 595 acatatacacgccaagttagacagaggaacaatgaacccttatcaagcaggtgaag 654
      |||
Sbjct: 595 acatatacacgccaagttagacagaggaacaatgaacccttatcaagcaggtgaag 654

Query: 655 caaattatgtcaaccaaggaggctctgttcaactgattagcaagaaaagtaccatggt 714
      |||
Sbjct: 655 caaattatgtcaaccaaggaggctctgttcaactgattagcaagaaaagtaccatggt 714

Query: 715 cactataaagaagtttgggatcacatcgccagttgttagcactgcacatatgaaggt 774
      |||
Sbjct: 715 caataaagaagtttgggatcacatcgccagttgttagcactgcacatatgaaggt 774

Query: 775 ttacgaagaagagtgactttcgggtgataaagaccgtgctgctt-acagcatct 833
      |||
Sbjct: 775 ttacgaagaagagtgactttcgggtgataaagaccgtgctgctt-acagcatct 833
```

Windows taskbar with icons for File Explorer, Word, Edge, Chrome, Excel, and other applications. System tray shows ENG INTL, 8:22 AM, and 3/18/2019.

# Viroma Peruano de la papa – Plataforma Web

Pathogens x Pathogens x +

Not secure | potpathodiv.org/vsinfo?sid=Cus-100B#BLASTX

*R. solanacearum* <  
Data  
*P. infestans* <  
Data  
Virome <  
Data  
Admin <  
*P. infestans* complete set  
Upload data  
Logout  
Tutorial

Sample Cleaning

sample ID	Total Reads	Reads to be cleaned	% to be cleaned	Final Clean Reads	% Final Clean Reads
Cus-100B	8378743	3882636	46.34	4496107	53.66

Download Clean Reads

Length Distribution

Sequence Length Distribution

Virus Identified by nucleotide similarity (BLASTN) >

Virus Identified by translated protein similarity (BLASTX) >

Data interpretation Download Virus Contigs (BLASTX)

Reference	Length	Coverage (%)	#contig	Depth	Depth (Norm)	%identity	%iden Max	%iden Min	Genus	Description
AFJ22628.1	1974	209 (10.6)	8	266.5	59.9	80.57	95.00	65.79	carlavirus	Potato virus S isolate BB-AND, complete genome.
AER27673.1	180	18 (11.3)	1	34.6	7.7	88.89	88.89	88.89	carlavirus	Potato virus S isolate Tasajo coat protein (CP) gene, partial ods.
AAA42421.1	997	894 (89.7)	6	462.1	102.8	73.72	85.00	69.39	comovirus	Andean potato mottle virus polyprotein encoding small and large coat proteins and potential movement protein mRNA, complete ods.
AAA42422.1	729	159 (21.8)	4	278.5	61.9	91.82	100	89.58	comovirus	Andean potato mottle virus RNA polymerase mRNA, 3' end.
AIG59705.1	186	148 (79.6)	3	262.3	58.3	72.73	85.71	68.04	comovirus	Andean potato mottle virus strain PV-0057 coat protein gene, partial ods.
ACV41391.1	1860	1008 (54.1)	4	634.1	141.0	39.03	43.07	34.25	comovirus	Turnip ringspot virus isolate Toledo segment RNA 1, complete sequence.

