BELGIAN WILDLIFE DISEASE SOCIETY (BWDS)

federale overheidsdienst
VOLKSGEZONDHEID, VEILIGHEID VAN DE VOEDSELKETEN EN LEEFMILIEU

Université de Liège

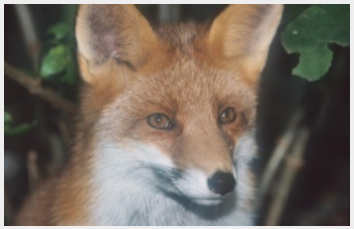
Wildtool

A flexible first-line tool for risk assessment with prioritization of wildlife-borne pathogens

WILDTOOL

Granted by the Belgian Federal Government :

WILDSURV project (RT 07/05) : 01.03.2008 - 01.03.2010



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- *IAS carry infectious agents (bacteria, viruses, parasites)*
- *Impact and transmission patterns change when host species becomes IAS*
- *DRA = necessary part of IAS risk assessment*

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RA + prioritize

(pathogenic)

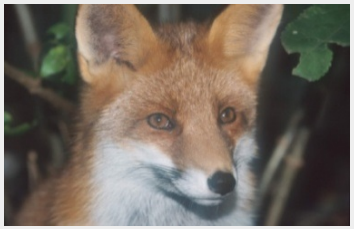
infectious agents

Harmonia

RA + prioritize

(invasive)

animal species



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Objectives

→ ***Flexible*** *(1)*, ***"First line"*** *(2) tool*
for DRA of wildlife-borne pathogens

(1) - different fields of interest (public health, livestock breeding, companion animal medicine, conservation, game management)

*→ different **target groups**: man, production animals, companion animals, game, threatened species*

*- applicable at **regional or national** levels (B)*

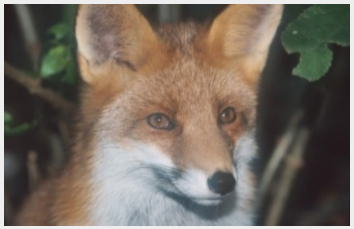
*- **scarcity of data***

*- **relative importance of criteria** for different users*

*- **regular updates** with most recent information*

*(2) - **broad scope** of pathogens : "horizon scanning"*

*- **identify pathogens** to be considered for in depth risk analysis*



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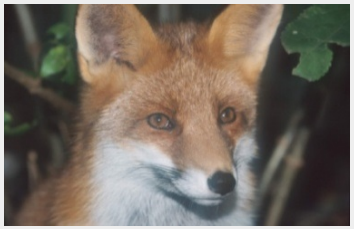
Methods / *Principles*

Risk analysis for import of diseases (international trade):

OIE: Terrestrial Animal Health Code :

- *Hazard identification*
- *Risk assessment*
  - ***Release assessment***
  - ***Exposure assessment***
  - ***Consequence assesment***
  - ***Risk estimation***



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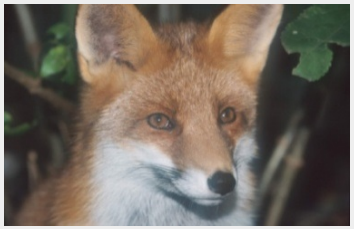
Methods / *Hazard identification*

- Basis : OIE list of notifiable wildlife diseases (version 2008)

- "pathogens" instead of "diseases" -

- Not restrictive: any other pathogen can be included IF information appears about a possible release or exposure in Belgium



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Methods / *Criteria*

-> Need for criteria (according to the elements of a standard OIE risk assessment) to compare pathogens

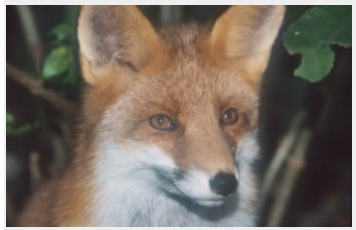
-> Preliminary literature search to identify the kind of information currently available for most pathogens

