Vector-Borne Diseases - North African Regional meeting

WORLD ORGANISATION
FOR ANIMAL HEALTH

Bluetongue and epizootic hemorrhagic disease: incursion, recent developments and control strategies in the context of North Africa

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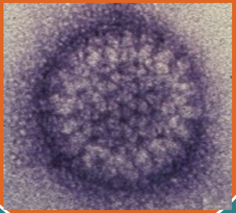
TO BE COVERED

in brief

- I VIRUSES, VECTORS & HOSTS
- II INCURSION OF VIRUSES
- III RECENT DEVELOPEMENTS
- IV CONTROL STRATEGIES
- V CONCLUDING REMARKS

VIRUSES, VECTORS & HOSTS

When to expect the disease

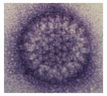


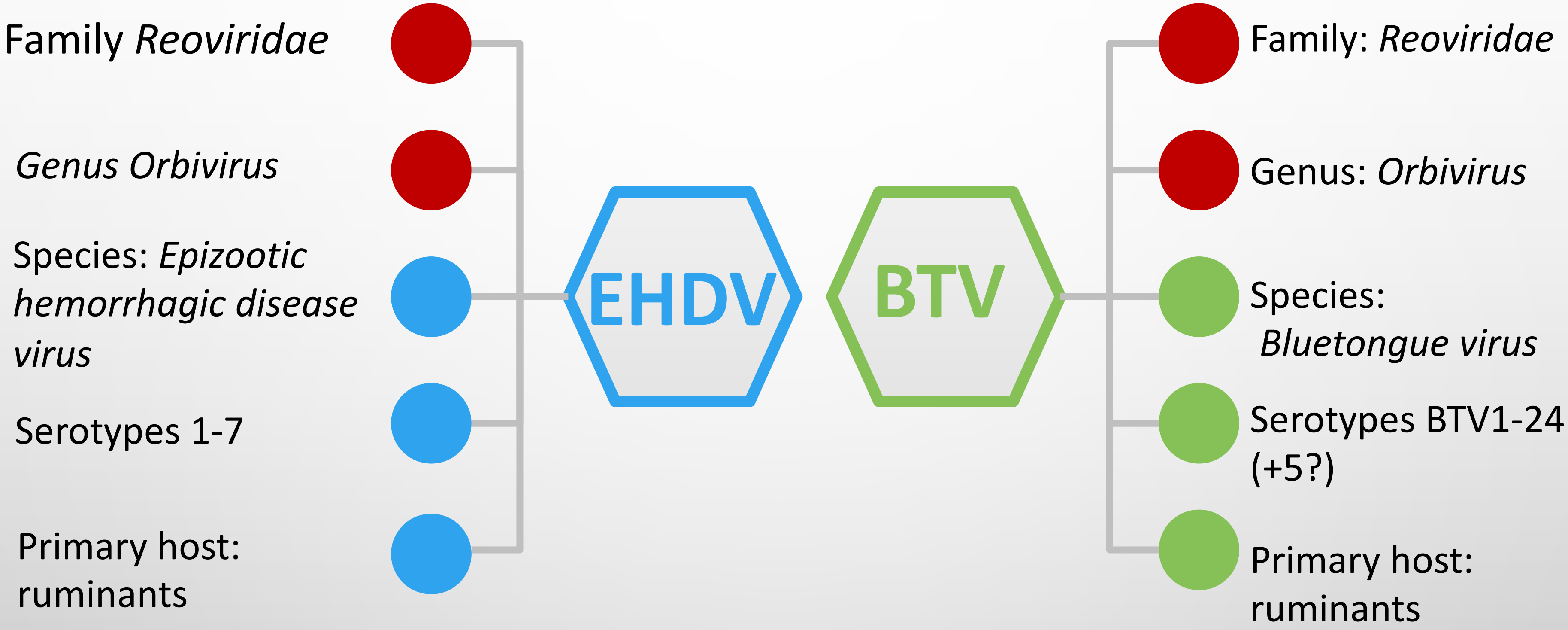
https://www.cdc.gov/EID/content/13/4/614.htm

