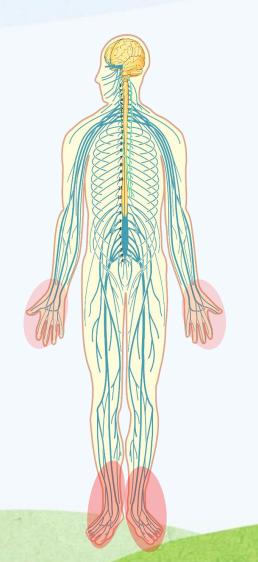


What is HIV-associated Sensory Neuropathy?

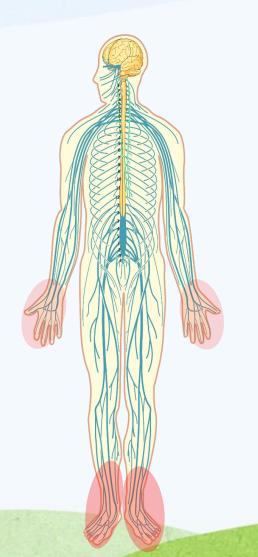


Painful & debilitating neurological condition

Affects up 60% of people living with HIV

Results from HIV infection directly or from the use of neurotoxic ART – particularly stavudine

What is HIV-associated Sensory Neuropathy?

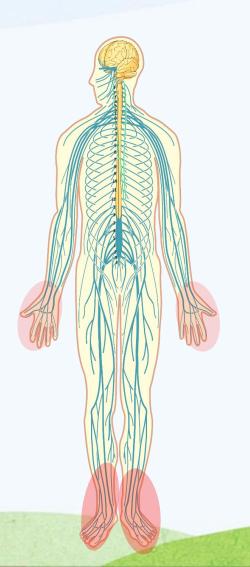


Symptoms may include:

- o reduced ankle reflexes
- o Burning, numbness, pins & needles
- o Pain hypersensitivity (Hyperalgesia)
- o Pain without painful stimuli (Allodynia)

Impacts ability to work and quality of life!

What is HIV-associated Sensory Neuropathy?



Clinical pathology:

- o Neuronal loss in the dorsal root ganglion
- o Dieback degeneration of long axons
- o Destruction of primary afferent terminals

Underlying inflammatory pathology:

- o Infiltration of macrophages
- o Increased cytokine and chemokine production

But HIV-SN has a genetic component!

A genetic study by our group investigated 3 genes:

P2X7R: inflammatory signalling

P2X4R: neurotransmission

CAMKK2: neuronal repair & energy homeostasis

153 HIV+ South African patients treated with stavudine with African ancestry and were assessed for neuropathy

Blood collected, DNA extracted, genotyped for 45 SNPs

Haplotypes derived using fastPHASE

SNPs in CAMKK2 associate with HIV-SN

SNP	GENE	CHI ²
rs1186055	P2X7R	0.17
rs208307	P2X7R	0.15
rs10160951	P2X7R	0.17
rs2230912	P2X7R	0.08
rs2686387	P2X4R	0.15
Rs2668252	P2X4R	0.13
Rs1169719	P2X4R	0.11
rs1653587	CAMKK2	0.12
rs7975295	CAMKK2	0.007
rs2686344	CAMKK2	0.018
rs1560568	CAMKK2	0.023
rs2686367	CAMKK2	0.004

Strong association found with CAMKK2

rs2686344 associated with REDUCED risk

rs7975295, rs1560568 & rs2686367 associated with INCREASED risk

Weaker effect observed in P2X7R and P2X4R

HAPLOTYPE (>1% Frequency)	GENE	CHI ²
1111112111121211111111	P2X7R	0.18
211121211112121111111	P2X7R	0.12
211111111	P2X4R	0.20
211111212	P2X4R	0.17
212111111	P2X4R	0.13
11111111112	CAMKK2	0.14
11111111121	CAMKK2	0.002
11111112112	CAMKK2	0.14
11112111111	CAMKK2	0.03
11112121111	CAMKK2	0.05
11121212111	CAMKK2	0.014
11121221111	CAMKK2	0.05
11121221112	CAMKK2	0.13
21111111121	CAMKK2	0.03

