Netherlands Food and Consumer
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*Ministry of Agriculture, Fisheries, Food
Security and Nature*

Evaluation of three assessments from the EFSA Panel on Plant Health quantifying the probability of introduction of a pest into the European Union

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Abstract

Following a request from the National Plant Protection Organization of the Netherlands, the Office for Risk assessment & Research (BuRO) evaluated quantitative assessments of the probability of introduction of three pests into the European Union (EU), *Thaumatotibia leucotreta*, *Citripestis sagittiferella* and *Elasmopalpus lignosellus,* from the Panel on Plant Health of the European Food Safety Authority. This request was put forward because of (i) discrepancies between the outcomes of the qPRAs of *T. leucotreta* and *C. sagittiferella* and lack of outbreaks of these pests which could be linked to the pathways assessed and (ii) because of differences in the methodology applied in the three qPRAs. The assessment of *T. leucotreta* estimates the number of adults that emerge every year from cut roses imported into the EU and the proportion of mated females among these adults. The structure of the model to calculate the number of emerging adults was considered accurate. However, the parameter estimate for the percentage of infested cut roses was considered too high resulting in an overestimation of the number of emerging adults. The estimated proportion of mated females was also considered too high, partly due to an inaccurate calculation method. The title of the risk assessment (Assessment of the probability of introduction of *Thaumatotibia leucotreta* into the European Union with import of cut roses) indicates that the probability of entry and establishment of *T. leucotreta* was assessed as ‘introduction’ includes both the entry and establishment of a pest. However, the model actually calculates the number of mated females in regions assessed suitable for establishment but not the number of founder (established) populations. The assessment of *C. sagittiferella* estimates the number of founder populations per year in the EU through the import of citrus fruit. The model used to estimate this number was not considered accurate and very likely considerably overestimated the true number of founder populations per year. The assessment of *E. lignosellus* estimates the number of founder populations per year in the EU through the import of asparagus spears. The structure of the model used for this estimation was considered accurate, but some of the parameter estimates were insufficiently substantiated and were considered either too high or too low. Based on the evaluation of the three quantitative pathway assessments, BuRO provides several suggestions to improve the assessment of the probability of introduction of pests in quantitative pest risk assessments.

Reading guide

This report contains the evaluation by the Office for Risk assessment & Research (BuRO) of assessments of the probability of introduction of three pests into the EU. These assessments were published by the Panel on Plant Health of the European Food Safety Authority (the Panel) in 2023 as part of the following qPRAs:

- Assessment of the probability of introduction of *Thaumatotibia leucotreta* into the European Union with import of cut roses,
- Pest risk assessment of *Citripestis sagittiferella* for the EU, and
- Pest risk assessment *of Elasmopalpus lignosellus* for the European Union.

Recommendations and main conclusions of the evaluation are found in the following sections of the report:

- Section 6.4: **recommendations** to improve the assessment of the probability of introduction of pests in quantitative pest risk assessments (qPRAs).
- Sections 6.1 and 6.2: discussion of the **main conclusions across all three assessments**.
- Section 3.5, 4.5 and 5.5: the **main conclusions per assessment** (*T. leucotetra, C. sagittiferella* and *E. lignosellus*, respectively).

In more detail, Chapter 1 of the report provides the background information and introduces the specific questions to be answered in the evaluation. Chapter 2 presents the methodology, including a list of definitions. Chapters 3 to 5 present the results of the evaluation of the assessments of the probability of introduction of *T. leucotreta* through the import of cut roses, of *C. sagittiferella* through the import of citrus fruit and of *E. lignosellus* through the import of asparagus spears. The main conclusions are summarised in sections 3.5, 4.5 and 5.5, respectively. In Chapter 6, the following aspects are discussed: estimation of the number of infested units on arrival in the EU and the probability of transfer and establishment (section 6.1) comparison of model outputs with the actual number of recorded outbreaks (section 6.2), other statistical considerations relating to the methods used by the Panel (section 6.3), and recommendations to improve the assessment of the probability of introduction of pests in qPRAs (section 6.4).

Contents

1 Introduction

The National Plant Protection Organization of the Netherlands (NPPO-NL) requested the Office for Risk assessment & Research (BuRO) to evaluate the assessments of the probability of introduction (pathway assessments) in quantitative Pest Risk Assessments (qPRAs) prepared by the Panel on Plant Health of the European Food Safety Authority (the Panel). This request was put forward because of (i) discrepancies between the outcomes of some qPRAs and the lack of outbreaks in the European Union (EU) of the pests concerned and (ii) because of differences in the methodology applied in these qPRAs. In particular, the 'Assessment of the probability of introduction of *Thaumatotibia leucotreta* into the European Union with import of cut roses' and the 'Pest risk assessment of *Citripestis sagittiferella* for the EU' raised questions (EFSA Panel on Plant Health et al., 2023c; EFSA Panel on Plant Health et al., 2023d). Specifically, these questions focused on:

- the infestation rate of cut flowers (the proportion of infested cut roses) estimated in the qPRA of *T. leucotreta*;
- the number of mated females estimated in the qPRA of *T. leucotreta* as compared to the number of outbreaks detected in the EU;
- the model used to estimate the number of established populations in the qPRA of *C. sagittiferella*;
- the evidence provided for the likelihood of establishment of *C. sagittiferella*;
- the number of founder populations estimated in the qPRA of *C. sagittiferella* as compared to the number of outbreaks detected in the EU.