-> Criteria choice : main criteria + subcriteria

Methods / *Data Collection*

*- **Storage of literature data (expressed as scores)** in database according to six main criteria*

*- **Review** of pathogen-specific scores **by experts***






Elements of risk evaluation, main criteria and data sources

Corresponding part of risk evaluation :	**Main criteria** *(Data sources)*
Release assessment	**Host presence** *(1)*
Release assessment	**Vector presence** *(2)*
Release assessment	**Occurrence in wildlife** *(1), (3)*
Release + Exposure assessment	**Transmission** *(1) + (2)*
Exposure assessment	**Occurrence in targets** *(1) , (3)*
Consequence assessment	**Impact** *(1) + (2)*

(1) Literature

(2) Expert consultation

(3) National and international reports

Main criteria and kinds of scores

Main criteria	Scores	
Host presence	Y / N	Host presence subcriteria scores (numerical : 1-100)
Vector presence	Y / N	Vector presence subcriteria scores (numerical : 1-100)
Occurrence in wildlife	Y / N	Occurence in wildlife subcriteria scores (numerical : 1-100)
Transmission	Transmission subcriteria scores (H/M/L/NE)	
Occurrence in targets	Y / N	
Impact	Impact subcriteria scores (H/M/L/NE)	

Subcriteria

Impact						
Case fatality (man, production animals, companion animals)	NE	L	M	H		U
Morbidity (all target groups)	NE	L	M	H		U
Mortality (all target groups)	NE	L	M	H		U
Impact on life comfort (all target groups)	NE	L	M	H		U
Risk of population decrease (game, threatened spp., pest spp)	NE	L	M	H		U
Economic impact (all target groups)	NE	L	M	H		U
Notifiable disease (national, OIE)	N				Y	
Probability of eradication achievement (all target groups)		H	M	L	NE	U
Treatment possibilities (all target groups)		H	M	L	NE	U
Vaccination efficiency (all target groups)		H	M	L	NE	U
Risk concerning use as a weapon in bioterrorism	NE	L	M	H		U
Transmission characteristics						
Contagiousness and/or efficiency of transmission by vectors		L	M	H		U
Genetic stability		H	M	L		U
Importance of occupational / circumstantial exposure		H	M	L		U
Risk of introduction	NE	L	M	H	End	U
Probability of transmission from wildlife to “target group”		L	M	H		U
Transmission efficiency between different wildlife species	NE	L	M	H		U
Risk of secundary transmission (intra- or extra- target group)	NE	L	M	H		U
Transmission influenced by extrinsic factors (environment, anthropogenic)	NE	L	M	H		U
Resistance: in environment, to desinfectants		L	M	H		U
Numerical score	**1**	**2**	**3**	**4**	**5**	**1/2/3/4/5**

Subcriteria

Host presence	
Number of months present in "region" : 1-12	(1/12 to 12/12) x 100
Migrating : Y or N	100 or 1
% UTM squares occupied in "region" :	1 - 100
Fraction of total European population in "region"	n x 100 / total Europ. population
Increasing trend in "region" : Y or N	100 or 1
Vector presence (only if vector-borne pathogen)	
Vector presence in Belgium : Y or N	100 or 0
Vector present in "region" : Y or N	100 or 0
Occurrence in wildlife	
Number of European countries in which reported in wildlife	n x 100 / total Europ. countries
Number of neigbouring countries (incl. Belgium) in which reported in wildife	n x 100 / total neighb. countries
Most recent year of reporting in wildlife anywhere in Europe: subtract from current year: 0-1 / 2-5 / 6-10 / 11-20 / 20 -100 years ago	100 / 80 / 60 / 40 / 20
Most recent year of reporting in neighbouring countries (incl. Belgium) in wildlife: subtract from current year: 0-1 / 2-5 / 6-10 / 11-20 / 20-100 years ago	100 / 80 / 60 / 40 / 20