https://creativecommons.org/

Photo: S. HAMMAMI

Viruses





Family *Reoviridae*

Genus Orbivirus

Species: *Epizootic hemorrhagic disease virus*

Serotypes 1-7

Primary host: ruminants

EHDV

BTV

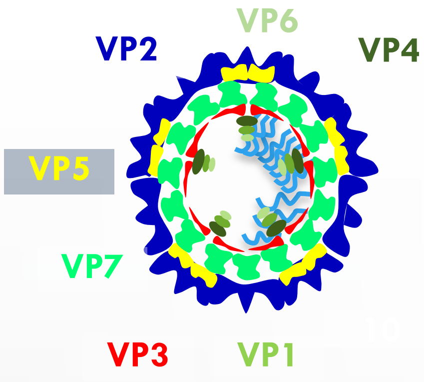
Family: *Reoviridae*

Genus: *Orbivirus*

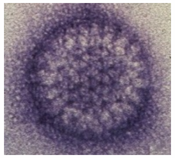
Species: *Bluetongue virus*

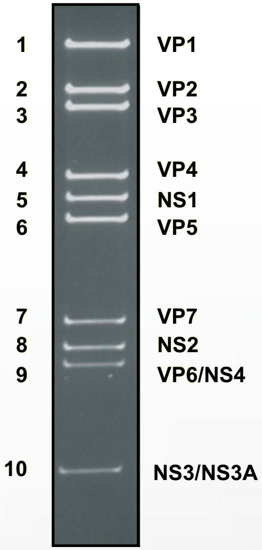
Serotypes BTV1-24 (+5?)

Primary host: ruminants



Viruses



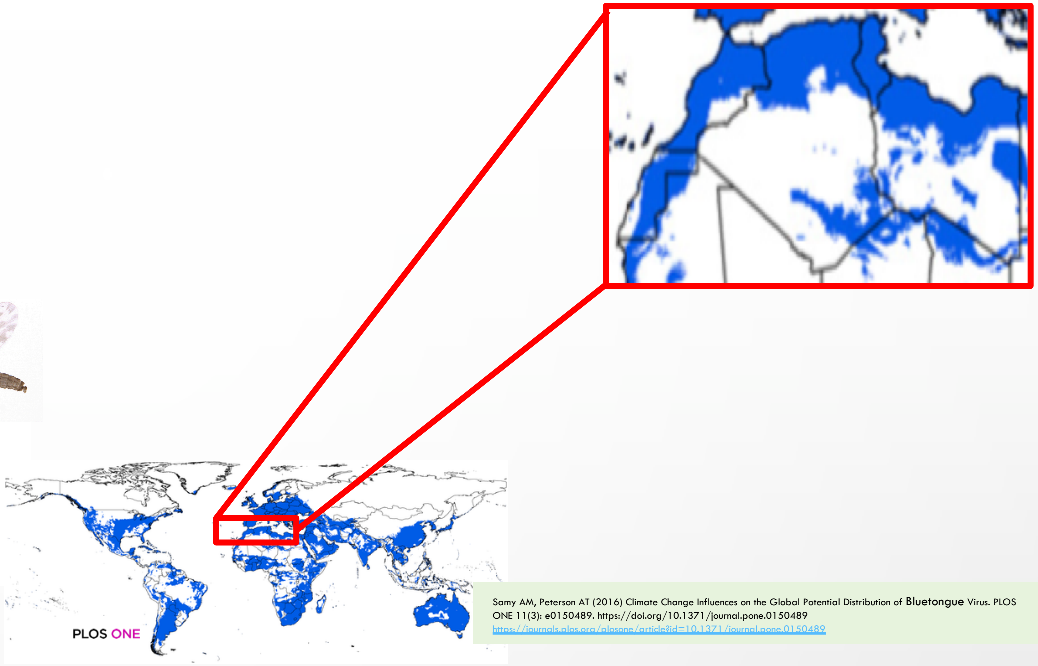


Characteristics	Practical implications
Non-enveloped	Resistance in nature
Segmented linear dsRNA (10 segments)	Reassortment : novel phenotypes (potential consequences)
Serotypes BTV (1-24,classic)+ new types? EHDV: EHDV1-7	Vaccination difficulty
VP2 main antigen with 70% variability	Interacts with serotype- specific antibodies VP5 helps determining the serotype

Culicoides spp.