To address these questions from the NPPO, BuRO evaluated the assessments of the probability of introduction in the following documents published by the Panel:

- Assessment of the probability of introduction of *Thaumatotibia leucotreta* into the European Union with import of cut roses (EFSA Panel on Plant Health et al., 2023a), and
- Pest risk assessment of *Citripestis sagittiferella* for the EU (EFSA Panel on Plant Health et al., 2023c).

In addition, BuRO also evaluated a third qPRA published by the Panel:

- Pest risk assessment of *Elasmopalpus lignosellus* for the European Union (EFSA Panel on Plant Health et al., 2023d).

This qPRA was evaluated because it had been published in the same year (2023) as the qPRAs of *T. leucotreta* and *C. sagittiferella*, while a different pathway model had been used to assess the probability of introduction. In total, the Panel completed four qPRAs in 2023. The fourth qPRA, 'Risk assessment of *Resseliella citrifrugis* for the EU' (EFSA Panel on Plant Health et al., 2023b), was not evaluated because the Panel used the same pathway model in that qPRA as in the qPRA of *C. sagittiferella* (i.e. this assessment did not add another methodology).

2 Methodology

BuRO took the following steps for each qPRA when performing the evaluation:

- a brief description of the biology of the pest (references are provided for more detailed information),
- a description of the model as presented in the qPRA including a description of the pathway unit and transfer unit (for definitions see section 2.1),
- an evaluation of the model through the following criteria:
  - the model:
    - does it assess the number of founder populations as defined in the European Food Safety Authority's (EFSA) guidance on quantitative pest risk assessment (EFSA Panel on Plant Health et al., 2018)?
    - is the (sub)model accurate:
      - does it include all steps needed to estimate the number of founder populations?
      - are the parameters combined in a logical way?
      - are the parameters in the model independent?
  - parameter estimates and the final output:
    - do the applied (statistical) techniques sufficiently capture the uncertainty of the parameter values used in the calculations (and hence in the outcome of the calculations itself)?

  - are parameter estimates sufficiently substantiated by data, scenarios and/or arguments.
  - does the final output appear realistic taking into account the number of units that had already been imported and the number of known outbreaks of the pest in the EU at the time when the qPRA was adopted.

Finally, the models in the three qPRAs were compared and recommendations were made to improve assessments of the probability of introduction in qPRAs.

The goal of the evaluation was not to carry out new qPRAs but in some cases alternative calculations were made to demonstrate the effect of certain choices made in the qPRAs by the Panel. The evaluation was limited to the models used to assess the probability of introduction and their parameter estimates (i.e. the evaluation did not include an evaluation of the assessments of spread and impact nor of the methodology used to assess the potential area of establishment of the pests in the EU).

2.1 Definitions

Definitions were taken from EFSA's guidance on quantitative pest risk assessment (EFSA Panel on Plant Health et al., 2018) unless stated otherwise.

EFSA's guidance	EFSA's guidance on quantitative pest risk assessment (EFSA Panel on Plant Health et al., 2018)
EKE	Expert Knowledge Elicitation is a systematic, documented and reviewable process to retrieve expert judgements from a group of experts in the form of a probability distribution (EFSA, 2014)
Entry (of a pest)	Movement of a pest into an area where it is not yet present, or present but not widely distributed and being officially controlled (FAO, 2024)
Establishment (of a pest)	Perpetuation, for the foreseeable future, of a pest within an area after entry (FAO, 2024)
Founder population	A viable population of a species which is able to successfully colonize and to establish in a new area
Incursion	An isolated population of a pest recently detected in an area, not known to be established, but expected to survive for the immediate future (FAO, 2024)
Interception	The detection of a pest during inspection or testing of an imported consignment (FAO, 2024)
Introduction (of a pest)	The entry of a pest resulting in its establishment (FAO, 2024)
Outbreak	A recently detected pest population, including an incursion, or a sudden significant increase of an established pest population in an area (FAO, 2024)
Pathway subunit	A pathway subunit is an element within a pathway unit, for which the abundance of a pest can be measured. For example, one rose in a box of roses, one tuber in a ton of seed potatoes. A pathway subunit may or may not be affected
Pathway unit	A unit of material or other means potentially affected by the pest that can be used to measure the flux along the pathway (number of pathway units per time unit). Examples are: a specific/certain number of crates of nectarines, metric ton of seed potatoes, cubic meter for wood/timber. The flux can be expressed in terms of a certain number of pathway units, e.g. per year. A pathway unit may or may not be affected
Transfer	Movement of a pest from an imported commodity to a place where the pest can establish (EFSA Panel on Plant Health et al., 2018). In case of arthropod pests (excluding viviparous species) it includes (mating and) first egg laying (Van der Gaag et al., 2019)
Transfer unit	A unit composed by one or more pathway units or subunits, which moves as a cluster within the risk assessment area and carries a pest population that goes to the final destination where establishment occurs (e.g. a