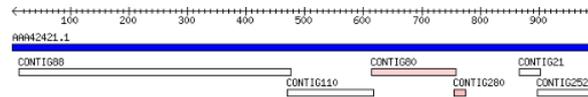
FastQC >

# Viroma Peruano de la papa – Plataforma Web



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- R. solanacearum
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- Virome
- Admin
- Tutorial

## Identification of virus AAA42421.1 from sample Cus-100B



Order	Query ID	Query Start	Query End	Subjet Start	Subjet End	Identity	E value	Strand
1	CONTIG110	1	441	470	616	102/147(69%)	4e-62	1

### Alignment:

```
Query: 1  RGAPNFRHTYRQNTKQWFLFTVMPLTTGIGLNGVNSVSSPKHLVNEYTISSESSIEW 180
      RGAP FRHTYRQ+TK+ F+FT+NP++TGIGLNGVNSV+S KHL NEYTISSE S+ W
Sbjct: 470  RGAPNFRHTYRQSTKLRFIPTINWPISITGIGLNGVNSVTSKHLTNEYTISSESVW 529

Query: 181  PACAGELRFLVDPNPGPYYSFDYFRQTGSRITHMVISPWTTTPTADCAIAWQVHTSEP 360
      PAC G L F V PNP CG YW+S+DYFRQTGSR+++ VISPW+ TPT DCA+AWQ+HV E
Sbjct: 530  PACQGVLEFSVSPNPGHYYSYDYFRQTGSRLSICVSPWSATPTTDCAVAWQIHVDDEQ 589

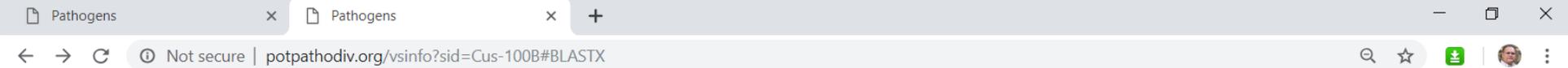
Query: 361  NSNSTFSWFFPPATHPVRRMNGLLFK 441
      M+ S F+ PA +PV+RMNGNL+FK
Sbjct: 590  MTHSIFNPQAPAVLPVKRMNGNLIFK 616
```

2	CONTIG21	109	2	901	886	27/38(75%)	2e-12	-1
---	----------	-----	---	-----	-----	------------	-------	----

### Alignment:

```
Query: 109  WKKGTLHFKIKLLGKSSIKRADNSSTTRIDVRRAPG 2
      WK+G LHF+K+K+LGKS++KR+HNSST+RIDVRRAPG
Sbjct: 866  WKRGLHFKIKLLGKSNVKSNSSTSRIDVRRAPG 901
```

# Viroma Peruano de la papa – Plataforma Web



- Home
- Map
- R. solanacearum
- Data
- P. Infestans
- Data
- Virome
- Data
- Admin
- P. Infestans complete set
- Upload data
- Logout
- Tutorial

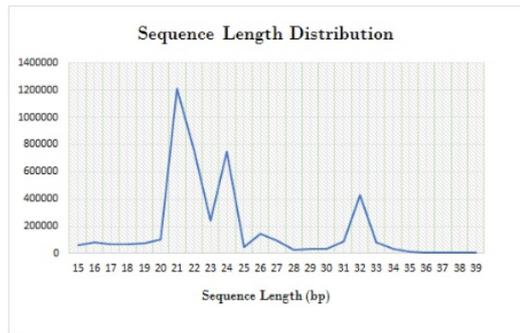
## Sample Cus-100B analyzing results

### Sample Cleaning

sample ID	Total Reads	Reads to be cleaned	% to be cleaned	Final Clean Reads	% Final Clean Reads
Cus-100B	8378743	3882636	46.34	4496107	53.66

Download Clean Reads

### Length Distribution



Virus Identified by nucleotide similarity (BLASTN)

Virus Identified by translated protein similarity (BLASTX)

FastQC



# Viroma Peruano de la papa – Plataforma Web

Pathogens x Pathogens x +

Not secure | potpathodiv.org/vsinfo?sid=Cus-100B#fastqc

Virus Identified by translated protein similarity (BLASTX)

FastQC

FastQC Report  
Sun 11 Mar 2018  
Cus-100B.clean.fq

## Summary

- ✓ Basic Statistics
- ✓ Per base sequence quality
- ✗ Per tile sequence quality
- ✓ Per sequence quality scores
- ✗ Per base sequence content
- ✓ Per sequence GC content
- ✓ Per base N content
- ⚠ Sequence Length Distribution
