

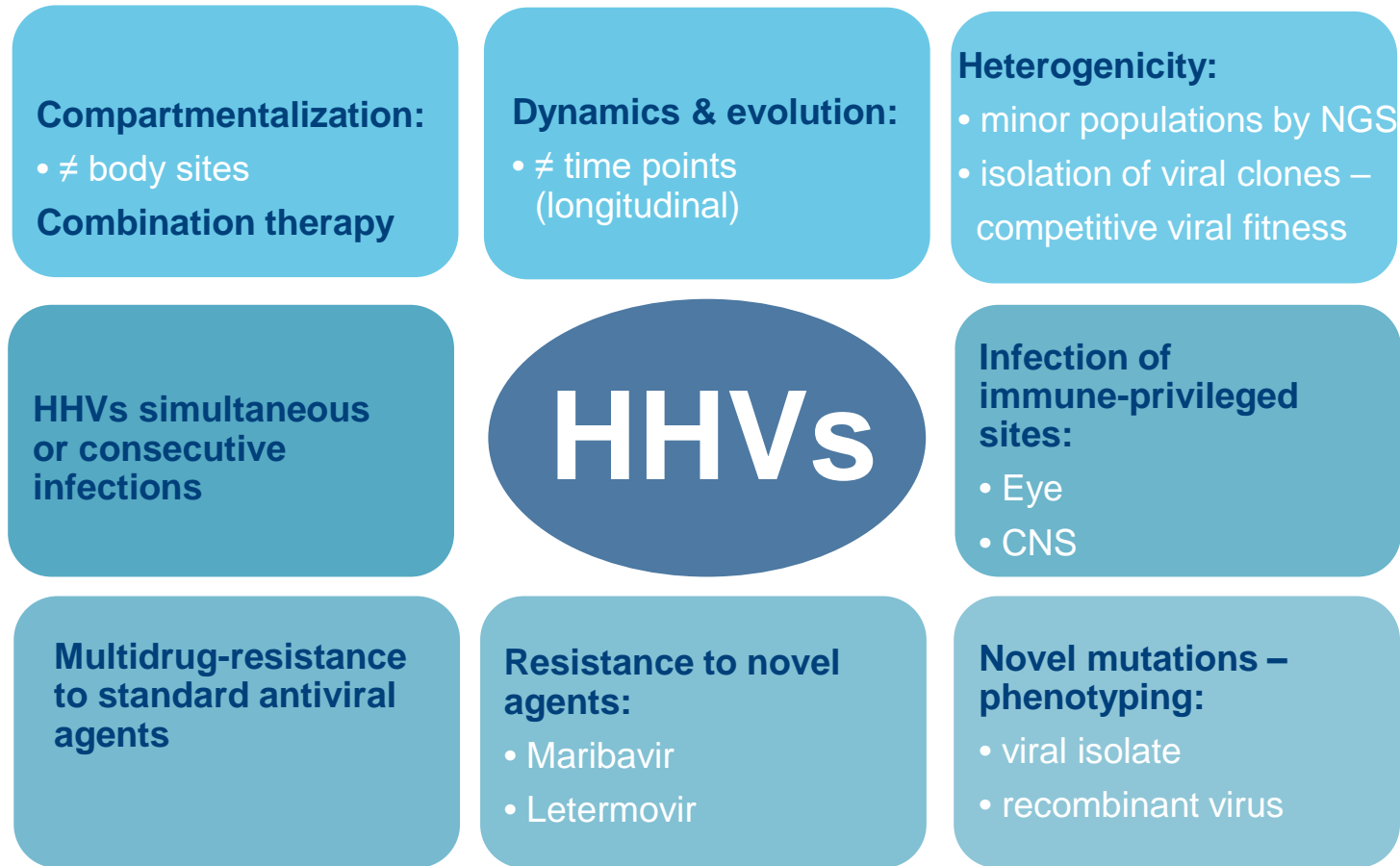


Introduction to the translational Research platform RegaVir

Robert Snoeck & Graciela Andrei

Leuven, January 30, 2024

RegaVir platform for translational research

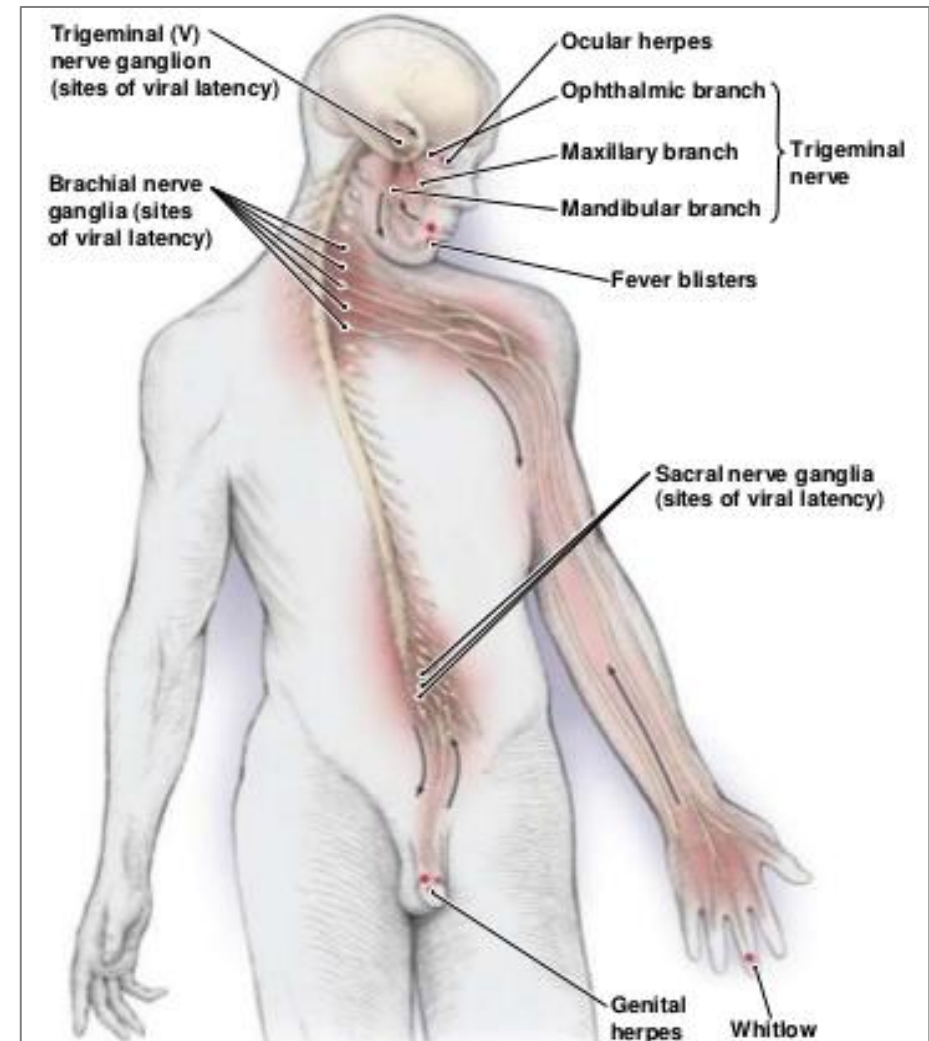


HSV infections

- Herpes simplex virus (HSV) infections are ubiquitous globally.
- **An estimated 3.7 billion people under age 50 (67%) globally have herpes simplex virus 1 (HSV-1) infection, the main cause of oral herpes.**
- **An estimated 491 million people aged 15–49 (13%) worldwide have herpes simplex virus 2 (HSV-2) infection, the main cause of genital herpes.**

HSV infections

- After a primary infection, HSV remains latently in sensory ganglia with the potential to reactivate.
- Most HSV infections are asymptomatic or unrecognized, but symptoms of herpes include painful blisters or ulcers that can recur over time.