field) and which can come into contact with the host and potentially be a founder population. Example: 100 tubers of seed potatoes to be planted in the same field.

3 *Thaumatotibia leucotreta*

3.1 Biology

Thaumatotibia leucotreta (Lepidoptera: Tortricidae, EPPO code: ARGPLE), commonly known as the false codling moth (FCM), is a pest that feeds on many different plant species including *Rosa* spp. After mating, adult females lay their eggs mostly singly on fruit or on flower buds of host plants. Larvae develop inside the fruit or flower bud. Mature larvae (fifth instar larvae) leave the fruits or flower buds and pupate in a sheltered place (European Food Safety Authority et al., 2020).

3.2 Description of the model

3.2.1 Introduction

The qPRA estimates ”*the number of T. leucotreta adults escaping from the cut roses imported from African countries into the NUTS 2*[1] *regions identified as suitable for establishment*” (p. 12)[2]. It also estimates the proportion of mated females for every emerging adult.

The pathway unit is a single cut rose and as assumed in the qPRA an infested cut rose carries no more than one *T. leucotreta* specimen, i.e. one egg or larva. The transfer unit is a bunch of 10 cut roses (not explicitly defined in the qPRA).

The model to estimate the number of adults that emerge in regions suitable for establishment includes three submodels:

- **a cut rose distribution model** that calculates the number of infested cut roses that enter NUTS 2 regions in the EU that have suitable conditions for establishment (also referred to as ‘suitable NUTS 2 regions’ or ‘suitable regions’ in the present evaluation);
- **a developmental model** that calculates the proportion of specimens that emerge as adults from cut roses in the importing country during storage and transport, during the vase life of the cut roses and after waste disposal of the cut roses by the consumer before the waste is treated (all cut roses will finally end in commercial or household waste);
- **a waste model** that calculates the proportion of specimens that survive and escape different waste treatments.

In sections 3.2.2–3.2.5, the three submodels and the overall model are briefly described. Section 3.2.6 describes the method used by the Panel to calculate the proportion of mated females for every emerging adult.

3.2.2 Cut rose distribution model

The cut rose distribution model calculates the number of infested cut roses that ends up in commercial waste and the number of infested cut roses that ends up in household waste in a suitable NUTS 2 region in a specific season. The model to calculate the number of cut roses ending in household waste comprises two main pathways: direct import from African countries and Israel and indirect import through other EU Member States. The latter one is divided into two main clusters: ‘The Netherlands/Belgium’ and ‘Germany/Luxembourg’. These are the EU Member States that import cut roses from Africa and trade (re-export) them to EU Member States with suitable NUTS 2 regions. Other EU Member States were not considered because of minor import volumes (p. 17).

The number of infested cut roses ending in commercial waste (waste from auctions and importers) in a suitable NUTS 2 region in a specific season ($FCM_{commercial,NUTS2,Season}$) was calculated as (p. 17):

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[1] NUTS: Nomenclature of territorial units for statistics; classification system used by the EU to divide EU countries into different regions. NUTS 1 are major socio-economic regions, NUTS 2 basic regions and NUTS 3 small regions (https://ec.europa.eu/eurostat/web/nuts)

[2] Page numbers refer to the page in the original qPRA where the information is provided.

$$FCM_{commercial,NUTS2\ Season} = Infestation_{AF} \times Trade_{AF-EURA,Season} \times Population_{NUTS2/EURA} \times Grading.$$

The number of *T. leucotreta* specimens (FCM) ending in household waste in a suitable NUTS 2 region in a specific season ($FCM_{household,NUTS2,Season}$) was calculated as (p. 17):

$$\begin{aligned}
&FCM_{household,NUTS2,Season} \\
&\qquad = Infestation_{AF} \times (Trade_{AF-EURA,Season} \times Population_{NUTS2/EURA} \times (1 - Grading) \\
&\qquad + Trade_{AF \rightarrow NLBE,Season} \times Dilution_{NLBE,Season} \times Population_{NUTS2/EURA} \\
&\qquad + Trade_{AF \rightarrow DELU,Season} \times Dilution_{DELU,Season} \times Population_{NUTS2/EURA}).
\end{aligned}$$

Parameters are described in Table 1. The dilution factors ($Dilution_{NLBE,Season}$ and $Dilution_{DELU,Season}$) were calculated as the proportion of cut roses imported from countries where *T. leucotreta* is present in relation to the total number of cut roses imported and produced by the re-exporting EU clusters of Member States (NLBE: the Netherlands & Belgium, DELU: Germany & Luxembourg, see p. 17 in the qPRA for details and the formula used).