- ✗ Sequence Duplication Levels
- ✗ Overrepresented sequences
- ✓ Adapter Content
- ✗ Kmer Content

### Basic Statistics

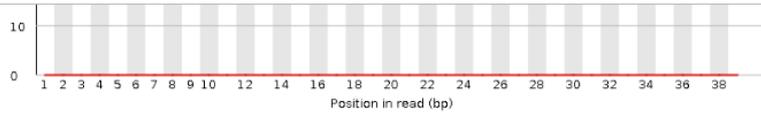
Measure	Value
Filename	Cus-100B.clean.fq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	4496107
Sequences flagged as poor quality	0
Sequence length	15-39
%GC	40

### Per base sequence quality

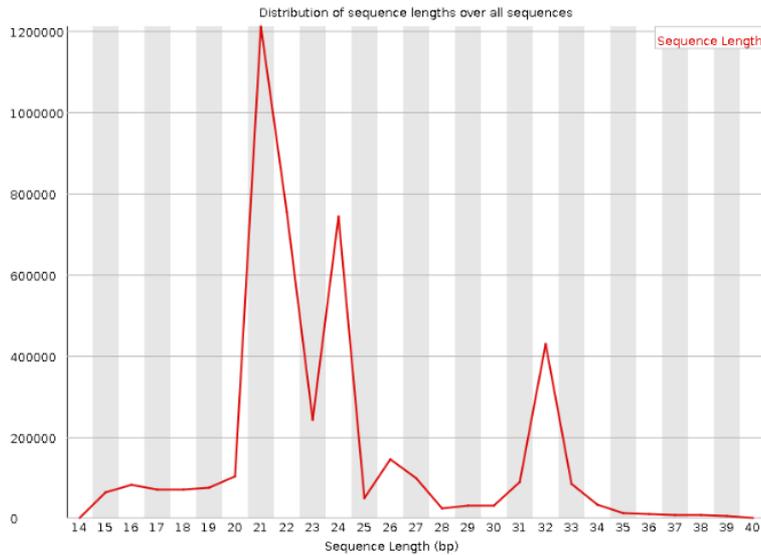
Quality scores across all bases (Sanger / Illumina 1.9 encoding)

The graph displays a blue line representing the quality score across the sequence. The score begins at a low point of about 32.5, quickly rises to a plateau of approximately 36 by the 10th position, and then continues to rise, stabilizing between 39 and 40 for the rest of the sequence. A horizontal dashed line is drawn at approximately 37.5, likely representing a quality threshold. The background of the graph is shaded in light green.

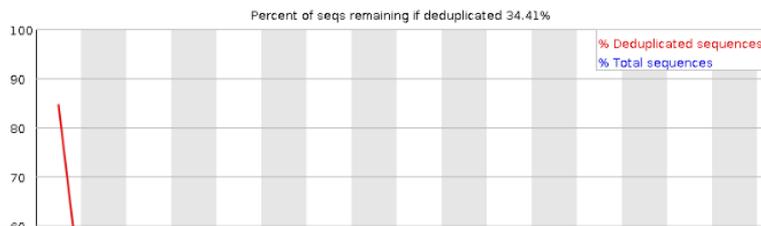
# Viroma Peruano de la papa – Plataforma Web



## Sequence Length Distribution



## Sequence Duplication Levels



# Viroma Peruano de la papa – Plataforma Web



- [Home](#)
- [Map](#)
- [R. solanacearum](#)
- [P. Infestans](#)
- [Virome](#)
- [Data](#)
- [Admin](#)
- [Tutorial](#)

## Virome data

Field List Samples

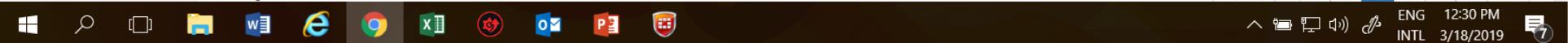
Show 10 entries

Search:

Sample	Field	Year	Pathogen host	Cultivar/Specie	Cultivar age (months)	Phenologic state	Intercultivar	Field number	Field size	Field picture	Plant picture	Leaf picture	Seed Origin	Management system	Pesticides	Common Virus	New Viru
Cus-093	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	<a href="#">Ver</a>	<a href="#">Ver</a>	<a href="#">Ver</a>	Cusco			PVY	APM
Cus-094	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	<a href="#">Ver</a>	<a href="#">Ver</a>	<a href="#">Ver</a>	Cusco			PVY	PVY
Cus-095	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	<a href="#">Ver</a>	<a href="#">Ver</a>	<a href="#">Ver</a>	Cusco			PVY, PVB	
Cus-096	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	<a href="#">Ver</a>	<a href="#">Ver</a>	<a href="#">Ver</a>	Cusco			PVY, PVB, PVY, PVV	PVY
Cus-097	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	<a href="#">Ver</a>	<a href="#">Ver</a>	<a href="#">Ver</a>	Cusco			PVY, PVB, PVY, PVV	PVY
Cus-098	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	<a href="#">Ver</a>	<a href="#">Ver</a>	<a href="#">Ver</a>	Cusco			PVY, PVV, PVX?	