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Methods / *Choice of parameters:*

User chooses :

- *target group*

- *region*

- *weights for pathogen-specific subcriteria*
  → *relative importance of the subcriteria*
  → *differentiation between the scores*

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Methods / *Data processing :*

1.- algoritm (Y/N scores)

2.- translation of the qualitative scores (H/M/L/NE) to numerical values (for the "impact" and "transmission" subcriteria)

3.- multiplication of the numerical scores with the weights assigned to the subcriteria by the end user

4.- sum of the products = end-score per pathogen ("normalised": expressed as a % of the maximal possible score for that pathogen within the chosen target group)

5.- ranking of pathogens (highest score first)

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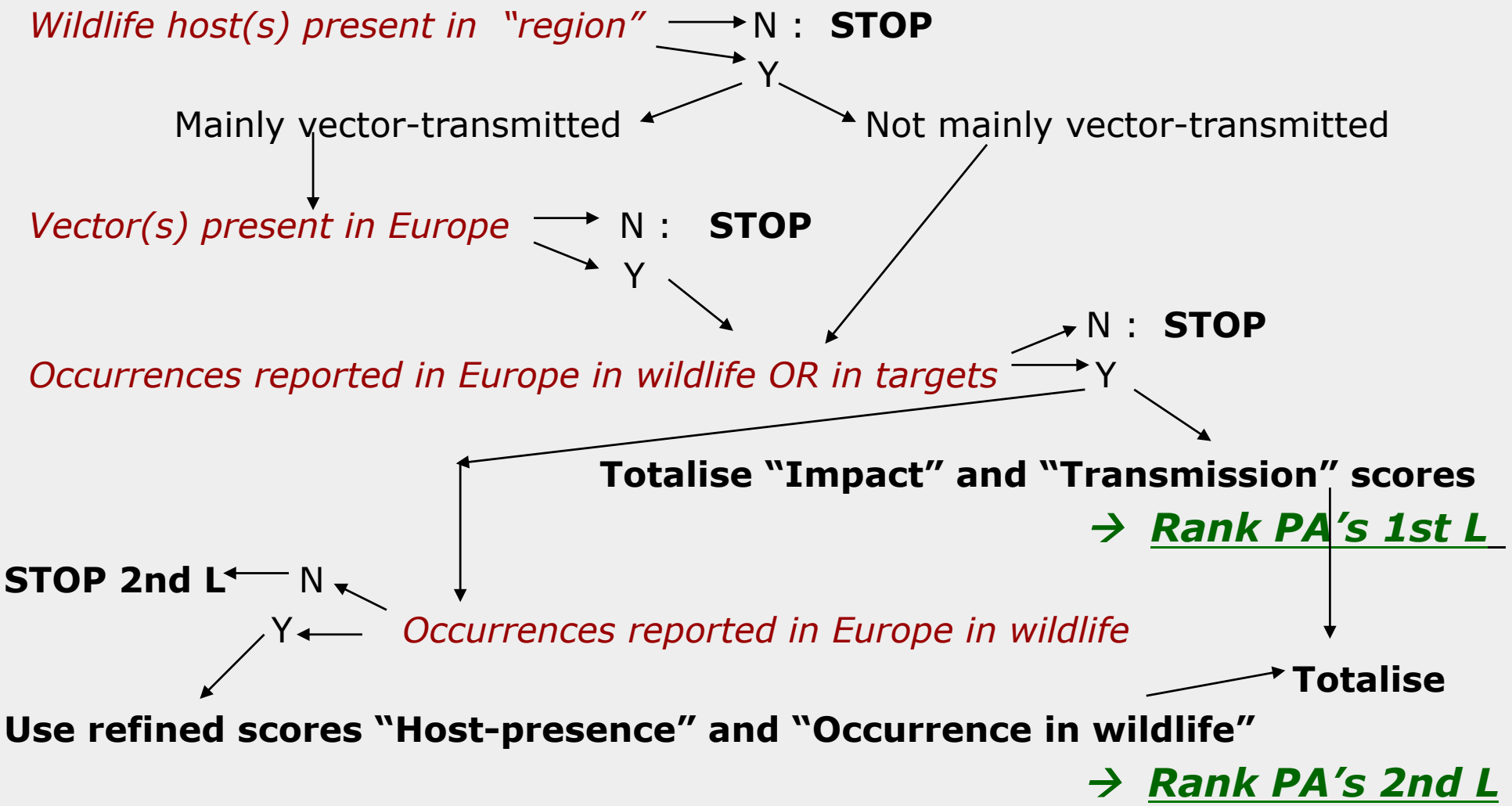
Methods / *Algoritm*