Table 1. Description of the parameters used in the cut rose distribution model which is part of the pathway model '*Thaumatotibia leucotreta* – cut roses' (amended from Table 6 on p. 18 in EFSA Panel on Plant Health et al. (2023a))

Parameter	**Description**
$FCM_{commercial,NUTS2,Season}$ $FCM_{household,NUTS2,Season}$	Number of *T. leucotreta* individuals ending in commercial or household waste in a suitable NUTS 2 region during a specific season
AF	African countries and Israel with reported occurrence of *T. leucotreta*
EURA	European countries/clusters with suitable NUTS 2 regions
NUTS2	NUTS 2 region climatically suitable for establishment
NLBE	Cluster of re-exporting countries: the Netherlands/Belgium
DELU	Cluster of re-exporting countries: Germany/Luxembourg
Season	Stratification by season: winter, spring, summer, autumn
$Infestation_{AF}$	Average infestation rate of cut roses from AF
$Trade_{AF-EURA,\ Season}$	Direct trade of cut roses from AF to European climatically suitable countries/clusters
$Population_{NUTS2/EURA}$	Proportion of the human population in the NUTS 2 region climatically suitable in relation to the whole country or cluster
Grading	Proportion of direct imported cut roses, which on average is discarded due to quality issues
$Trade_{AF\ NLBE,\ Season}$ $Trade_{AF\ DELU,\ Season}$	Trade of cut roses from AF to the European re-exporting clusters[1] in a specific season
$Dilution_{NLBE,Season}$ $Dilution_{NLBE,Season}$	Dilution of *T. leucotreta*-infested cut roses, imported from Africa and Israel, by other imports and own production in a specific re-exporting cluster and season

[1] Two clusters are being distinguished: NLBE: the Netherlands & Belgium and DELU: Germany & Luxembourg.

3.2.3 Developmental model

The developmental model calculates the proportion of *T. leucotreta* adults that emerges from the cut roses before waste treatment through simulation but no equation is provided in the qPRA (p. 20). The model takes into account the life stages of *T. leucotreta* arriving at the border, the level of maturity within a specific life stage, the development rate of the life stages and the temperature during the stay in a 'compartment'. The compartments are: transport & storage, retail & private home and the period between waste disposal and waste treatment) (p. 19-21). The probability that an adult emerges before waste treatment was estimated for (Table A.86, p. 148):

- four groups of NUTS 2 regions with different climatic suitability (ranging from low to high suitability),
- for different seasons (winter, spring, summer and autumn), and
- for different times between initial disposal of the cut roses and waste treatment (3, 7, 14 and 28 days).

3.2.4 Waste model

The waste model estimates the proportion of *T. leucotreta* specimens that escape as adults from different waste treatments (private compost and the communal treatments landfill, composting an incineration). The proportion of each treatment is estimated for household and commercial waste (p. 21).

No data were available for the time between initial disposal of waste and waste treatments for household waste. Therefore, calculations were made for 3, 7, 14 and 28 days between waste disposal and waste treatment (p. 21-24).

The final result of the waste model also includes the proportion of specimens that escapes before the cut roses are treated by different forms of waste treatment as calculated in the developmental model (Table 8 on p. 23, Appendix 8.2 on p. 148).

The formula to calculate the proportion of adults escaping the cut roses from consumer's places or from household waste was as follows (p. 22):

$$\begin{aligned} &ESC_{Household,NUTS2,Season} \\ &\quad = P_{pivate} \times ESC_{private} + (1 - P_{pivate}) \times ESC_{time,xd,CSClàss,Sesaon} + (1 - P_{private} \times (1 \\ &\quad - ESC_{time,xd,CSClass,Season}) \times P_{HH,Landfill,country} \times ESC_{Landfill} + (1 - P_{prvate}) \times (1 \\ &\quad - ESC_{time,xd,CSClass,Season}) \times P_{HH,Compostl,country} \times ESC_{Compost} + (1 - P_{private}) \times (1 \\ &\quad - ESC_{time,xd,CSClass,Season}) \times P_{HH,Incineration,country} \times ESC_{incineration}. \end{aligned}$$