Cus-099	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	<a href="#">Ver</a>	<a href="#">Ver</a>	<a href="#">Ver</a>	Cusco			PVY, PVV, PVY	PVY
Cus-100	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	<a href="#">Ver</a>	<a href="#">Ver</a>	<a href="#">Ver</a>	Cusco			PVX, PVY	
Cus-100B	Cus	2016	Potato	Canchan	2	Vegetativo		10	3000	<a href="#">Ver</a>	<a href="#">Ver</a>	<a href="#">Ver</a>	Cusco			PVX, PVY	PVS APM
Cus-101	Cus	2016	Potato	Cica	4	Floración		11	1500	<a href="#">Ver</a>	<a href="#">Ver</a>	<a href="#">Ver</a>	Mercado Cusco			PVX, PVY	

Showing 351 to 360 of 987 entries

Previous 1 ... 35 36 37 ... 99 Next



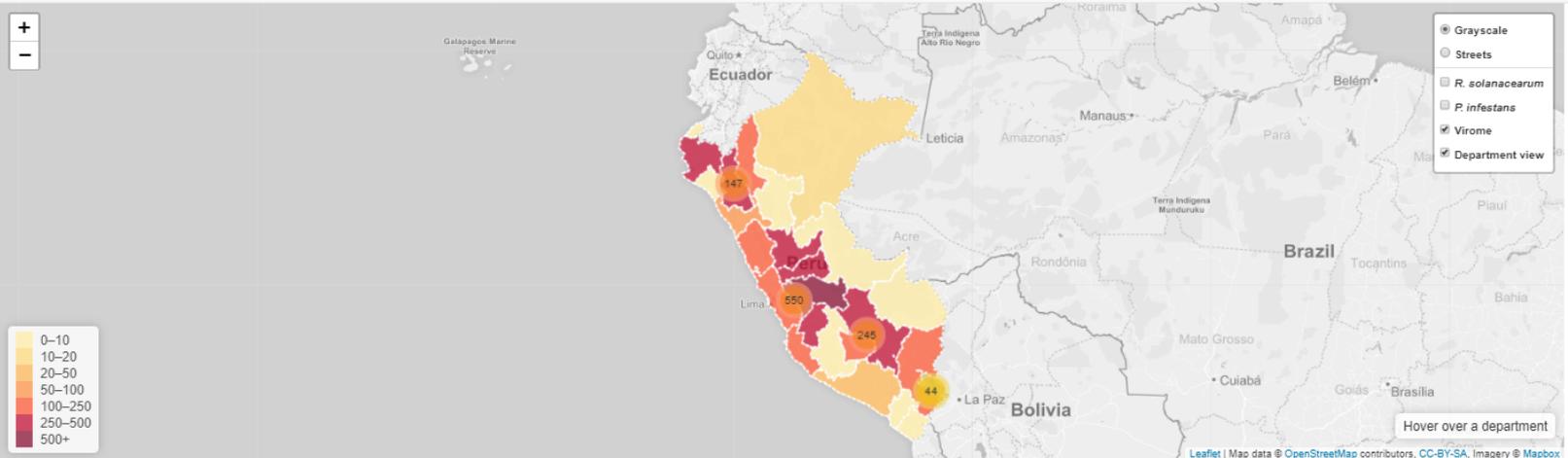
# Viroma Peruano de la papa – Plataforma Web

Pathogens x Evento Proyecto\_PPT\_2019 - One x +

Not secure | potpathodiv.org/map.html



Home  
Map  
*R. solanacearum*  
*P. infestans*  
Virome  
Admin  
Tutorial



Legend:

- Grayscale
- Streets
- R. solanacearum*
- P. infestans*
- Virome
- Department view

Legend (Number of Viromes):

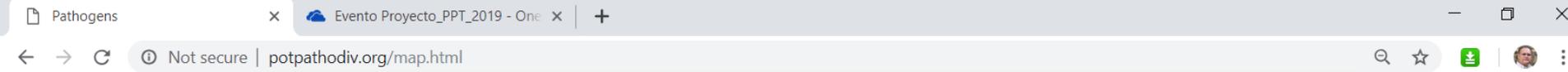
- 0-10
- 10-20
- 20-50
- 50-100
- 100-250
- 250-500
- 500+

