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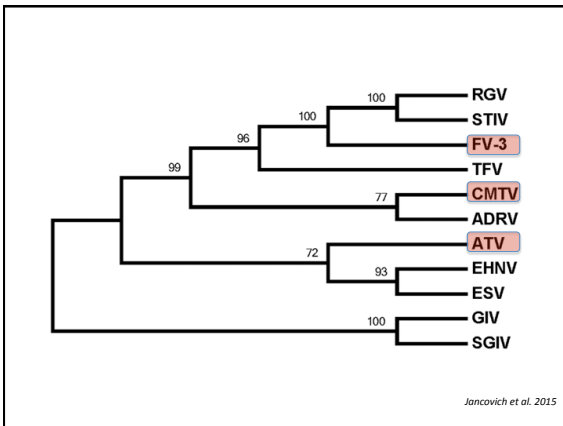
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**Table 1** Sequenced genomes from members of the genus *Ranavirus*

Ranavirus	Abbreviation	Host	Genome size (kb)	GC (%)	Predicted ORFs	Accession #	Reference
<i>Ambystoma davidianus ranavirus</i>	ADRV	Salamander	106,519	55	101	KF033124	Wang et al. (2014)
			106,734			KC865735	Chen et al. (2013)
<i>Ambystoma tigrinum virus</i>	ATV	Salamander	106,332	54	96	AY150217	Janovich et al. (2003)
Common midwife toad ranavirus	CMTV	Frog	106,878	55	104	JQ231222	Mavian et al. (2012a)
<i>Epizootic hematopoietic necrosis virus</i>	EHNV	Fish	127,011	54	100	FJ433873	Janovich et al. (2010)
ESV		Fish	127,732	54	136	JQ724856	Mavian et al. (2012b)
European sheathfish virus	EV3	Frog	105,903	55	98	AY548484	Tan et al. (2004)
<i>Frog virus 3</i>	FV3	Frog	105,903	55	98	AY548484	Tan et al. (2004)
Groupers iridovirus	GIV	Fish	139,793	49	139	AY666015	Tsai et al. (2005)
<i>Rana gryllus virus</i>	RGV	Frog	105,791	55	106	JQ654586	Lei et al. (2012)
Singapore grouper iridovirus	SGIV	Fish	140,131	48	162	AY521625	Song et al. (2004)
Soft-shelled turtle iridovirus	STIV	Turtle	105,890	55	105	EU627010	Huang et al. (2009)
Spotted salamander Maine	SSME	Salamander	105,070	55	95	KJ175144	Morrison et al. (2014)
Tiger frog virus	TFV	Frog	105,057	55	105	AF389451	He et al. (2002)

Ranavirus names in *italics* indicate recognized species within the genus *Ranavirus*

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Where about?

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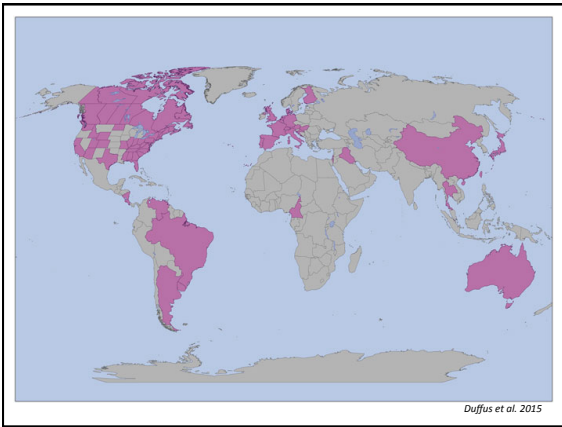
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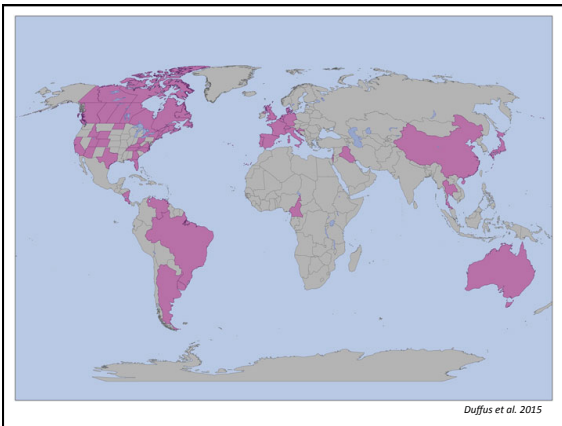
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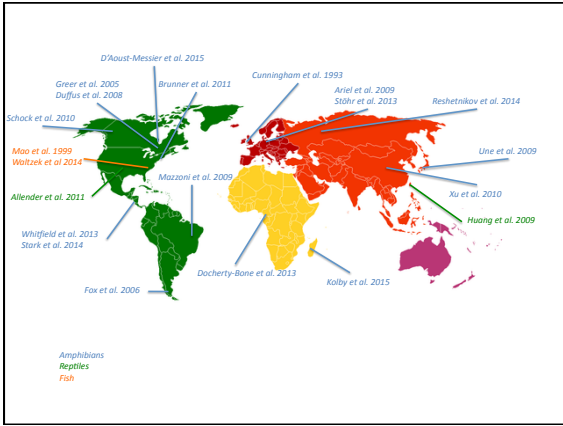
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Who is affected?