The formula to calculate the proportion of adults escaping from commercial waste which may happen before the treatment within 3 days after wasting or during the waste treatment (landfill, composting or incineration) was as follows (p. 22):

$$\begin{aligned} &ESC_{Commercial,NUTS2,Season} \\ &\quad = ESC_{time,3d,CSClass,Season} + \left(1 - ESC_{time,3d,CSClass,Season}\right) \times P_{C,Landfill,country} \times ESC_{Landfill} \\ &\quad + \left(1 - ESC_{time,3d,CSClass,Season}\right) \times P_{C,Compostl,country} \times ESC_{Compost} \\ &\quad + \left(1 - ESC_{time,3d,CSClass,Season}\right) \times P_{c,Incineration,country} \times ESC_{Incineration}. \end{aligned}$$

Parameters are described in Table 2.

Table 2. Description of the parameters used in the waste model which is part of the pathway model '*Thaumatotibia leucotreta* – cut rose' (amended from Table 8 on p. 23 in EFSA Panel on Plant Health et al. (2023a))

Parameter	**Description**
$ESC_{\text{Household, NUTS2, Season}}$	Proportion of *T. leucotreta*, which will escape the cut roses used at consumer level or household waste
$ESC_{\text{Commercial, NUTS2, Season}}$	Proportion of *T. leucotreta*, which will escape the commercial waste of cut roses
P_{private}	Proportion of household waste, which goes to private composting (not subjected to regional waste treatment)
$ESC_{\text{time, xd, CSClass, Season}}$	Proportion of *T. leucotreta*, which will escape the cut roses until x days after initial disposal in a region of a specific climate suitability class (CSClass) and season[1]
$P_{\text{HH,Landfill,country}}$ $P_{\text{C,Landfill,country}}$	Proportion of household (HH) or commercial (C) waste treated by 'landfill'
$P_{\text{HH,Compostl,country}}$ $P_{\text{C,Compostl,country}}$	Proportion of household (HH) or commercial (C) waste treated by 'composting'
$P_{\text{HH,Incineration,country}}$ $P_{\text{C,Incineration,country}}$	Proportion of household (HH) or commercial (C) waste treated by 'incineration or anaerobic digestion'
ESC_{private}	Proportion of *T. leucotreta*, which will escape private compost
ESC_{Landfill}	Proportion of *T. leucotreta*, which will escape waste treated by 'landfill'
ESC_{Compost}	Proportion of *T. leucotreta*, which will escape waste treated by 'composting'
$ESC_{\text{Incineration}}$	Proportion of *T. leucotreta*, which will escape waste treated by 'incineration or anaerobic digestion'

[1] Calculated by the developmental model (see section 3.2.4)

3.2.5 Overall model

The overall model calculates the total number of adults that emerge per suitable NUTS 2 region as the sum of the number of adults that emerges from cut roses used at consumer level or household waste and those emerging from commercial waste in that region corrected for natural developmental mortality (p. 25):

$$
\begin{aligned}
FCM_{Escape,NUTS2} = {} & (1 - Mort_{natural}) \\
& \times \Sigma_{season} \big(FCM_{household,NUTS2,Season} \times ESC_{Household,NUTS2,Season} \\
& + FCM_{commercial,NUTS2,Season} \times ESC_{commercial,NUTS2,Season}\big).
\end{aligned}
$$

Parameters used in the overall model are described in Table 3.

Table 3. Description of the parameters used in the overall pathway model '*Thaumatotibia leucotreta* – cut roses' (amended from Table 9 on p. 25 in EFSA Panel on Plant Health et al. (2023a))

Parameter	**Description**	**Units**
$FCM_{\text{Escape, NUTS2}}$	Annual average number of *T. leucotreta* adults escaping from cut roses imported from AF (African countries with FCM occurrence and Israel) in a specific NUTS 2 region [climatically suitable for establishment of *T. leucotreta*]	Number of adults per year
$Mort_{\text{natural}}$	Natural developmental mortality	Proportion
$FCM_{\text{Commercial,NUTS2, Season}}$ $FCM_{\text{Household,NUTS2, Season}}$	Number of FCM *T. leucotreta* specimens ending in commercial or household waste in a NUTS 2 region climatically suitable in a specific season	Number of specimens per year
$ESC_{\text{Household,NUTS2, Season}}$	Proportion of *T. leucotreta* which will escape the cut roses used at consumer level or household waste [in a specific season]	Proportion
$ESC_{\text{Commercial,NUTS2, Season}}$	Proportion of *T. leucotreta* which will escape the commercial waste of cut roses [in a specific season]	Proportion

3.2.6 Calculation of the number of mated females

The number of mated females per year in a suitable NUTS 2 region was calculated by (cluster scenario 2 on p. 25):

$$Number\ of\ mated\ females\ _{NUTS2}/year\ =\ FCM_{Escape,NUTS2}/435.$$

The proportion of mated females for every emerging (escaping) adult (1/435) was estimated based on the assumption that mating will take place when at least one female and one male adult emerge from a bunch of 10 cut roses (see 3.3.6 for details).