Map labels: Ecuador, Quito, Leticia, Amazonas, Manaus, Pará, Belém, Brazil, Mato Grosso, Goiás, Brasília, Tocantins, Bahia, Rondônia, Acre, Terra Indígena Alto Rio Negro, Terra Indígena Mundurucu, Piuí, Mato Grosso do Sul, Cuiabá, Bolivia, La Paz.

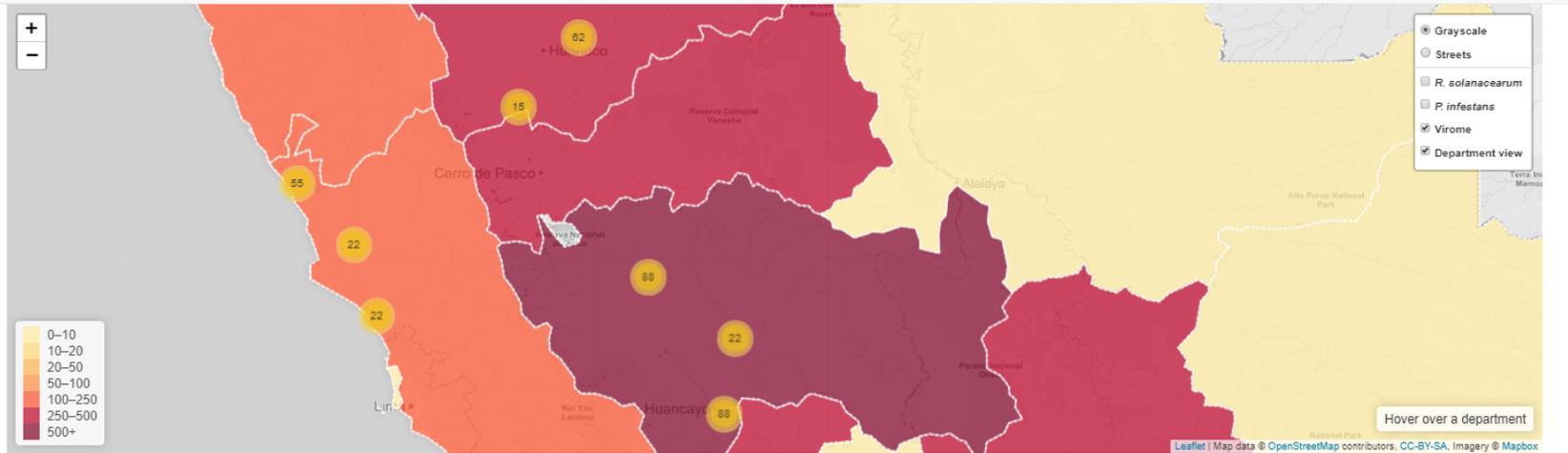
Leaflet | Map data © OpenStreetMap contributors, CC-BY-SA, Imagery © Mapbox

Windows taskbar: ENG 12:48 PM, INTL 3/18/2019

# Viroma Peruano de la papa – Plataforma Web



- Home
- Map
- R. solanacearum*
- P. infestans*
- Virome
- Admin
- Tutorial



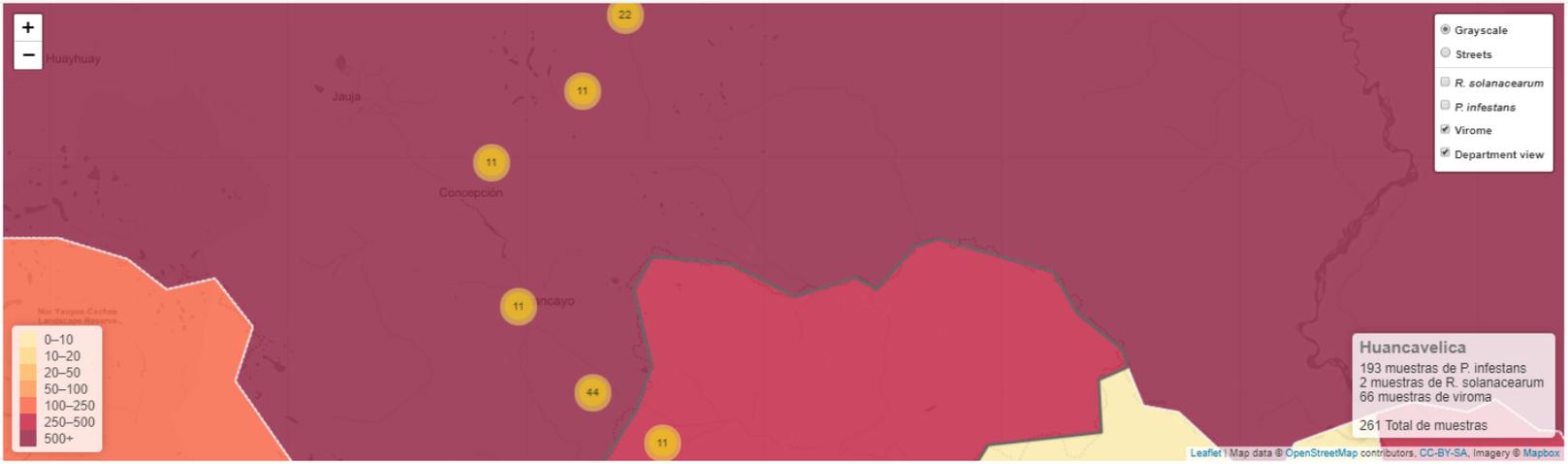
# Viroma Peruano de la papa – Plataforma Web

Pathogens x Evento Proyecto\_PPT\_2019 - One x +

Not secure | potpathodiv.org/map.html



Home  
Map  
R. solanacearum  
P. Infestans  
Virome  
Admin  
Tutorial



Legend:

- 0-10
- 10-20
- 20-50
- 50-100
- 100-250
- 250-500
- 500+

Legend:

- Grayscale
- Streets
- R. solanacearum
- P. infestans
- Virome
- Department view

Huancavelica

- 193 muestras de P. infestans
- 2 muestras de R. solanacearum
- 66 muestras de virome
- 261 Total de muestras

Leaflet | Map data © OpenStreetMap contributors, CC-BY-SA, Imagery © Mapbox

Windows taskbar: ENG 12:53 PM, INTL 3/18/2019