Per PA :



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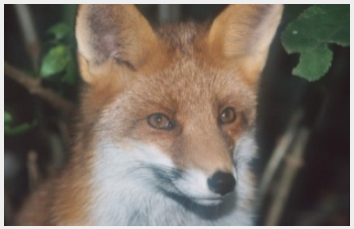
Methods / *Two level ranking*

Why is refinement of the "rough" 1st level Y/N scores necessary ?

- *if "host presence" is very limited / very important*
- *if "occurrence in wildlife" in Europe is very limited / very important*

→ Standard procedure = 1st level ranking ("comprehensiveness")

→ Refinement = 2nd level ranking (focus on release assessment)
←→ Scarcity of "Occurrence in wildlife" data for many pathogens !






Processing of the subcriteria scores : 1st and 2nd L (per PA)

Impact						
Case fatality (man, production animals, companion animals)	NE	L	M	H		U
Morbidity (all target groups)	NE	L	M	H		U
Mortality (all target groups)	NE	L	M	H		U
Impact on life comfort (all target groups)	NE	L	M	H		U
Risk of population decrease (game, threatened spp., pest spp)	NE	L	M	H		U
Economic impact (all target groups)	NE	L	M	H		U
Notifiable disease (national, OIE)	N				Y	
Probability of eradication achievement (all target groups)		H	M	L	NE	U
Treatment possibilities (all target groups)		H	M	L	NE	U
Vaccination efficiency (all target groups)		H	M	L	NE	U
Risk concerning use as a weapon in bioterrorism	NE	L	M	H		U
Transmission characteristics						
Contagiousness and/or efficiency of transmission by vectors		L	M	H		U
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Risk of secundary transmission (intra- or extra- target group)	NE	L	M	H		U
Transmission influenced by extrinsic factors (environment, anthropogenic)	NE	L	M	H		U
Resistance: in environment, to desinfectants		L	M	H		U
Numerical score	**1**	**2**	**3**	**4**	**5**	**1/2/3/4/5**

Processing of the subcriteria scores : 2nd L (per PA)

Host presence	
Number of months present in "region" : 1-12	(1/12 to 12/12) x 100
Migrating : Y or N	100 or 1
% UTM squares occupied in "region" :	1 - 100
Fraction of total European population in "region"	n x 100 / total Europ. population
Increasing trend in "region" : Y or N	100 or 1
Vector presence (only if vector-borne pathogen)	
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Methods / *Unknown scores*

"Unknown" subcriteria scores : - no information in the literature
- unknown by experts

An "unknown" score is given the median numerical value "3"

→ the subcriterion concerned + its weight are conserved (≠ 0)
=> consistent comparison between pathogens
→ no influence on scoring result

Methods / *Uncertainty estimation*

Uncertainty = % of "unknown" subcriteria
(2nd L : uncertainty % averaged with 1st L uncertainty %)

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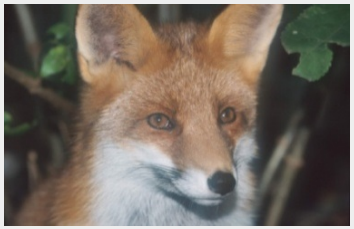
Interpretation

→ ***Check 2nd level ranking order for those pathogens ranking high in 1st level :***

- high rank conserved: important for surveillance !