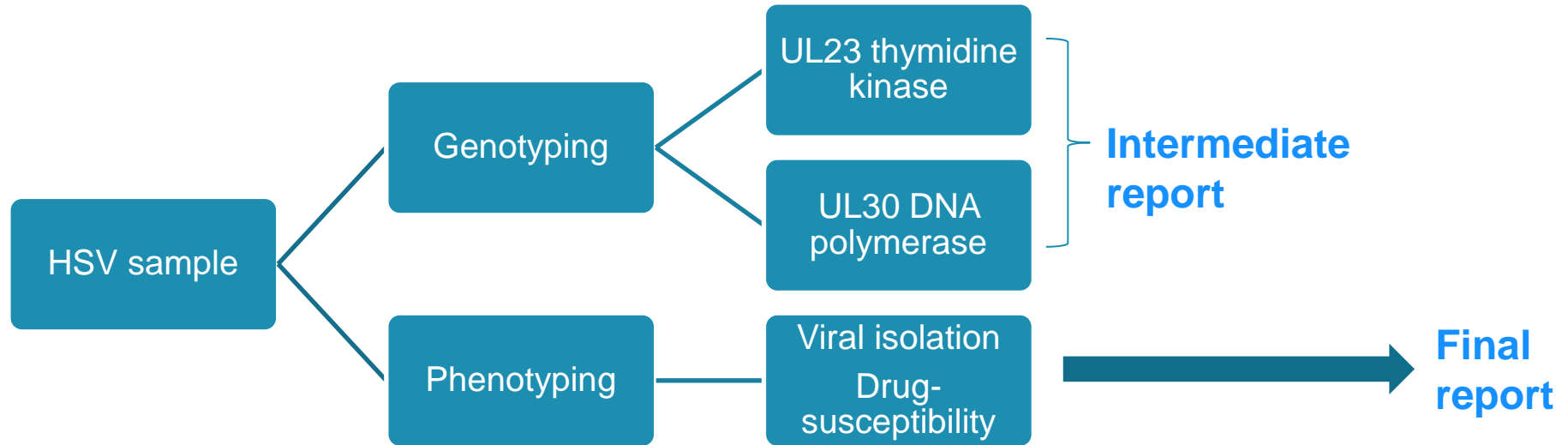
HSV infections

- In immunocompromised individuals, **antiviral prophylaxis with acyclovir (ACV)** may be effective at preventing reactivation.
- Routine use of ACV prophylaxis has led to a **reduction in the incidence of early reactivation of HSV** after allogeneic bone marrow transplant.
- **ACV is the most used drug for HSV infection therapy.**

Emergence of resistance to new anti-HCMV agents in a pediatric HSCT patient with IEI

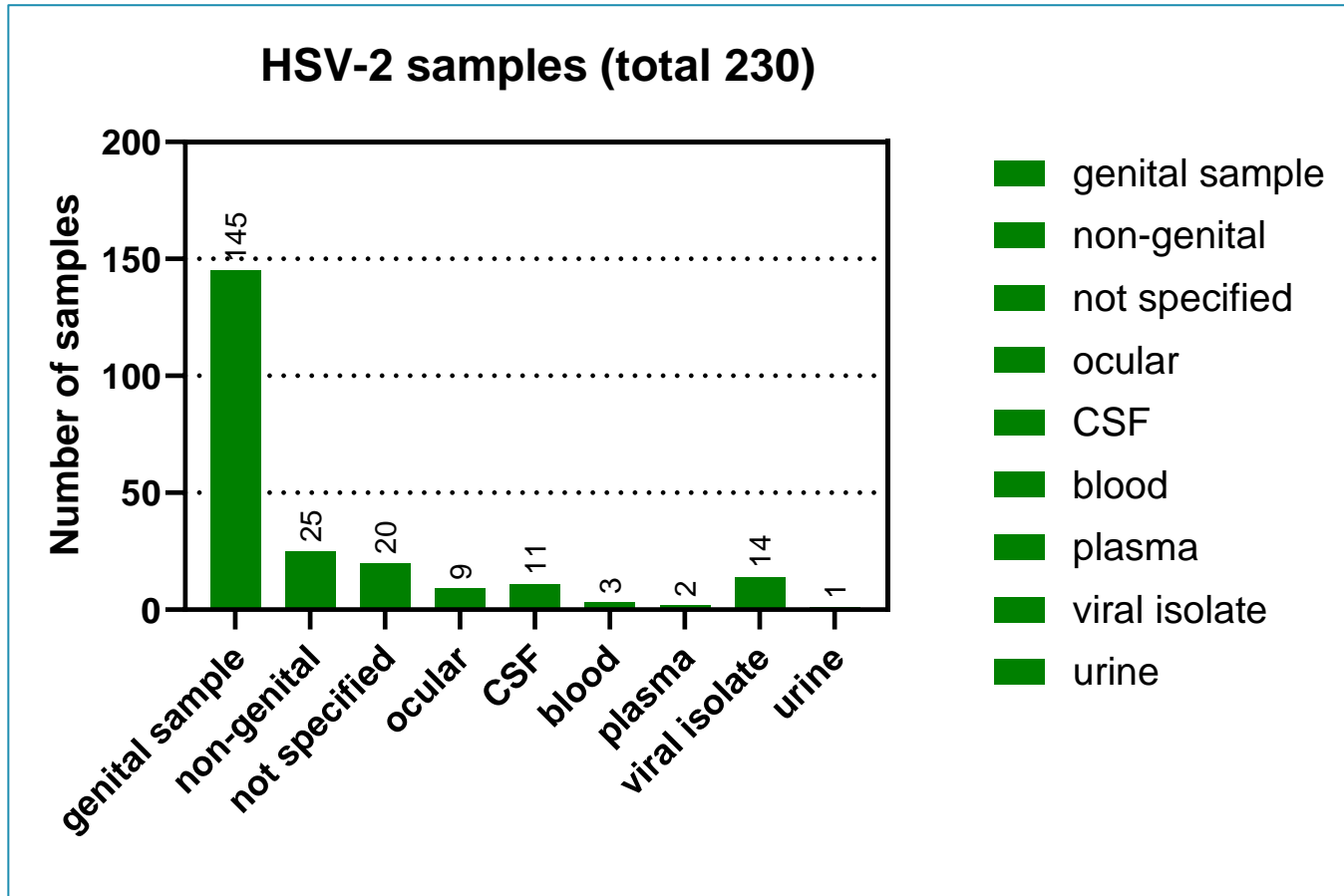
- **Emergence of ACV-resistance (ACV-R)** has been increasingly reported and is associated with long-term ACV prophylaxis or therapy in immunocompromised patients.
- Due to the high polymorphism in genes involved in drug resistance, **phenotypic methods**, although work-intensive, are still required to test drug susceptibility.