# Viroma Peruano de la papa – Plataforma Web

Pathogens x Evento Proyecto\_PPT\_2019 - One x +

Not secure | potpathodiv.org/map.html



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Grayscale  
Streets  
R. solanacearum  
P. infestans  
Virome  
Department view

0-10  
10-20  
20-50  
50-100  
100-250  
250-500  
500+

Virome  
Provincia: Concepción  
District: Santa Rosa de Ocopa  
Field: Ver

22  
11  
44  
11

Leaflet | Map data © OpenStreetMap contributors, CC-BY-SA, Imagery © Mapbox

ENG 12:54 PM  
INTL 3/18/2019

The image shows a web browser window displaying a map of Peru. The browser's address bar shows the URL 'potpathodiv.org/map.html'. The page features a navigation menu on the left with options like 'Home', 'Map', and 'Virome'. The main content is a map of Peru with a color-coded legend indicating the density of virome data, ranging from 0-10 (lightest) to 500+ (darkest). A tooltip is visible over a specific location, providing details: 'Virome', 'Provincia: Concepción', 'District: Santa Rosa de Ocopa', and 'Field: Ver'. The map also shows several numbered markers (22, 11, 44, 11) and a 'Department view' button. The Windows taskbar at the bottom shows the system time as 12:54 PM on 3/18/2019.