- lower ranking order: release less important then for higher ranked pathogens

- absent in 2nd level = no refined data found






1st Level : Production animals / Flanders

1	Eastern equine encephalitis virus	44.43	19.05
2	West Nile virus	44.24	9.52
3	Chlamydophila psittaci	43.71	4.76
4	Bluetongue virus	43.29	14.29
5	Rinderpest morbillivirus	42.67	4.76
6	Avian paramyxovirus 1 (Newcastle disease)	42.43	9.52
7	Porcine circovirus	42.43	4.76
8	Cryptosporidium parvum	42.38	23.81
9	Salmonella enterica subsp. Enterica	42.38	14.29
10	Rabbit haemorrhagic disease virus	42.33	4.76
11	Myxomatosis virus	42.24	9.52
12	Avian influenza HP strains	42.05	0
13	African swine fever virus	41.81	14.29
14	Giardia duodenalis (G. intestinalis, G. lamblia)	41.67	19.05
15	Pasteurella multocida (Fowl cholera)	41.48	14.29

2nd Level : Production animals / Flanders

1	Chlamydophila psittaci	77.33	2.38
2	Pasteurella multocida (Fowl cholera)	74.26	7.14
3	Avian influenza LP strains	72.71	7.14
4	Duck virus hepatitis	71.9	16.67
5	Mycobacterium microti	70.45	19.05
6	Salmonella enterica subsp. Enterica	69.69	7.14
7	Sarcocystis spp. (others)	69.35	21.43
8	Leptospira	69.29	4.76
9	Erysipelothrix rhusiopathiae	68.54	15
10	Avian influenza HP strains	67.89	0
11	Mycobacterium avium subsp. Paratuberculosis	67.78	2.38
12	Anaplasma phagocytophilum	67.01	7.14
13	Pseudamphistomum truncatum	66.38	28.57
14	Coxiella burnetii	66.18	11.9
15	Echinococcosis (E.multilocularis and E.granulosus)	66.15	15

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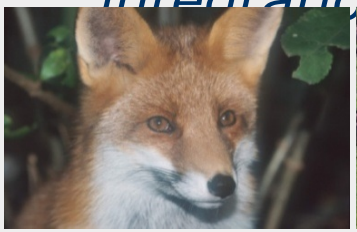
Current version = prototype

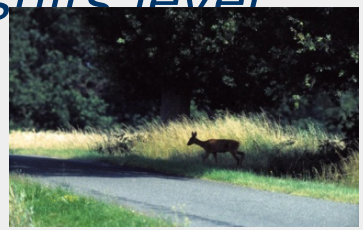
Future points of attention :

→ *Continued update literature data !*
= «Occurrences»
= «Host Presence»
→ *Refine processing*
→ *Operated by a team: improvements, data collection, queries*

Integration with Harmonia ?

YES , BUT : *different objectives / procedures :*
→ ***FIRST determine exactly the «common objective»:***
which kind of information do we want to obtain concretely ?
THEN work out practicalities
→ *DRA separately (cf conclusions workshop september):*
integration at the results level



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Publication :

Wildtool, a flexible first-line risk assesment system for wildlife-borne pathogens

Tavernier P., Dewulf J., Roelandt S., Roels S (2011)

European Journal of Wildlife Research 57(5), 1065-1075

Website :

http://wildtool.var.fgov.be

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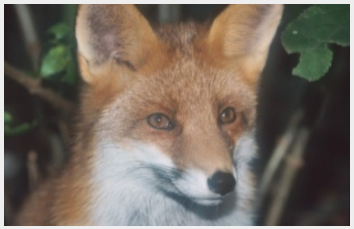




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