RegaVir HSV workflow

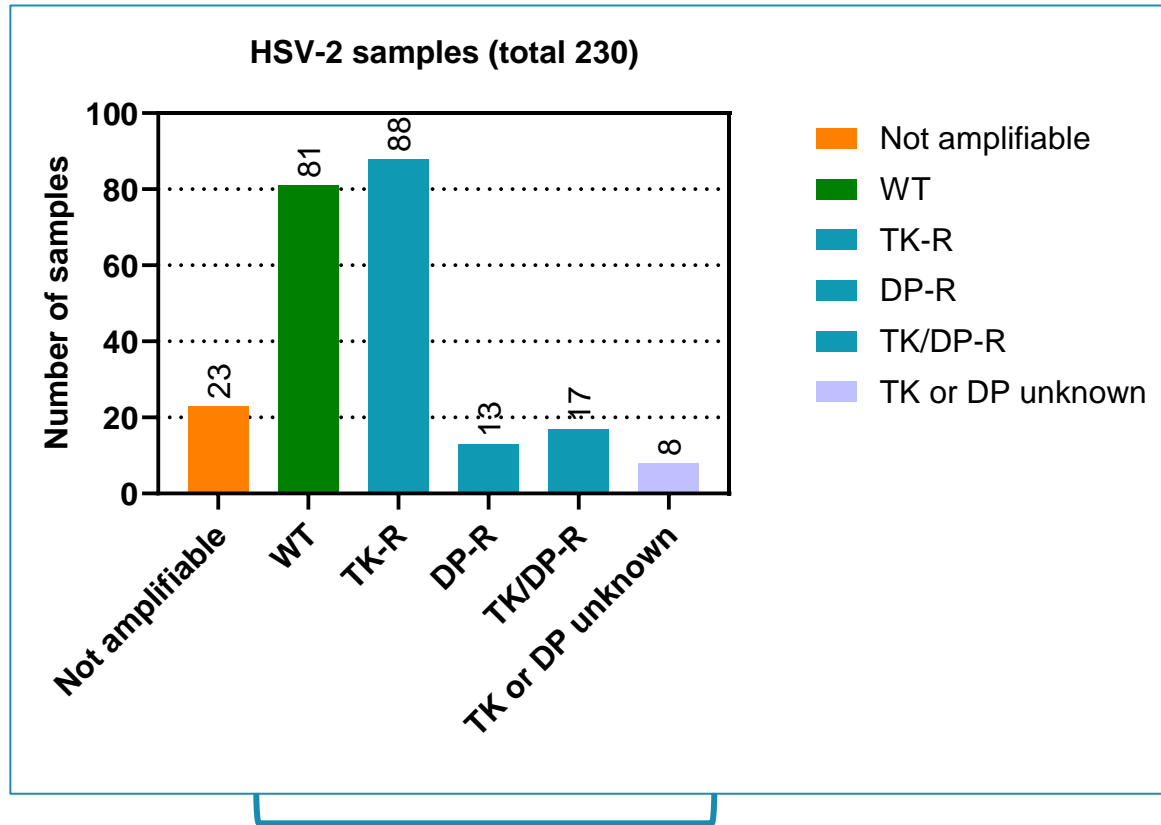


- Phenotyping not done for CSF, ocular, and blood/plasma samples.
- **Swabs in UTM required for viral isolation (please, do not use eSwabs)**
- Between January 2009 and January 2024, **230 HSV-2 samples** were analyzed by RegaVir.

HSV-2 sample type



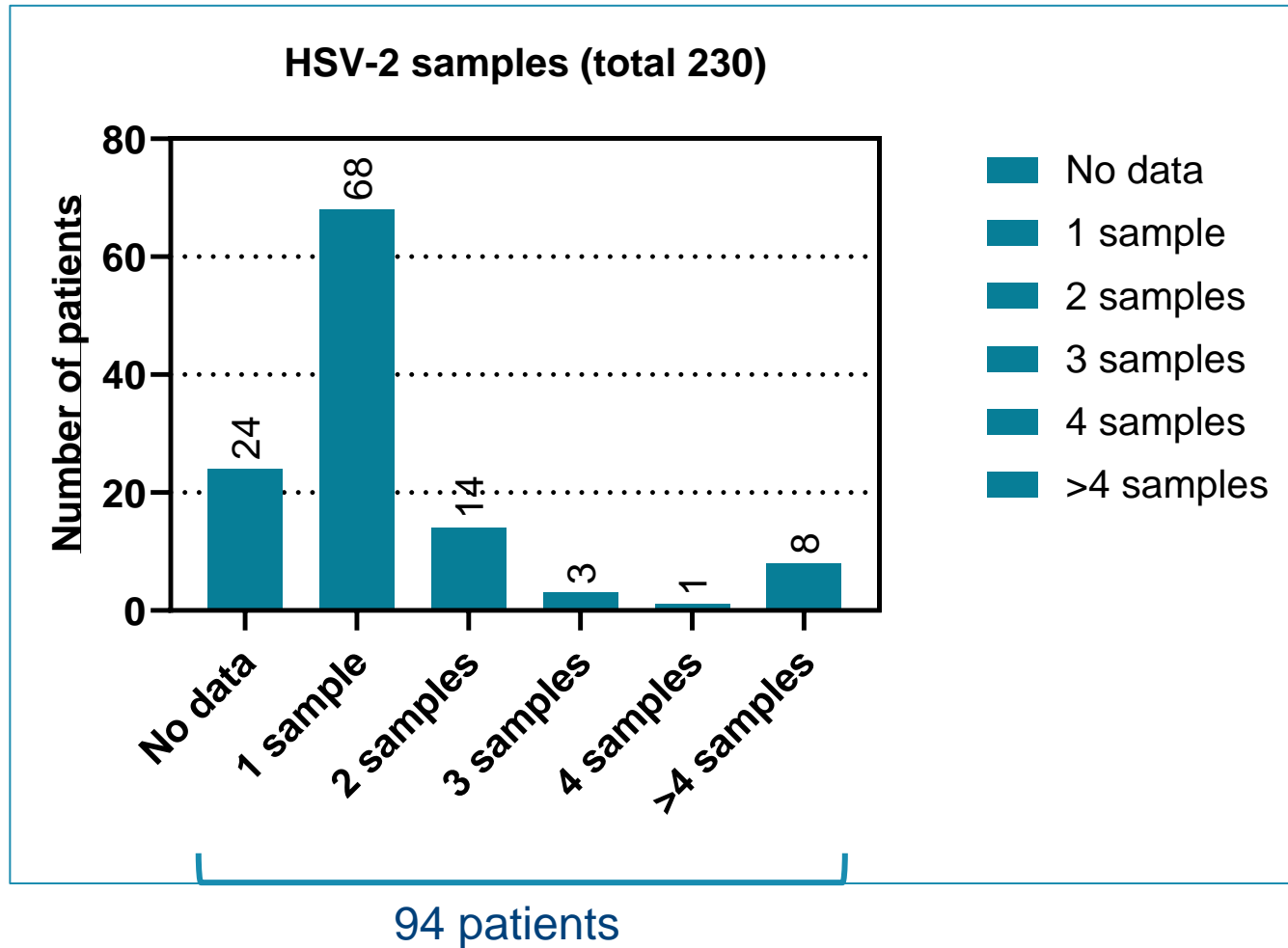
HSV-2 resistance samples



207 amplifiable samples . 230: 90%

118 confirmed resistance . 207 amplifiable samples: 57%

Patients analyzed for HSV-2



HSV-2 anogenital infections in HIV positive patients

- 77-years old men with recurrent anogenital HSV-2
- HIV positive
- Anogenital swabs recovered over 7 years