3.3 Evaluation of the model

3.3.1 Founder populations

The model estimates the number of mated females but not the number of founder populations although the title of the qPRA '*Assessment of the probability of introduction of Thaumatotibia leucotreta into the European Union with import of cut rose*' suggests otherwise. Introduction includes entry and establishment (FAO, 2017), which is also mentioned in the qPRA (p. 6, 39). Thus, the model is missing a parameter to estimate the number of founder populations, i.e. it is missing a parameter for the probability that a mated female will oviposit leading to a founder population (or two parameters, one for the probability of oviposition and another one for the probability of establishment after oviposition). Therefore, the title of the qPRA is not fully consistent with its contents.

3.3.2 Cut rose distribution model

The structure of the cut rose distribution model was considered accurate.

3.3.3 Developmental model

The structure of the developmental model was considered accurate.

3.3.4 Waste model

The structure of the waste model was considered accurate.

3.3.5 Overall model

The structure of the overall model that calculates the total number of adults that emerge was considered accurate.

3.3.6 Likelihood of finding a mating partner

3.3.6.1 Natural mortality

The formula used in the qPRA to calculate the proportion of mated females does not take into account that the density of specimens (i.e. the proportion of infested cut roses) decreases due to natural mortality after arrival in the EU. Therefore, the formula overestimates the proportion of mated females which is discussed in detail below.

In the qPRA, the following information was used to estimate the proportion of mated females for every emerging (escaping) adult:

- in samples of 400 cut roses taken at import 41% of the specimens intercepted were present with at least one other specimen (based on Dutch interception data, Table 5 on p. 10),
- a sex ratio of 2:1 (two females per one male) based on literature (p. 11).

In addition, the following assumptions were made (p. 11):

- no more than one *T. leucotreta* specimen is present per cut rose,
- cut roses are distributed in bunches of 10 cut roses,
- specimens are uniformly distributed among the bunches, and
- if a male and female are present in a bunch mating will take place.

The Panel calculated the minimum percentage of mated females as:

$$0.41 \times 0.025 \times 2/3 \times 1/3 \times 100 = 0.23\% \text{ (p. 11)},$$

which means one mated female for every 435 emerging adults of *T. leucotreta*. However, it was also estimated that on average 48% of the larvae and pupae survived (p. 161). Thus, the likelihood that at least one adult female and one adult male are present in a bunch of 10 cut roses should instead be:

$$0.41 \times 0.025 \times 0.48 \times 2/3 \text{ x } 1/3 \times 100 \approx 0.11\%.$$

In addition, assuming 2 specimens per 400 cut roses (as in the model on p. 11), the likelihood that 2 specimens are present in a bunch of 10 cut roses would be $1 \times 9/399 \approx 0.0226$ instead of 0.025. Thus, the likelihood that at least one female and male are present in a bunch of 10 cut roses would be:

$$0.41 \times 0.0226 \times 0.48 \times 2/3 \times 1/3 \times 100 \approx 0.10\%,$$

which means one mated female for every 1,004 escaping adults of *T. leucotreta*. However, this calculation – like the one in the qPRA – does not take into account that three specimens can be present in a sample of 400 cut roses (at import), rather than just two. The presence of more than two specimens increases the probability of mating. Therefore, BuRO carried out the following simulation process using R (see Appendix A for details):

1. Ten million samples with 400 cut roses each were randomly generated with 1, 2 or 3 specimens per sample using a probability of 167/217, 32/217 and 18/217 for having 1, 2 or 3 specimens, respectively (these probabilities were based on interception data that are presented in Table 5 on p. 10 in the qPRA: 1, 2 and 3 specimens (never more than 3) had been detected in 167, 32 and 18 samples, respectively, out of 217 samples found infested. The same data were used by the Panel to calculate the proportion of mated females).
2. Each specimen is randomly assigned a female ($p = 2/3$) or male ($p = 1/3$) status.
3. Random survival of each specimen ($p = 0.48$) and selection of those samples in which both a female and male survive (at least one female and one male should be present for mating to occur).
4. Random distribution of 400 cut roses in 40 bunches of 10 cut roses each (which means a maximum of 1 bunch with 2 or more specimens).
5. Checking for at least one female and at least one male in a bunch of 10 cut roses.
6. Counting all females in bunches that fulfil condition 5.

This simulation resulted in one mated female for every 690 escaping adults which is still lower (approximately 1.6 times) than the rate of one per 435 adults estimated in the qPRA.