# Viroma Peruano de la papa – Plataforma Web



- Home
- Map
- R. solanacearum*
- P. Infestans*
- Virome
- Admin
- Tutorial

## Field (Jun) information

Field ID:	Jun
Country:	Peru
Department:	Junín
Province:	Concepción
District:	Santa Rosa de Ocopa
Locality:	
Latitude:	-11.87439°
Longitude:	-75.28642°
Altitude:	3435 m

## Field Map



## Samples in field Jun

Show 10 entries

Search:

Sample	Date	Pathogen Host	Cultivar	Sequenced
Jun-081	2016	Potato	Canchan	1
Jun-082	2016	Potato	Canchan	1
Jun-083	2016	Potato	Canchan	1
Jun-084	2016	Potato	Canchan	1
Jun-085	2016	Potato	Canchan	1
Jun-086	2016	Potato	Perrichilli	1

# Viroma Peruano de la papa – Plataforma Web

Pathogens x Pathogens x +

Not secure | potpathodiv.org/vsinfo?sid=Cus-100B#fastqc

Data

P. Infestans

Data

Virome

Data

Admin

P. Infestans complete set

Upload data

Logout

Tutorial

### Sample Cleaning

sample ID	Total Reads	Reads to be cleaned	% to be cleaned	Final Clean Reads	% Final Clean Reads
Cus-100B	8378743	3882636	46.34	4496107	53.66

[Download Clean Reads](#)

### Length Distribution

**Línea base para monitorear cambios en el futuro**

### Virus Identified by nucleotide similarity (BLASTN)

Reference	Length	Coverage (%)	#contig	Depth	Depth (Norm)	%Identity	%Iden Max	%Iden Min	Genus	Description
AF493951	949	522 (55)	6	102.2	22.7	90.63	96.72	86.51	carlavirus	Potato virus S strain Andean coat protein mRNA, complete cds.
JQ647830	8482	4127 (48.7)	49	100.9	22.4	89.90	100	82.10	carlavirus	Potato virus S isolate BB-AND, complete genome.
JX683388	8117	3770 (46.4)	48	100.2	22.3	88.96	100	82.72	carlavirus	Potato virus S isolate RL5 RNA-dependent RNA polymerase gene, partial cds; and 12K protein, 7K protein, coat protein, and 11K protein genes, complete cds.
AJ863510	8464	3247 (38.4)	37	127.6	28.4	89.55	100	81.46	carlavirus	Potato virus S complete genome, isolate Vitava.
LN851194	8482	2754 (32.5)	31	139.5	31.0	88.46	100	79.75	carlavirus	Potato virus S complete genome, isolate Ewa.
KC430335	8488	2471 (29.1)	27	146.2	32.5	88.54	100	80.23	carlavirus	Potato virus S isolate Yunnan YN, complete genome.

[data interpretation](#) [Download Virus Contigs \(BLASTN\)](#)

100%

ENG 2:41 PM  
INTL 9/22/2018

**CIP:**

Jan Kreuze,  
Segundo Fuentes,  
Ana Perez,  
Angel Allauca,  
Melody Amao,  
Pamela Chavez

Lilia Salinas,  
Viviana Infantas,  
Maria Elena Lanatta,

Ximena Ganoza,

Henry Juarez,  
Ciro Rosales,

Percy Cabello,  
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**UNALM:**

Carlos Cadenas,  
Alejandro Risco,  
Tomas Melgarejo,

**Consultor:**

Mirella Flores

**Oficinas Agrarias**  
**Oficinas SENASA**  
**Oficinas del INIA**



**Muchas Gracias !**