Date of arrival	RegaVir ID	Genotyping		Phenotyping
		TK	DNA pol	
06.04.09	RV_11	C insertion nts 551-556 (6C's → 7 C's)	Natural polymorphisms: S15P, P60L, P801T, G904A, E905A, A906G	TK-resistance
13.10.11	RV_257	C deletion Nt 306 leading to a framshift mutation (truncated protein at amino acid 101)	Natural polymorphisms: S15P, P60L, P801T, G904A, E905A, A906G	TK-resistance
01.04.10	RV_101	C insertion nts 551-556 (6C's → 7 C's)	Natural polymorphisms: S15P, P60L, P801T, G904A, E905A, A906G	TK-resistance
19.09. 14	RV_718	C deletion Nt 306 leading to a framshift mutation (truncated protein at amino acid 101)	Natural polymorphisms*: P801T, G904A, E905A, A906G	TK-resistance
28.04.16	RV_988	C insertion nts 551-556 (6C's → 7 C's)	Natural polymorphisms*: P801T, G904A, E905A, A906G	TK-resistance
19.10.16	RV_1078	C deletion Nt 306 leading to a framshift mutation (truncated protein at amino acid 101)	Natural polymorphisms: S15P, P60L, P801T, G904A, E905A, A906G	TK-resistance

*Partial sequence but all known drug-R mutations verified

HSV-2 Thymidine kinase

POLYMORPHISMS

A19V
R26H
A27T
S29A
E39G

R75C ?
D78N
L92P
E96D

A119T

A135P
D137E
F140L
T159I

A199V
A215T
R220K

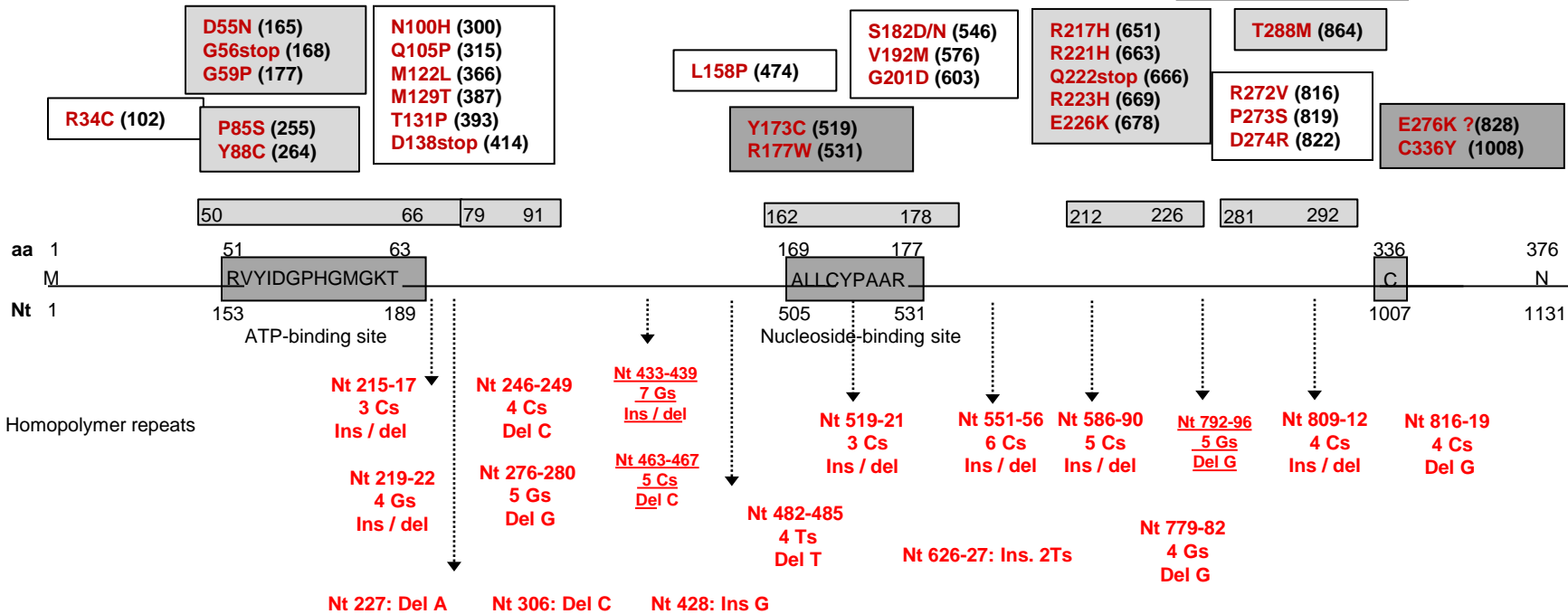
N245SD
277G

R284S
A300V
I302D
I349V
R371S

RESISTANCE

Y133S (369)

Y239stop (717)



Mutations previously described that are known to be associated with genetic polymorphism are indicated in green while those known to confer drug-resistance are marked in red. Mutations that confer drug resistance located in the ATP-binding site, the nucleoside-binding site, and Cys-336 are shown in dark grey boxes. Mutations found in other conserved regions of the viral TK are shown in pale grey boxes, and mutations located in non-conserved regions of the viral enzyme are shown in white boxes. Mutations found in HSV-2 clinical isolates received during the RegaVir project are underlined, being the novel mutations associated with drug-resistance in a purple box.

Phenotyping in human embryonic lung fibroblasts

Strain	EC ₅₀ (µg/ml)						
	Acyclovir	Penciclovir	Brivudin	Ganciclovir	Foscavir	Cidofovir	Adefovir
RV-988	12.63 20	12.63 20	>10 >10	3.42 2.99	14.63 1956	0.8 0.8	20.07 30.59
Reference HSV-2 (G strain)	0.023	0.16	>10	0.0019	13.68	0.47	13.68
RV-1078	6.84 20	5.98 12.63	4.47 5.25	1.45 1.05	3.58 5.8	0.42 0.39	10.46 13.68
Reference HSV-2 (G strain)	0.06	0.16	>10	0.0055	10.46	0.8	16.36

EC₅₀ : Concentration required to reduce virus induced cytopathicity by 50%

HSV-2 infections in HIV positive patients

- ~70% of persons with HIV are HSV-2 seropositive.
- ~95% of persons with HIV are seropositive for either HSV-1 or HSV-2.
- HSV-2 infection increases the risk of HIV acquisition 2- to 3-fold.
- In coinfecting patients, HSV-2 reactivation results in increases in HIV RNA levels in blood and genital secretions.
- **Sexual transmission of HSV most often occurs during episodes of asymptomatic viral shedding.**
- Treatment failure due to acyclovir resistance should be suspected if herpes-related lesions do not begin to resolve within 7 days to 10 days after initiation of anti-HSV therapy.
- High prevalence of ACV-R HSV-2 in HIV positive patients unresponsive to therapy.