3.3.6.2 Difference in the use of interception data

For the calculation of the proportion of mated females for every emerging adult, the Panel used different data or estimates for the infestation rate of cut roses than for the calculation of the number of emerging adults. To calculate the proportion of mated females for the period 2022 – 2026 (the period covered by the qPRA, p. 7), the Panel assumed that the probability that an infested sample of 400 cut roses carries two or more specimens is the same as for the period January 2019 – September 2022. Interception data with numbers of specimens per sample of 400 cut roses were used from that period. However, to calculate the number of emerging adults per year, the Panel estimated the infestation rate of the cut roses by EKE. Interception data were only used to inform the EKE (these interception data were from a period that largely overlaps with the one used to calculate the likelihood of finding a mating partner (January 2018- December 2021 versus January 2019-September 2022) and one may expect similar infestation rates and level of clustering for the two periods). The Panel finally obtained the infestation rate to calculate the number of emerging adults by fitting a curve through the elicited values. This infestation rate was lower (median value 0.0021) than the infestation rate calculated from the interception data (0.00319). The Panel does not give an explanation, why the infestation rate to calculate the number of emerging adults was estimated by EKE (resulting in a lower infestation rate than the Panel had calculated from the interception data) while the number of specimens in an infested sample of 400 cut roses was directly derived from interception data. A lower infestation rate would logically result in a lower number of specimens per sample of 400 cut roses which would result in a lower proportion of mated females.

3.3.6.3 Scenarios

BuRO argues that the proportion of mated females may also be overestimated by the assumption in the qPRA that mating will always take place when at least one female and one male are present in a bunch of ten cut roses. The qPRA describes two scenarios for the clustering of specimens in a bunch of ten cut roses: a scenario in which an infested cut rose harbours at least two specimens (called 'worst case') and a second scenario in which no more than one specimen is present on a cut rose (called 'realistic case') (pp. 10-11). The Panel considered the first scenario unrealistic because of the lack of reports from border inspections of more than one specimen per cut rose and used the 'realistic case' for the calculations (p. 11). BuRO agrees that the first scenario is unrealistic but considers the 'realistic case' still a 'worst case' because it assumes that specimens "*develop in parallel and escape at similar time in the same location from the bunch*" and mating will always happen when a female and a male are present in the same bunch of cut roses. Specimens may, however, be of different age and one specimen may be able to escape as an adult while other ones will go to a waste treatment before they can escape. In addition, the developmental model calculates that some specimens will pupate while cut roses are still in a 'climatized environment' as illustrated by Figures A.11 – A.14 on p. 144-147 in the qPRA. Thus, some adults will be formed indoors. Adults (the moths) are active at night and when windows are closed or insect screens are used during the night, moths may not be able to escape which may also decrease the probability of mating.

3.4 Uncertainty, estimation of parameter values and final output

3.4.1 <u>Uncertainty</u>

The Panel estimated uncertainty distributions by EKE for most parameter values used to estimate the number of emerging adults of *T. leucotreta*. Only for the natural developmental mortality minimum and maximum values were calculated using data from literature. The Panel used Monte Carlo simulations to assess the number of adults that emerge from roses (p. 25) and also conducted a sensitivity analysis (p. 45). The infestation rate and the relative proportion of waste treated as private compost contributed most to the overall uncertainty with percentages depending on the time to waste treatment. Assuming 14 days for the time before the waste was treated, the infestation rate and proportion of waste treated as private compost contributed for 63.4 and 34.8% to the overall level of uncertainty, respectively (p. 45). Key uncertainties are listed on p. 45 in the qPRA and uncertainty is clearly expressed in the conclusions and abstract of the qPRA. However, uncertainty concerning the probability of mating was not accounted for. The Panel assumed that if one female and one male adult escaped from the same bunch of cut roses mating will always occurs. However, BuRO argues that this may not always be the case (see 3.3.6.3 for arguments).

3.4.2 Trade volume and production data

The Panel used trade data from Eurostat for the period 2011–2020 (total volume and average weight per cut rose). Table A.32 (p. 102) shows the "*Average re-export of cut roses from African countries with reported presence of Thaumatotibia leucotreta and from Israel to Spain and Portugal via the Netherlands and Belgium stratified by season. (Eurostat, EU trade since 1988 by HS2-4-6 and CN8, CN 06031100, monthly statistics 12-2010-12.2020, online, accessed on 13 January 2023)"*. This table includes a big outlier. In the winter of 2011, the re-export volume was 54.9 million pieces of cut roses while the re-export volume varied from 3.6 million to 5.7 million cut roses in the same season in other years (2012–2020). This outlier, which has a large effect on the average value, may be a clerical error as the total export of cut roses from the Netherlands and Belgium to Spain and Portugal in the winter of 2011 (December 2010 – February 2011) was only 433,218 kg corresponding to approximately 8.5 million of cut roses using an average weight of 0.057 kg per cut rose as in the qPRA (Eurostat, EU trade since 1988 by HS2-4-6 and CN8, CN 06031100, monthly statistics 2010-12 – 2011-02 and 2011-12 – 2012-02, online, accessed on 10 March 2025). Even if the value of 54.9 million pieces is in fact correct, it would have been better not to use this outlier to predict the average import volume for the winters of 2022 – 2026 but to use it only for the calculation of the standard deviation. Now, the import volume is probably overestimated.