>1400 species worldwide

- Main vector in North Africa: ***C. imicola***
- Wind movement



Samy AM, Peterson AT (2016) Climate Change Influences on the Global Potential Distribution of Bluetongue Virus. PLOS ONE 11(3): e0150489. https://doi.org/10.1371/journal.pone.0150489
https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0150489

- Persistent infectious virus in susceptible species

Photo: S. HAMMAMI

- Long-lasting protection to reinfection by homologous BTV serotype

INCURSION

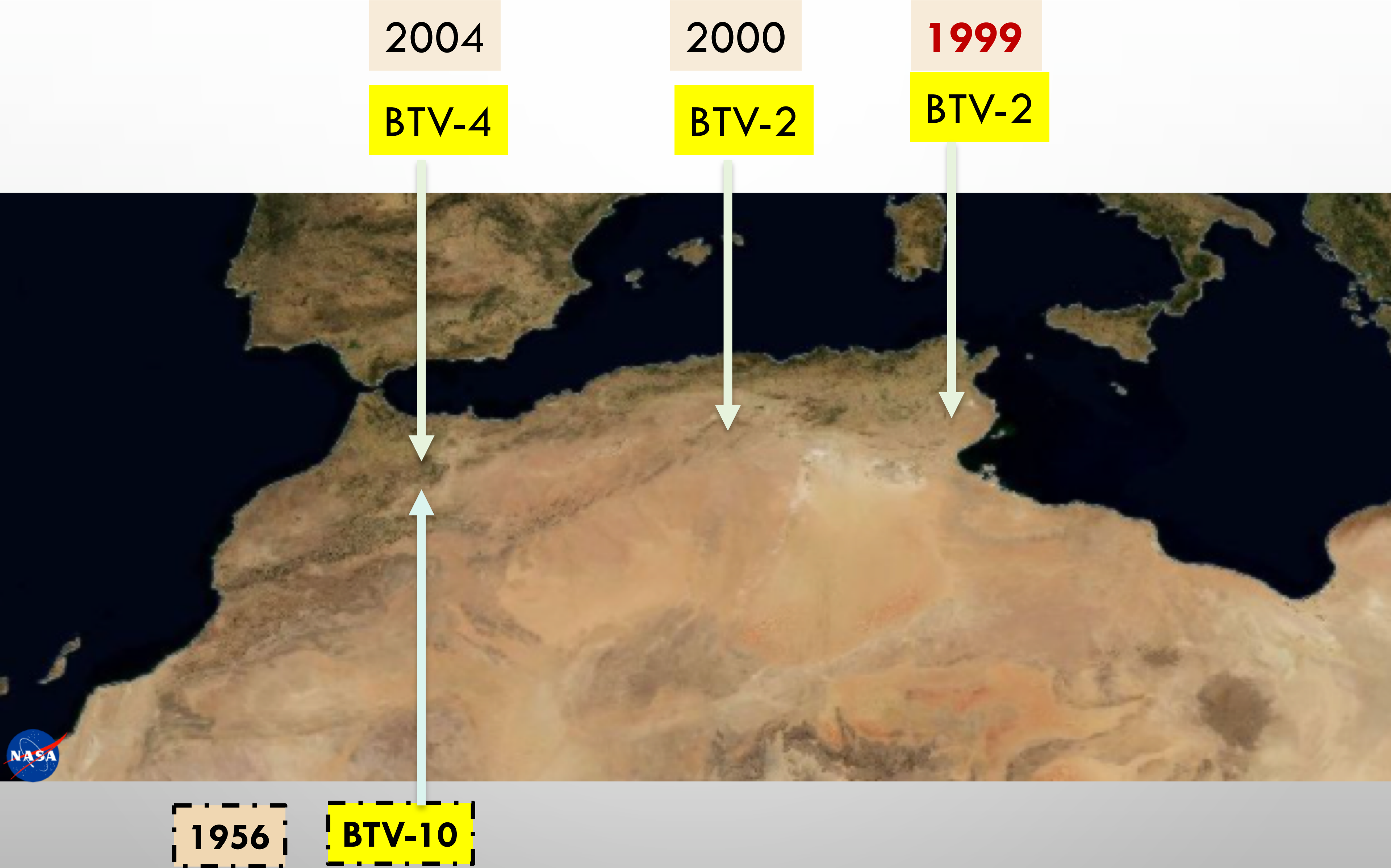
1999: Morbidity rate 8.35%
Mortality rate 5.5%,
Lethality rate 39%

2000: Endemic

2002: Limited number of cases

Species and age category	Total	Positivity(%) (Serology)
Bovines + Ovines	**2108**	**22,6% (476)**
Cows	**235**	**63,6% (148)**
Heifers	**175**	**40,6% (71)**
Ewes	**886**	**27,1% (240)**
Lambs	**812**	**2,1% (17)**

BTV incursions in North Africa



2004

BTV-4

2000

BTV-2

1999

BTV-2

1956

BTV-10

EHDV incursions in North Africa

2006: Morocco and Algeria Tunisia
2015: Tunisia

Genome segments 2, 3, 6, 7 and 10 of EHDV sequenced: EHDV serotype 6 (**EHDV-6**) present in Tunisia in 2006.