HSV-2 ocular infection (UZ Gent)

- 46-years old woman with intra-ocular HSV infection (08.12.2021)
- No predisposition, no immunosuppression
- Antiviral treatment received: prophylactic – therapeutic (in case of acute infection)
 - **Acyclovir**
(08.12.2021 10 mg.kg 3x.day IV)
(18.12.2021 *per os* 5x 800 mg.day)
 - **Foscarnet**
intravitreal 2x.week (2.4 mg)
- Not improving under antiviral therapy - Increasing inflammation, retinal detachment

HSV-2 ocular infection (UZ Gent)

Arrival date to RegaVir	RegaVir ID	Sample date	Sample type	Viral load	HSV-2 genotype
03.01.2022	RV-2408	17.12.2021	DNA extract anterior chamber fluid	Ct = 27.4	Wild-type <i>DP natural polymorphisms: P801T, G904A, E905A, A906G</i>
03.01.2022	RV-2409	27.12.2021	DNA extract anterior chamber fluid	Ct = 25.8	Wild-type <i>DP natural polymorphisms: P801T, G904A, E905A, A906G</i>
25.01.2022	RV-2421	21.01.2022	DNA extract anterior chamber fluid	HSV-2 positive	Wild-type <i>DP natural polymorphisms: P801T, G904A, E905A, A906G</i>
07.02.2022	RV-2432	24.01.2022	DNA extract anterior chamber fluid	Ct = 29.65	Wild-type <i>DP natural polymorphisms: P801T, G904A, E905A, A906G</i>
07.02.2022	RV-2433	27.01.2022	DNA extract anterior chamber fluid	Ct = 30.15	Wild-type <i>DP natural polymorphisms: P801T, G904A, E905A, A906G</i>
07.02.2022	RV-2434	28.01.2022	DNA extract anterior chamber fluid	Ct = 27.97	Wild-type <i>DP natural polymorphisms: P801T, G904A, E905A, A906G</i>

Report 11.02.2022

Ocular HSV-2 infection (Saint Luc – UCL Louvain)

- 24-years old woman
- Not immunosuppressed
- Ocular HSV infection
- Treatment not provided – in the last 10 days no treatment

Arrival date to RegaVir	RegaVir ID	Sample date	Sample type	Viral load	HSV-2 genotype
10.05.2022	RV-2500	10.05.2022	Anterior chamber fluid (right eye)	Not provided	Wild-type <i>TK natural polymorphism: G39E</i> <i>DP natural polymorphisms: P801T, G904A, E905A, A906G</i>

HSV-2 ocular infection (UZ Leuven)

- **29-years old man suffering from panuveitis (generalized inflammation of the whole uveal tract and also of the retina and vitreous humor) & papillitis (optic neuritis) on the right eye (07.05.2018).**
- Left eye same infection (panuveitis) in 2010 → vision light perception without localization.
- **Antiviral treatment:**
 - Therapeutic acyclovir IV 3x 300 mg (since 07/05//18)
 - Therapeutic foscarnet 0.1 cc intravitreal 3x (28/05/18, 31/05/18, 04/06/18)
- **Immunosuppressive treatment**
 - Medrol *per os*
 - Prednisolone forte (prednisolone acetate ophthalmic suspension) topical

HSV-2 ocular infection (UZ Leuven)

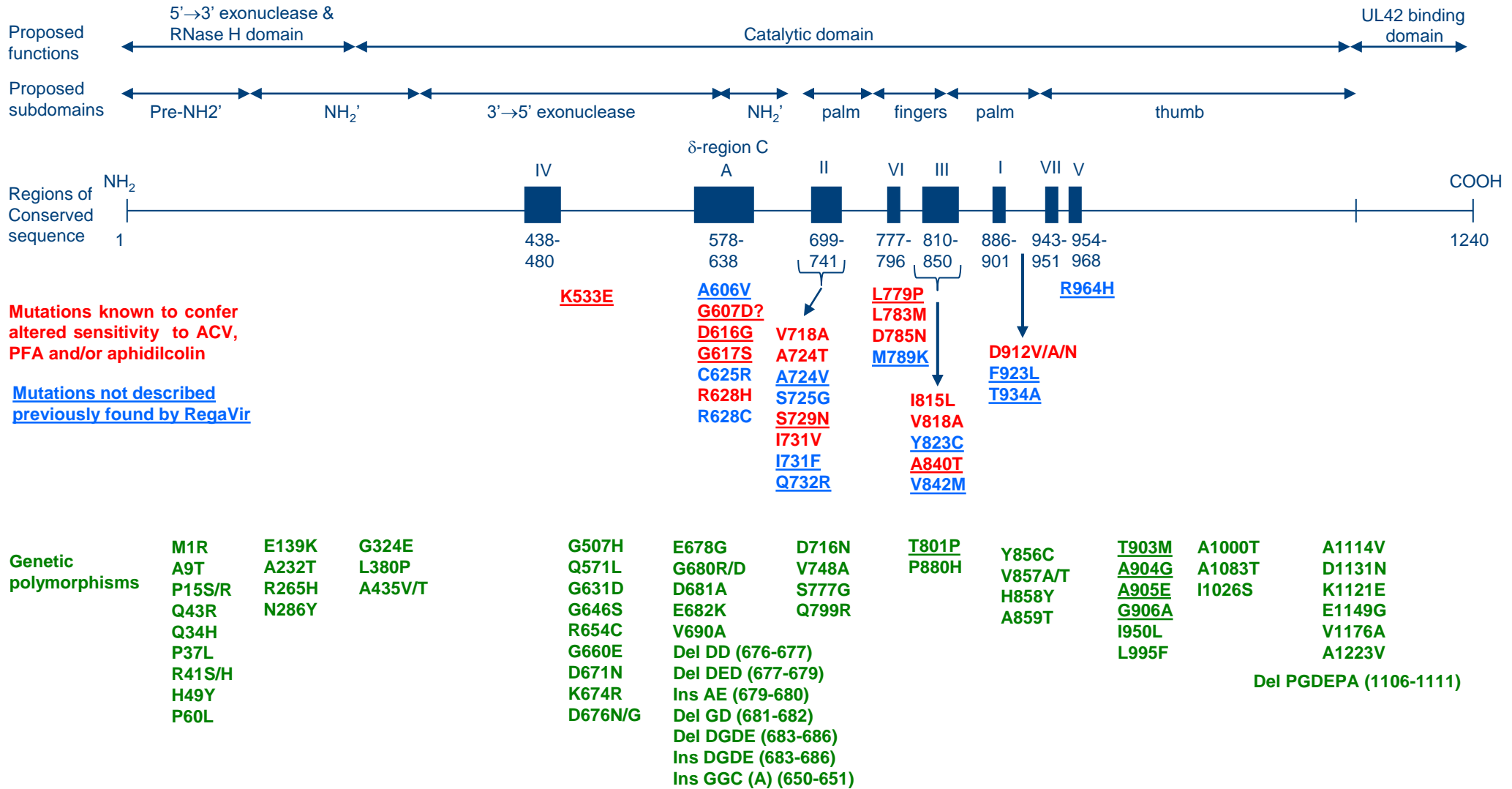
Arrival date to RegaVir	RegaVir ID	Sample date	Sample type	Viral load
29.05.2018	RV-1472	28.15.2018	Anterior chamber fluid	Not provided
12.06.2018	RV-1484	11.06.2018	Anterior chamber fluid	Not provided