CAMKK2 haplotypes associate with HIV-SN

Significant association found with 6 CAMKK2 haplotypes

5 haplotype associated with REDUCED risk

1 haplotype associated with INCREASED risk Contains the 2 of the risk SNPs

Weaker effect observed in P2X7R and P2X4R

Variable	Odds Ratio	P value	95% confidence interval		
n=137 p<0.0001 R ² =0.19					
Age	1.08	0.007	0.02-1.13		
Height	1.05	0.03	1.00-1.11		
rs208307 (P2X7R)	1.96	0.10	0.86-4.88		
rs2668252 (P2X4R)	2.10	0.09	0.90-4.93		
rs1169719 (P2X4R)	0.37	0.11	0.11-1.23		
rs1560568 (CAMKK2)	2.39	0.03	1.09-5.25		
rs2686367 (CAMKK2)	2.85	0.01	1.26-6.42		

The logistic regression model predicts HIV-SN

The optimum model included demographics and genetics:

Age and Height

2x CAMKK2 SNPs which mark risk significantly independently associated with HIV-SN

Predicted 19% of the risk of HIV-SN

LIMITATIONS!

Limitation: Patients received stavudine, a risk factor of HIV-SN

Solution: Assess another cohort without exposure to stavudine May identify if associations are due to stavudine, HIV or other ART

Limitation: SNPs vary by ethnicity so may only associate in Africans

Solution: Assess in a cohort of a different ethnicity.

Associations present in multiple populations may be critical in HIV-SN

Our Study

Indonesia



COMPLETE: 203 DNA Samples

Indonesian and South African HIV+ & Stavudine Naïve

Assessed for HIV-SN using the BPNS

Blood collected & DNA extracted

Genotyped for 64 SNP across P2X7R, P2X4R & CAMKK2

Haplotypes derived using fastPHASE

South Africa



IN PROGRESS: 83 DNA Samples

Unpublished, 2017: Fitri Octaviana, Yanuar Ahmed, Denise Dewanto, Huguette Ngassa Mbenda, Jessica Gaff, et al.

CAMKK2 significantly associated with HIV-SN

SNP	GENE	CHI ²
rs25644	P2X4R	0.07
rs1718158	CAMKK2	0.18
rs10849861	CAMKK2	0.046
rs1653586	CAMKK2	0.17
rs1653587	CAMKK2	0.17
rs1653587	CAMKK2	0.12
rs7975295	CAMKK2	0.011
rs1560568	CAMKK2	0.011
rs1132780	CAMKK2	0.010

4 CAMKK2 SNPs significantly associated with HIV-SN in Indonesian HIV+ patients

2 SNPs are associated with increased risk

Also associated with increased risk in South Africans – individually and in the risk haplotype

4 CAMKK2 SNPs showed a weaker effect

CAMKK2 haplotypes weakly associate with HIV-SN

HAPLOTYPE (>1% Frequency)	GENE	CHI ²
2211211211121	P2X7R	0.02
1121111211121	P2X7R	0.10
1211121111111	P2X7R	0.14
2212111	P2X4R	0.13
1211112 2 1 2 21111111	CAMKK2	0.09
212211211111111111	CAMKK2	0.06
1111211111111112212	CAMKK2	0.19
1111121121111111112	CAMKK2	0.14

4 CAMKK2 haplotypes weakly associated with HIV-SN

1 CAMKK2 haplotype contains 2 SNPs associated with increased risk in both Indonesians & South Africans

CAMKK2 is implicated in HIV-SN

Logistic regression is yet to be completed...



A role for the expressed protein of CAMKK2 in HIV-SN

Do the encoded proteins also impact HIV-SN?

