

G-RAID = Generic approaches for Risk Assessment of Infectious animal Disease introduction.

Background

- There is a continual threat of animal diseases entering the EU due to movement of animals, animal products and humans.
- Generic risk assessment (RA) tools have been independently developed to:
 - Assess /prioritise the risks from multiple animal diseases.
 - Provide results rapidly in response to emerging or re-emerging diseases.
- **Objective: To compare existing generic risk assessment tools with respect to their objectives, data and algorithms.**

Seven generic risk assessment tools

- Seven tools, developed by four organisations.
- Two quantitative, four semi-quantitative, one qualitative.
- All designed for rapid risk assessment.
- Objectives differ but all can be applied to multiple animal diseases (Table 1).
- All of the tools considered multiple risk pathways (Table 1). Most common:
 - Trade in live animals and products of animal origin.
 - Wild boar.

Table 1: Description of the risk assessment tools included in G-RAID, including summary of pathways.

Generic RA tool	Organisation	Objective	Prioritisation of:	Output	Number of original Case studies	Pathways included											
						Live animals	Products of animal origin	Germplasm	Vectors	Wildlife	Human travel	Transport	Feed and bedding	Laboratory material	Airborne spread		
SPARE	APHA (UK)	Early warning of disease introduction risks	Regions	Quantitative	3	X	X		X	X							
COMPARE	APHA (UK)	Identification of hotspots for risk-based surveillance	Regions, Pathways	Quantitative	3	X	X		X	X	X						
MINTRISK	WBVR (NL)	Comparison and prioritisation of vector borne diseases	Diseases, Regions	Semi-quantitative	7	X	X	X	X	X	X	X	X	X	X	X	X
RRAT	WBVR (NL)	Prioritisation of exotic livestock diseases to support decisions.	Diseases, Regions, Pathways	Semi-quantitative	10	X	X	X									
IDM	APHA (UK)	Incursion risk for high priority exotic notifiable diseases to support decisions	Diseases, Pathways	Semi-quantitative	34	X	X	X	X	X		X		X			
NORA	Ruokavirasto (FIN)	Rapid risk assessment to provide consistent results to support decisions	Regions, Pathways	Semi-quantitative	5	X	X	X	X	X	X	X	X				X
SVARRA	SVA (SE)	Systematic, structured and transparent rapid risk assessment.	Pathways	Qualitative	5	X	X	X	X	X	X	X	X				

Algorithms

- Despite all estimating the risk of exotic disease importation, the outputs of the tools varied (Figure 1).
- All of the tools used the basic principles of a Binomial model to estimate the probability of entry (N: number of pathway units; p: probability of infection).
- COMPARE, MINTRISK and IDM use R_0 to evaluate transmission of the disease once introduced. COMPARE and MINTRISK include it mathematically; IDM uses it to visualise potential impact of each disease.
- Economic and socio-ethical consequences are considered by MINTRISK and NORA.
- When developing a generic tool compromises are made relating to the complexity of the algorithms:
 - Exposure and consequence assessments aren't carried out at a high resolution.
 - None of the tools consider in great detail the dynamics of disease transmission.
 - Not designed to evaluate control strategies.
 - Inclusion of uncertainty/variability was not always embedded within the tool (only COMPARE, MINTRISK, SVARRA).

Data sources

- All tools needed large quantities of data and most often used the same data sources.
- Differences in the data input related to the complexity of the tool i.e. which pathways and how they were modelled.
- Data inputs were categorised into 4 types:
 - 1. Movement from one area to another:** All tools use global databases such as TRACES, Comext (Eurostat) and Comtrade (UN). National tools also used their national datasets.
 - 2. Prevalence in area of origin:** WAHIS (OIE) was the primary data source to all tools. Empres-i, ADNS, FAO, EC Reports and COM-mail are also used.
 - 3. Susceptible animals in the target region:** Level of complexity and therefore data requirements varied between tools. Sources of data included Eurostat, FAO and national farm registries.
 - 4. Disease-related parameters:** Traditional literature searches undertaken or expert opinion elicited.

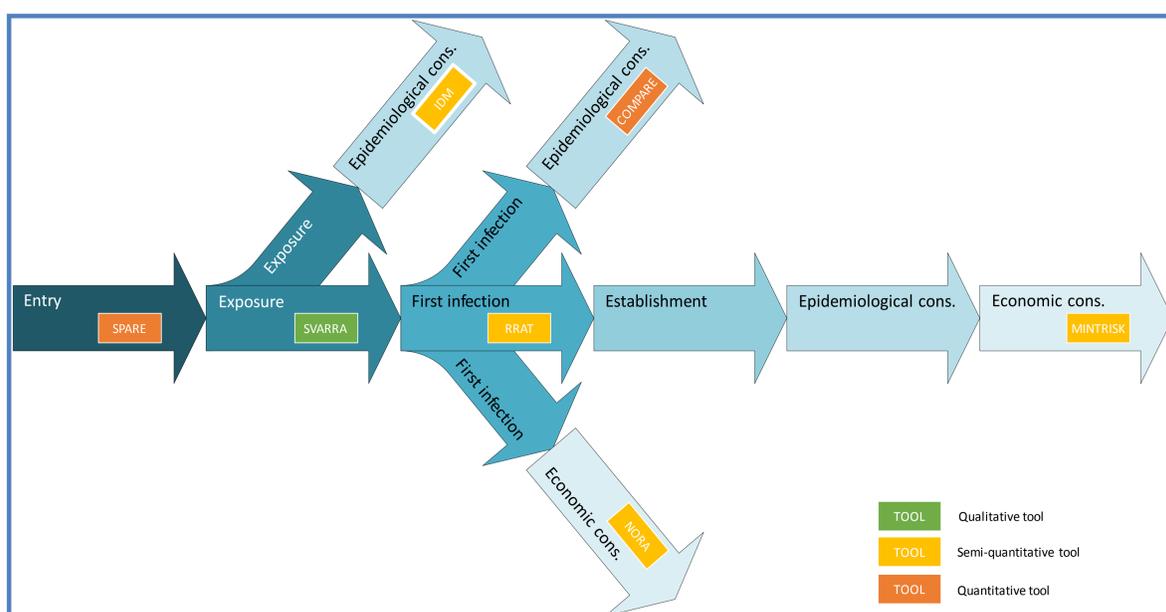


Figure 1. Outline of the steps involved in assessing disease incursion risks and the outputs of the G-RAID tools.

Key conclusions:

- **Similarities**
 - ✓ All of the tools can do rapid risk assessment.
 - ✓ All able to prioritise between disease, pathway and/or region.
 - ✓ All acknowledged the need for disease expertise in their development.
 - ✓ Same data sources to estimate movement from one area to another and prevalence in the area of origin.
 - ✓ Resolution limits the tools ability to evaluate intervention strategies (but not their primary aim).
- **Differences**
 - x Different outputs/end points.
 - x Level/type of expertise needed to use (computing, disease).
 - x Inclusion of uncertainty/variability not universal.

Overall conclusion: despite the different methods/objectives and independent development the tools have much in common.

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