	Mutations in the UL23 gene (thymidine kinase) (376 amino acids) Complete sequence		
	Related to genetic polymorphism (inter-strain variability)	Known to be associated with resistance to antiviral agents	Novel of unknown significance
RV-1472	G39E N78D A317V (novel) V335I (novel)	None	P271T
RV-1484	G39E N78D A317V (novel) V335I (novel)	None	P271T

	Amino acid changes in the UL30 (DNA polymerase) (1240 amino acids)	
	Known to be related to genetic polymorphism (inter-strain variability)	Known to be associated with resistance to antiviral agents
RV-1472 (partial sequence: amino acids 310-1240)	G646S A insertion 650-651 D667G* K674R EA insertion 677-678 D681A P801T G904A E905A A906G A977T* D985N* T987S* G990T* Q1013R* A1014E* G1016E* A1055P* V1088A* L1101H* A1105P* E1109D* PAPP deletion 1110-1113* L1116T* E1125P* P1127G* S1128A* H1129P* A1130R* D1131G* P1133E* G1135A* A1136G* S1137P*	None (all the positions verified)

* New polymorphisms

HSV-2 DNA polymerase



	Amino acid changes in the UL30 (DNA polymerase) (1240 amino acids)	
	Known to be related to genetic polymorphism (inter-strain variability)	Known to be associated with resistance to antiviral agents
RV-1484 partial sequence: amino acids 310-1068 * New polymorphisms	G646S A insertion 650-651 D667G* K674R EA insertion 677-678 D681A P801T G904A E905A A906G A977T* D985N* T987S* G990T* Q1013R* A1014E* G1016E* A1055P*	None (all the positions verified)

HSV-2 genital infection (UZ Gent)

- 24-years old woman with painful and recurrent gluteal HSV-2 lesions
- Antiviral treatment:
 - Valacyclovir daily 2x 500mg for 6 years
 - During exacerbations 3x 1g daily

Arrival date to RegaVir	RegaVir ID	Sample date	Sample type	Viral load
21.04.2016	RV-983	15.04.2016	Genital sample (vesicular fluid)	Not provided

HSV-2 genital infection (UZ Gent)

- 24-years old woman with painful and recurrent gluteal HSV-2 lesions
- Antiviral treatment:
 - Valacyclovir daily 2x 500mg for 6 years
 - During exacerbations 3x 1g daily

	Mutations in the UL23 gene (thymidine kinase) (376 amino acids) Complete sequence	
	Known to be related to genetic polymorphism (inter-strain variability)	Known to be associated with resistance to antiviral agents
RV-1472	G39E N78D	None (all positions verified)

	Amino acid changes in the UL30 (DNA polymerase) (1240 amino acids)		
	Known to be related to genetic polymorphism (inter-strain variability)	Novel	Known to be associated with resistance to antiviral agents
RV-983 (partial sequence: amino acids 309-1240)	D676G P801T G904A E905A A906G	A977T D985N T987S G990T Q1013R A1014E G1016E A1055P V1088A L1101H A1105P E1109D Deletion PAPP (1110-1113) L1116T E1125P P1127G S1128A H1129P A1130R D1131G P1133E G1135A A1136G	None (all the positions could be verified)

HSV-2 genital infection (UZ Gent)

Strain	EC ₅₀ (µg.ml)						
	Acyclovir	Penciclovir	Brivudin	Ganciclovir	Foscavir	Cidofovir	Adefovir
RV-983	0.024	0.072	>10	0.0023	25.26	1.2	21.87
	0.032	0.064	10	0.0025	25.26	1.1	21.87
Reference HSV-2 (G strain)	0.024	0.024	>10	0.00096	21.87	0.3	8.0

EC₅₀ : Concentration required to reduce virus induced cytopathicity by 50% in HEL cells.

HSV-2 genital infection (UZ Leuven)

- 66-years old woman with anogenital HSV-2 infection (sacro-anal)
- Not immunosuppressed
- Antiviral treatment:
 - Prophylactic valacyclovir 3x 1000 mg/day – cyclic, not continuous
 - Patient under self-medication taking high valacyclovir doses during several years

HSV-2 genital infection (UZ Leuven)

Arrival date to RegaVir	RegaVir ID	Sample date	Sample type	Viral load
22.06.2023	RV-2760	21.06.2023	Anogenital swab	Not provided
29.06.2023	RV-2765	28.06.2023	Anogenital swab	Not provided

	Mutations in the UL23 gene (thymidine kinase) (376 amino acids) Complete sequence		
	Known to be related to genetic polymorphism (inter-strain variability)	Known to be associated with resistance to antiviral agents	Novel of unknown significance
RV-2760	G39E N78D	None	P273L (P273S as a drug-R mutation) + E276K
RV-2765	G39E N78D	None	P273L (P273S as a drug-R mutation) + E276K

	Amino acid changes in the UL30 (DNA polymerase) (1240 amino acids)		
	Known to be related to genetic polymorphism (inter-strain variability)	Novel	Known to be associated with resistance to antiviral agents
RV-2760 (complete sequence)	A435T G646S A651ins D667G K674R AE679-680ins D681A P801T G904A E905A A906G	A9T T53A T144P A977T D985N T987S G990T Q1013R A1014E G1016E A1055P V1088A L1101H A1105P E1109D PAPP1110-1113del L1116T E1125P P1127G S1128A H1129P A1130R D1131G P1133E G1135A A1136G S1137P	None (all the positions could be verified)

	Amino acid changes in the UL30 (DNA polymerase) (1240 amino acids)		
	Known to be related to genetic polymorphism (inter-strain variability)	Novel	Known to be associated with resistance to antiviral agents
RV-2765 (complete sequence)	A435T G646S D667G K674R AE679-680ins D681A P801T G904A E905A A906G	A9T T53A T144P A977T D985N T987S G990T Q1013R A1014E G1016E A1055P V1088A L1101H A1105P E1109D PAPP1110-1113del L1116T E1125P P1127G S1128A H1129P A1130R D1131G P1133E G1135A A1136G S1137P	None (all the positions could be verified)

HSV-2 genital infection (UZ Leuven)