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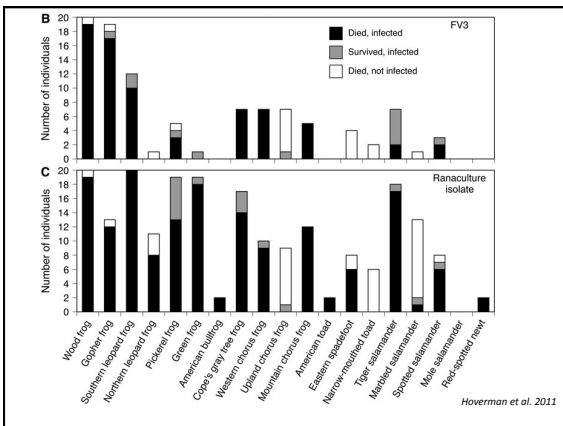
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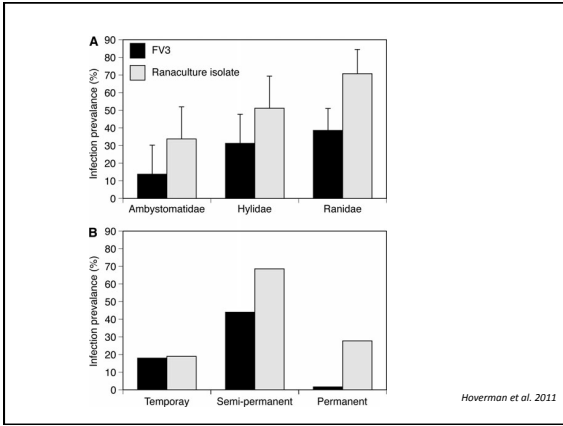
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Bd / FV3 co-occurrence?

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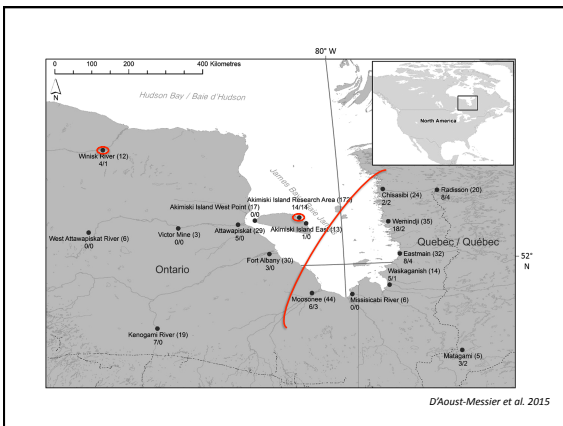
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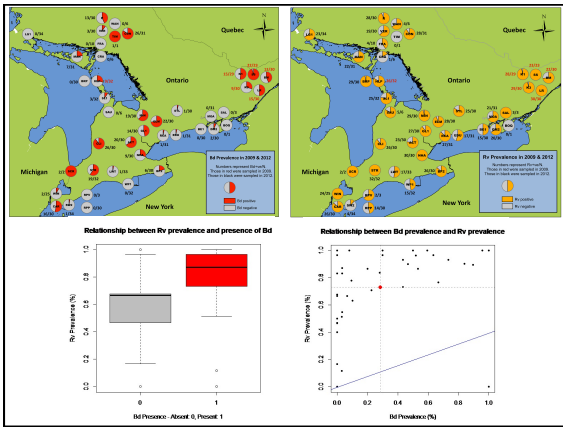
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Only one FV3?