Distal leg biopsies collected from:

- HIV-SN patients
- HIV+ patients without SN
- o Healthy Individuals

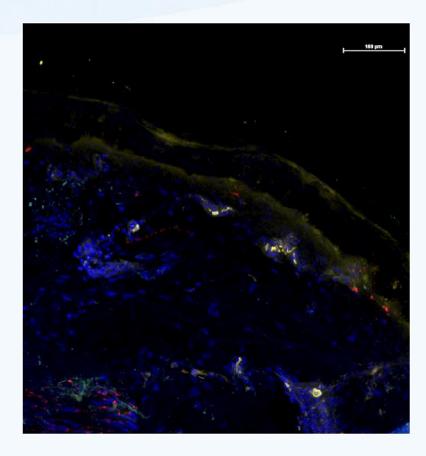


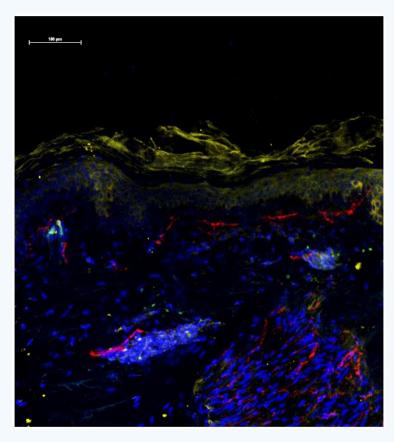
Fixed with 8% paraformaldehyde and cut into 50um sections

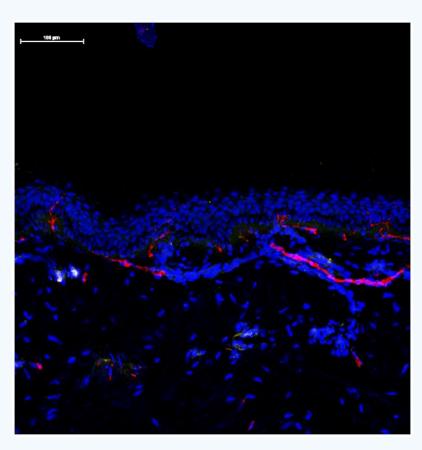
Treated with primary, secondary and fluorescently labelled antibodies