Photo: S. HAMMAMI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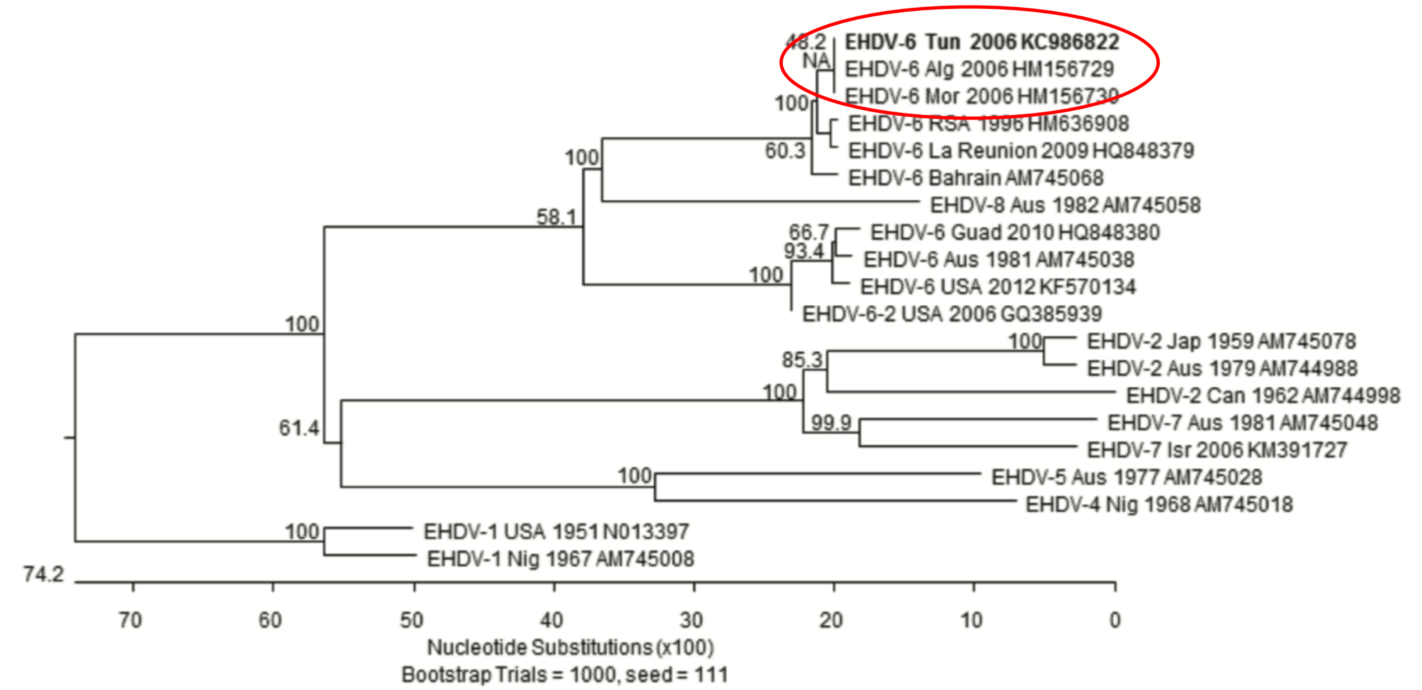
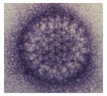


Segment 2 sequence analyses indicate that the EHDV-6 strain circulated in Tunisia in 2006 likely had the same origin as the EHDV-6 that circulated in Morocco and Algeria during 2006.

RECENT DEVELOPMENTS

Viruses



BTV sequencing and phylogenetic analyses (Seg-2)

All 24 known “typical” serotypes: 10 nucleotypes (A–J)

Serological cross-reactions observed between these serotypes

BTV-25 and BTV-27 cluster within nucleotype K, while BTV-26 belongs to nucleotype L

Phylogenetic tree of BTV genome segment 2.

(Maan et al., 2007; 2010, Schulz et al., 2016)