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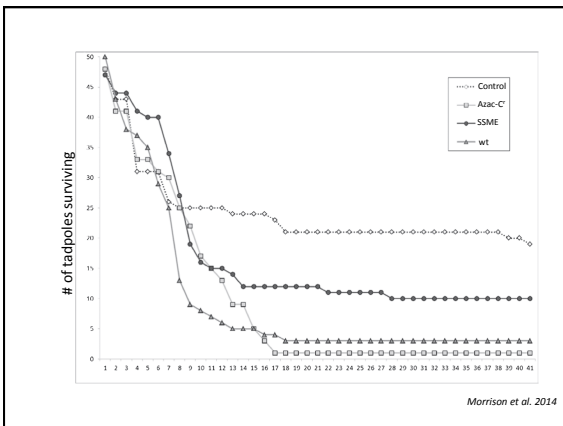
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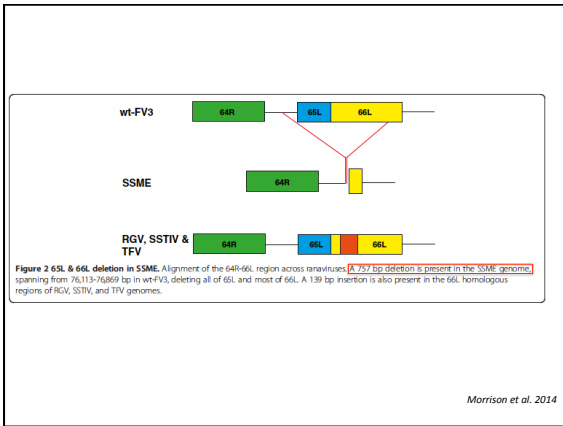
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Several strains + several hosts  
+ several environments = ?