Confocal z-stack images collected and protein expression assessed

P2X7R is upregulated in HIV patients





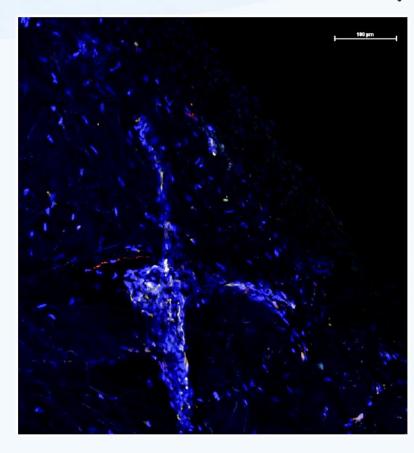


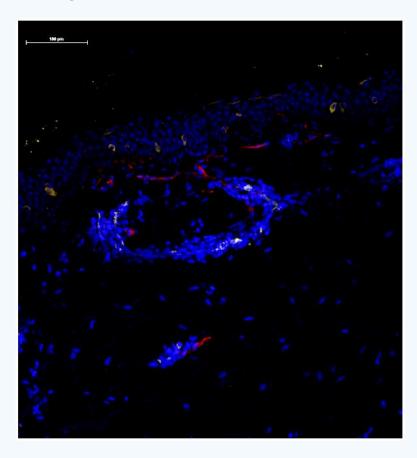
HIV+SN+

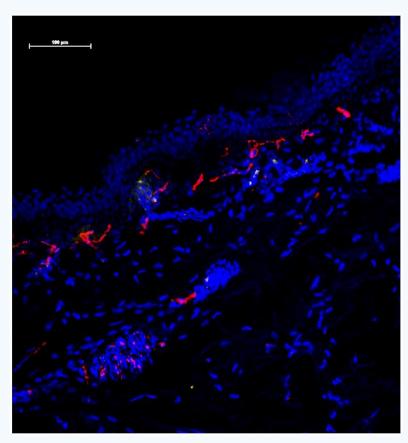
HIV+SN-

Healthy

P2X4R is upregulated in HIV-SN patients





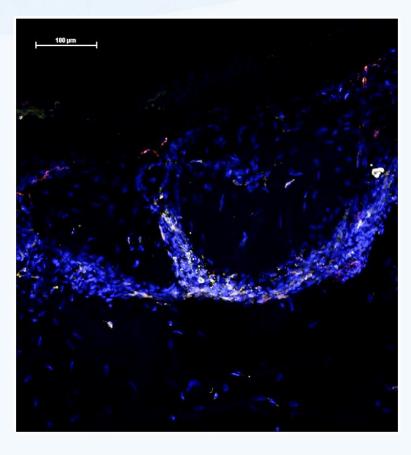


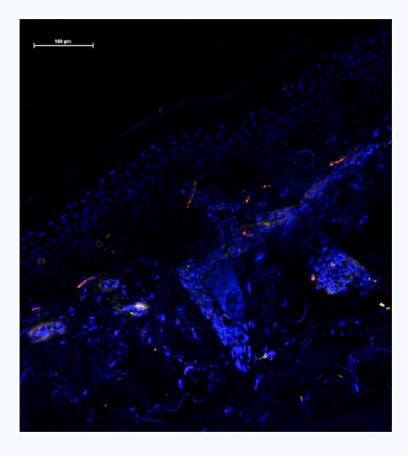
HIV+SN+

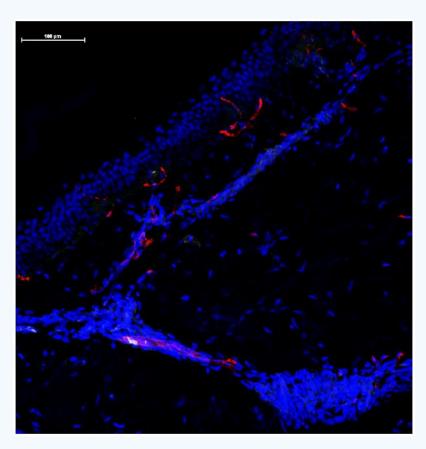
HIV+SN-

Healthy

CaMKK2 is upregulated in HIV-SN patients







HIV+SN+

HIV+SN-

Healthy

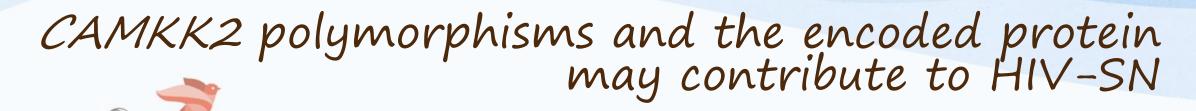
Summary

SNPs in CAMKK2 associate with HIV-SN in patients with and without exposure to Stavudine

SNPs in CAMKK2 associate with HIV-SN in both Indonesian and South African patients

CaMKK2 expression is upregulated in patients with HIV-SN P2X7R and P2X4R exhibit a weaker effect

CAMKK2 polymorphisms and the encoded protein may contribute to HIV-SN



These results may allow us to develop a prognostic test to identify individuals with increased risk to HIV-SN

and identifies possible mechanisms of the disease, which may provide a therapeutic target in the future!

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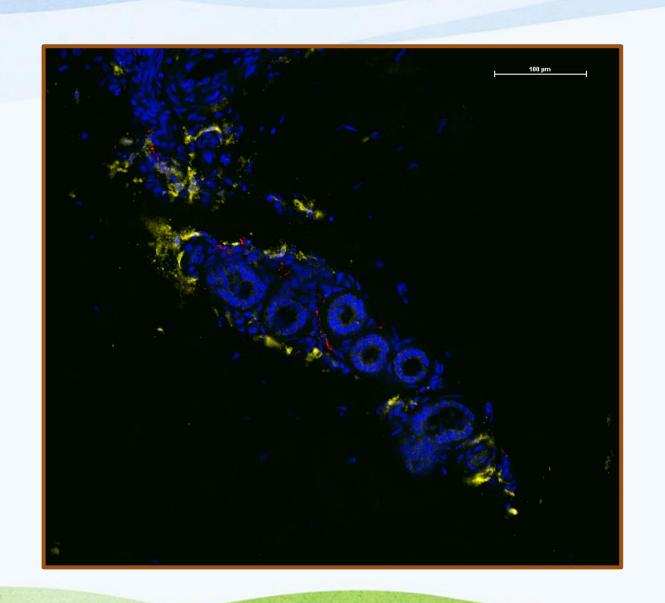
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Thank you!