Strain	EC ₅₀ (µg.ml)								
	Acyclovir	Penciclovir	Brivudin	Ganciclovir	Foscavir	Cidofovir	Adefovir	Trifluridine	Pritelivir
Reference HSV-2 (G strain)	0.068	0.094	>10	0.0072	23.39	0.22	5.35	2.99	0.0032
	0.054	0.057	>10	0.0021	20.62	0.37	10.46	2.0	0.016
	0.068	0.12	4.89	0.013	27.59	0.44	16.36	4.47	0.029
Mean	0.063	0.090	≥ 8.3	0.007	23.867	0.343	10.723	3.153	0.016
RV-2760	0.032	0.21	>10.0	0.012	25.26	0.55	11.6	3.28	0.025
	0.065	0.10	>10.0	0.032	52.31	1.62	19.03	4.09	0.030
	0.051	0.075	2.0	0.0083	23.39	0.55	4.37	0.84	0.0088
	0.042	0.12		0.012	25.26	0.55		0.89	0.023
Mean	0.048	0.13	≥ 7.33	0.016	31.56	0.82	11.67	2.28	0.022
Fold resistance	0.8	1.4	0.9	2.2	1.3	2.4	1.1	0.7	1.4
EC ₅₀ : Concentration required to reduce virus induced cytopathicity by 50% Fold resistance (EC ₅₀ sample.EC ₅₀ G strain)									

Alignment of the DNA polymerase

HSV-2 lab strains	[HSV-2_HG52	AVARLAGINITRTIYDQQIRVFTCLLRLAGQKGFILPDTQGRFRGLDKE-APKRPAVPR	659
		HSV-2_G	AVARLAGINITRTIYDQQIRVFTCLLRLAGQKGFILPDTQGRFRGLDKE-APKRPAVPR	659
HSV-2 RegaVir isolates	[HSV-2_RV-2514	AVARLAGINITRTIYDQQIRVFTCLLRLAGQKGFILPDTQGRFRGLDKE-APKRPAVPR	659
		HSV-2_RV-2726	AVARLAGINITRTIYDQQIRVFTCLLRLAGQKGFILPDTQGRFRGLDKE-APKRPAVPR	659
		HSV-2_RV-2852	AVARLAGINITRTIYDQQIRVFTCLLRLAGQKGFILPDTQGRFRGLDKE-APKRPAVPR	659
HSV-2 isolates with high DNA pol variability	[HSV-2v_RV-983	AVARLAGINITRTIYDQQIRVFTCLLRLAGQKGFILPDTQGRFRGLDKE-APKRPAVPR	659
		HSV-2v_RV-2760	AVARLAGINITRTIYDQQIRVFTCLLRLAGQKGFILPDTQGRFRSLDKEAAPKRPAVPR	660
		HSV-2v_RV-2765	AVARLAGINITRTIYDQQIRVFTCLLRLAGQKGFILPDTQGRFRSLDKE-APKRPAVPR	659
		HSV-2v_RV-1472	AVARLAGINITRTIYDQQIRVFTCLLRLAGQKGFILPDTQGRFRSLDKEAAPKRPAVPR	351
HSV-2 variant (HSV-2v) isolates	[HSV-2v_RV-1484	AVARLAGINITRTIYDQQIRVFTCLLRLAGQKGFILPDTQGRFRSLDKEAAPKRPAVPR	351
		HSV-2v_pat1	AVARLAGINITRTIYDQQIRVFTCLLRLAGQKGFILPDTQGRFRSLDKEAAPKRPAVPR	660
		HSV-2v_pat2	AVARLAGINITRTIYDQQIRVFTCLLRLAGQKGFILPDTQGRFRSLAKEAAPKRPAVPR	660
		HSV-2v_pat3	AVARLAGINITRTIYDQQIRVFTCLLRLAGQKGFILPDTQGRFRSLDKEAAPKRPAVPR	660
			*****.*****.* ** *****	
		HSV-2_HG52	GGERPGDGNDEDKDDD--EDGDEDGEREEVARETGGRHVG YQGARVLDPTS GFHVDP	717
		HSV-2_G	GGERPGDGNDEDKDDD--EDGDEDGEREEVARETGGRHVG YQGARVLDPTS GFHVDP	717
		HSV-2_RV-2514	GGERPGDGNDEDKDDD--EDGDEDGEREEVARETGGRHVG YQGARVLDPTS GFHVDP	717
		HSV-2_RV-2726	GGERPGDGNDEDKDDD--GDGDEDGEREEVARETGGRHVG YQGARVLDPTS GFHVDP	717
		HSV-2_RV-2852	GGERPGDGNDEDKDDD--EDGDEDGEREEVARETGGRHVG YQGARVLDPTS GFHVDP	717
		HSV-2v_RV-983	GGERPGDGNDEDKDG--EDGDEDGEREEVARETGGRHVG YQGARVLDPTS GFHVDP	717
		HSV-2v_RV-2760	GGERPGGGNGDEDRDDDEAEDGAEDGEREEVARETGGRHVG YQGARVLDPTS GFHVDP	720
		HSV-2v_RV-2765	GGERPGGGNGDEDRDDDEAEDGAEDGEREEVARETGGRHVG YQGARVLDPTS GFHVDP	719
		HSV-2v_RV-1472	GGERPGGGNGDEDRDDDEAEDGAEDGEREEVARETGGRHVG YQGARVLDPTS GFHVDP	411
		HSV-2v_RV-1484	GGERPGGGNGDEDRDDDEAEDGAEDGEREEVARETGGRHVG YQGARVLDPTS GFHVDP	411
		HSV-2v_pat1	GGERPGGGNGDEDRDDDEAEDGAEDGEREEVARETGGRHVG YQGARVLDPTS GFHVDP	720
		HSV-2v_pat2	GGERPGGGNGDEDRDDDEAEDGAEDGEREEVARETGGRHVG YQGARVLDPTS GFHVDP	720
		HSV-2v_pat3	GGERPGGGNGDEDRDDDEAEDGAEDGEREEVARETGGRHVG YQGARVLDPTS GFHVDP	720
			*****.*****:*.* ** *****	