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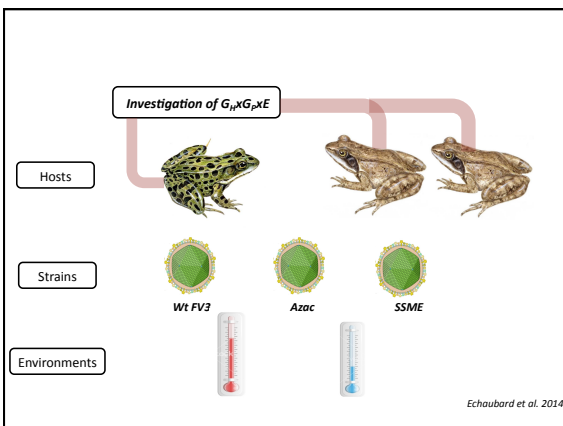
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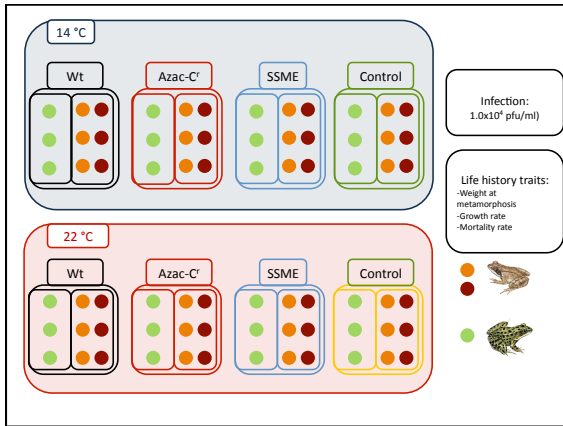
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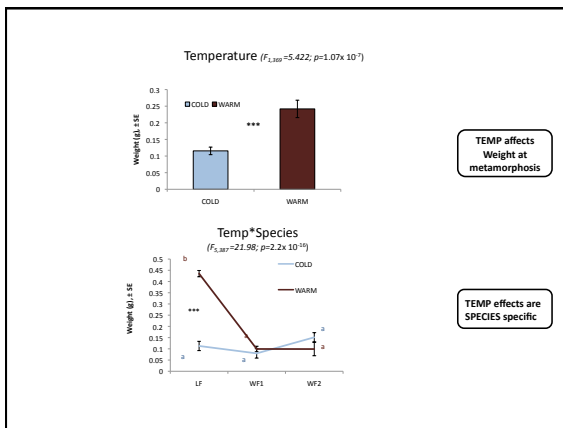
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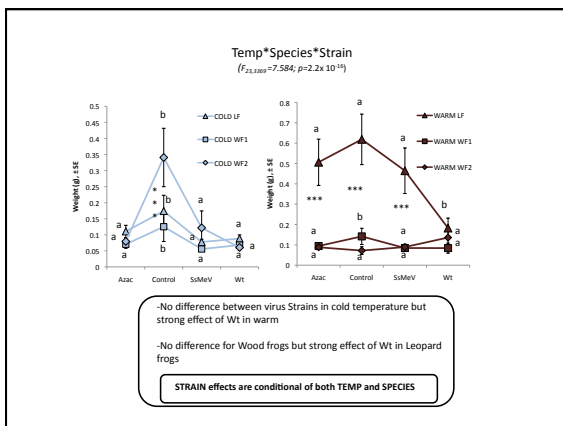
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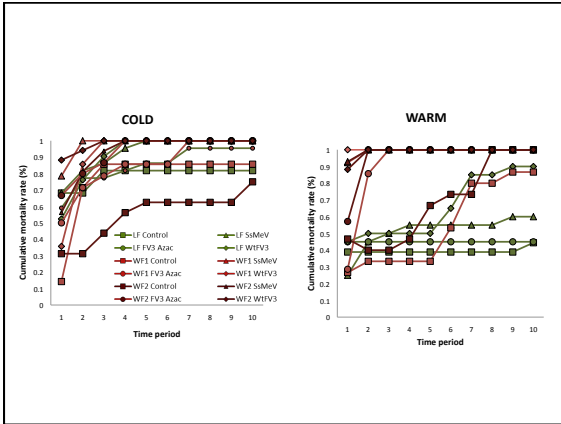
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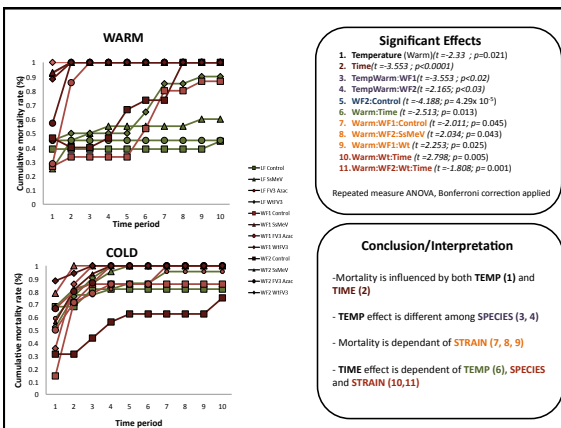
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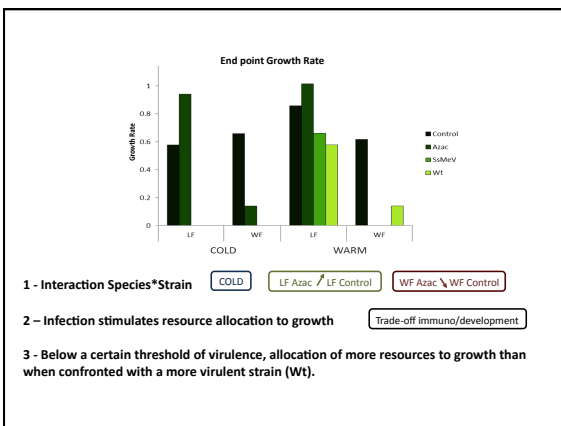
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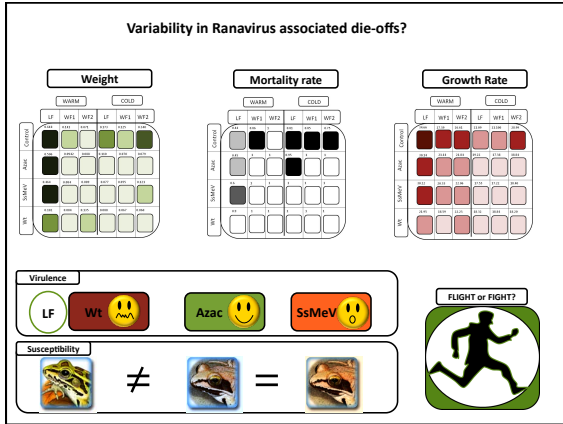
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