HSV-2_HG52	KGVDLVRKNNCAFINRTSRALVDLLFYDDTVSGAAAAAERPAEEWLARPLPEGLQAFGA	1017
HSV-2_G	KGVDLVRKNNCAFINRTSRALVDLLFYDDTVSGAAAAAERPAEEWLARPLPEGLQAFGA	1017
HSV-2_RV-2514	KGVDLVRKNNCAFINRTSRALVDLLFYDDTVSGAAAAAERPAEEWLARPLPEGLQAFGA	1017
HSV-2_RV-2726	KGVDLVRKNNCAFINRTSRALVDLLFYDDTVSGAAAAAERPAEEWLARPLPEGLQAFGA	1017
HSV-2_RV-2852	KGVDLVRKNNCAFINRTSRALVDLLFYDDTVSGAAAAAERPAEEWLARPLPEGLQAFGA	1017
HSV-2v_RV-983	KGVDLVRKNNCAFINRTSRITLVDLLFYNDVSVSTAAAAAERPAEEWLARPLPEGLREFEA	1017
HSV-2v_RV-2760	KGVDLVRKNNCAFINRTSRITLVDLLFYNDVSVSTAAAAAERPAEEWLARPLPEGLREFEA	1020
HSV-2v_RV-2765	KGVDLVRKNNCAFINRTSRITLVDLLFYNDVSVSTAAAAAERPAEEWLARPLPEGLREFEA	1019
HSV-2v_RV-1472	KGVDLVRKNNCAFINRTSRITLVDLLFYNDVSVSTAAAAAERPAEEWLARPLPEGLREFEA	711
HSV-2v_RV-1484	KGVDLVRKNNCAFINRTSRITLVDLLFYNDVSVSTAAAAAERPAEEWLARPLPEGLREFEA	711
HSV-2v_pat1	KGVDLVRKNNCAFINRTSRITLVDLLFYNDVSVSTAAAAAERPAEEWLARPLPEGLREFEA	1020
HSV-2v_pat2	KGVDLVRKNNCAFINRTSRITLVDLLFYNDVSVSTAAAAAERPAEEWLARPLPEGLREFEA	1020
HSV-2v_pat3	KGVDLVRKNNCAFINRTSRITLVDLLFYNDVSVSTAAAAAERPAEEWLARPLPEGLREFEA	1020

*****:*****:*. ** *****: * *

HSV-2_HG52	VLVDAHRRITDPERDIQDFVLTAELSRHPRAYTNKRLAHLTVYYKLMARRAQVPSIKDRI	1077
HSV-2_G	VLVDAHRRITDPERDIQDFVLTAELSRHPRAYTNKRLAHLTVYYKLMARRAQVPSIKDRI	1077
HSV-2_RV-2514	VLVDAHRRITDPERDIQDFVLTAELSRHPRAYTNKRLAHLTVYYKLMARRAQVPSIKDRI	1077
HSV-2_RV-2726	VLVDAHRRITDPERDIQDFVLTAELSRHPRAYTNKRLAHLTVYYKLMARRAQVPSIKDRI	1077
HSV-2_RV-2852	VLVDAHRRITDPERDIQDFVLTAELSRHPRAYTNKRLAHLTVYYKLMARRAQVPSIKDRI	1077
HSV-2v_RV-983	VLVDAHRRITDPERDIQDFVLTAELSRHPRAYTNKRLPHLTVYYKLMARRAQVPSIKDRI	1077
HSV-2v_RV-2760	VLVDAHRRITDPERDIQDFVLTAELSRHPRAYTNKRLPHLTVYYKLMARRAQVPSIKDRI	1080
HSV-2v_RV-2765	VLVDAHRRITDPERDIQDFVLTAELSRHPRAYTNKRLPHLTVYYKLMARRAQVPSIKDRI	1079
HSV-2v_RV-1472	VLVDAHRRITDPERDIQDFVLTAELSRHPRAYTNKRLPHLTVYYKLMARRAQVPSIKDRI	771
HSV-2v_RV-1484	VLVDAHRRITDPERDIQDFVLTAELSRHPRAYTNKRLPHLTVYYKLMA-----	759
HSV-2v_pat1	VLVDAHRRITDPERDIQDFVLTAELSRHPRAYTNKRLPHLTVYYKLMARRAQVPSIKDRI	1080
HSV-2v_pat2	VLVDAHRRITDPERDIQDFVLTAELSRHPRAYTNKRLPHLTVYYKLMARRAQVPSIKDRI	1080
HSV-2v_pat3	VLVDAHRRITDPERDIQDFVLTAELSRHPRAYTNKRLPHLTVYYKLMARRAQVPSIKDRI	1080

***** *****

HSV-2_HG52	PYVIVAQTREVEETVARLAALRELDAAAPGDEPAPPAALPSPAKRPRETPSHADPPGGAS	1137
HSV-2_G	PYVIVAQTREVEETVARLAALRELDAAAPGDEPAPPAALPSPAKRPRETPSHADPPGGAS	1137
HSV-2_RV-2514	PYVIVAQTREVEETVARLAALRELDAAAPGDEPAPPAALPSPAKRPRETPSHADPPGGAS	1137
HSV-2_RV-2726	PYVIVAQTREVEETVARLAALRELDAAAPGDEPAPPAALPSPAKRPRETPSHADPPGGAS	1137
HSV-2_RV-2852	PYVIVAQTREVEETVARLAALRELDAAAPGDEPAPPAALPSPAKRPRETPSHADPPGGAS	1137
HSV-2v_RV-983	PYVIVAQTREAEETVARLAALREHDAAPPGDDAA----TPSPAKRPRPTGAPRGPEGAGP	1133
HSV-2v_RV-2760	PYVIVAQTREAEETVARLAALREHDAAPPGDDAA----TPSPAKRPRPTGAPRGPEGAGP	1136
HSV-2v_RV-2765	PYVIVAQTREAEETVARLAALREHDAAPPGDDAA----TPSPAKRPRPTGAPRGPEGAGP	1135
HSV-2v_RV-1472	PYVIVAQTREAEETVARLAALREHDAAPPGDDAA----TPSPAKRPRPTGAPRGPEGAGP	827
HSV-2v_RV-1484	-----	759
HSV-2v_pat1	PYVIVAQTREAEETVARLAALREHDAAPPGDDAA----TPSPAKRPRPTGAPRGPEGAGP	1136
HSV-2v_pat2	PYVIVAQTREAEETVARLAALREHDAAPPGDDAA----TPSPAKRPRPTGAPRGPEGAGP	1136
HSV-2v_pat3	PYVIVAQTREAEETVARLAALREHDAAPPGDDAA----TPSPAKRPRPTGAPRGPEGAGP	1136



HSV-2 variant (HSV-2v)

- Both HSV-1 & HSV-2 species show overall **low levels of genomic variability**
- HSV-1 strains are generally more diverse than HSV-2 strains (mean pairwise distance of 0.8% for HSV-1 and 0.1% for HSV-2).
- In 2013, **a new HSV-2 variant (HSV-2v)** was identified in patients originating from **West Africa**, which showed an unexpectedly **high variability (2.4% divergence)** in the viral DNA pol.
- **HSV-2v** clearly differed from classical HSV-2 isolates in phylogenetic analyses and **may be linked to simian ChHV.**
- This new HSV-2 variant highlights the **possible occurrence of recombination between human and simian herpesviruses under natural conditions**, potentially presenting greater challenges for the future.

Ancient Recombination Events between Human Herpes Simplex Viruses

- Burrell et al , 2011: WGS of 18 HSV-2 clinical isolates characterized by divergent UL30 gene sequences to further elucidate the evolutionary history of this virus.
- **Two main HSV-2 lineages exist:**
 - One mostly restricted to **subSaharan Africa**
 - One has reached a **global distribution** (only the worldwide lineage is characterized by ancient recombination events with HSV-1).
- **Complexity of HSV-2 evolution**, a virus of putative zoonotic origin which later recombined with its human-adapted relative.
- **Coinfections with HSV-1 and 2** may have genomic and potentially functional consequences and should therefore be monitored more closely.



Thank you for your
attention

Any questions?