Another outlier in the same table (Table A.32) is the re-export of cut roses in the spring of 2016 (27.6 million of cut roses as compared to 2.9–9.6 million of cut roses in other years. This may also be a clerical error as the total export of cut roses from the Netherlands and Belgium to Spain and Portugal in spring 2016 was 412,878 kg corresponding to approximately 8.1 million of cut roses (Eurostat, EU trade since 1988 by HS2-4-6 and CN8, CN 06031100, monthly statistics 2016-03-2016-05, online, accessed on 11 March 2025).

The Panel used production data of cut roses (ha) from national statistical offices of EU Member States re-exporting cut flowers to Member States with suitable regions. In cases where such statistics were not available, it was assumed that the percentage of cut roses in the total area of production of flowers and ornamentals was the same as in another EU Member State. The production of cut roses in the Member States was calculated by multiplying the number of ha by the number of cut roses produced per ha per year (p. 109).

3.4.3 Infestation rate

The Panel estimated the infestation rate (i.e. the proportion of infested cut roses) by EKE. This estimation was informed by the proportion of infested cut roses calculated from interception data (all stages that can be present on cut roses - i.e. eggs and larvae - are visually detectable). The interception data that are shown in Tables 2 and 3 on p. 9 in the qPRA are, however, conflicting. For example, Table 2 shows 31 interceptions on cut roses in 2018 while Table 3 shows 96 interceptions. Irrespective of this discrepancy, calculations in the qPRA are based on the interception data retrieved from the NPPO of the Netherlands that are shown in Appendix A of the qPRA (p. 129–141):

- There were 217 interceptions of cut rose consignments from all countries where *T. leucotreta* is present during 2019–2022. In samples taken from these intercepted consignments, one (77% of the cases), two (15%) or three (8%) specimens were found (Table A.73 on p. 132; see also section 3.3.6.1 in the present evaluation).
- There were 190 interceptions of consignments from four different African countries out of 20,967 consignments that had been inspected from 2018–2021 (Table A.76 on p. 134, data summarised in Table 4 in the present evaluation).
- Not every consignment was inspected and inspection rates varied from 5.42% to 28.11% between the four African countries (Table A.79 on p. 137; Table 4 in the present evaluation).

Table 4. Number of inspected consignments, inspection rate, average consignment size, sample size and number of consignments found infested by *Thaumatotibia leucotreta* from four different African countries as reported by the NPPO-NL during 2018-2021 (Data from Table A.76 on p. 134 in EFSA Panel on Plant Health et al. (2023a))

Country	Number of consignments inspected	Inspection rate of consignments (%)	Average consignment size (no. of cut roses)	Sample size	Number of consignments found infested
Ethiopia	175	5.42	970,442	1,200	8
Kenya	19,779	10.33	42,305	400	136
Tanzania	767	28.11	36,798	400	30
Zambia	246	11.80	177,041	1,000	16

Table 5. Description of the parameters used in the model to calculate the infestation rate of *T. leucotreta* in the inspected cut rose consignments (p. 135 in EFSA Panel on Plant Health et al. (2023a))

Parameter	Description	Remarks
$r_{inspected}$	Infestation rate within the inspected consignments	
$p_{intercepted}$	Proportion of intercepted consignments	Triangular (P2.5, est, P97.5)
$r_{0\ specimens}$	Detection limit according to the sample size	Uniform (0, P95)
$q_{k\ spec}$	Proportion of interceptions with k specimens	Constant
$r_{k\ spec}$	Infestation level of interceptions with k specimens	Triangular (P2.5, est, P97.5)

The infestation rate of the inspected consignments was given by (p. 135 in the qPRA):

$$r_{inspected} = (1 - p_{intercepted}) \times r_{0\,specimens} + p_{intercepted}\,(q_{1\,spec} \times r_{1\,spec} + q_{2\,spec} \times r_{2\,spec} \times q_{3\,spec} \times r_{3\,spec}).$$

The parameters are described in Table 5. The parameter $r_{0\ specimens}$ is described in the qPRA as the 'detection limit according to the sample size' but may also be described as the 'infestation level of inspected consignments with 0 specimens'.

Apparently, the Panel assumed that the infestation rate in consignments in which no specimens were found (negative inspections) was different from the infestation rate in consignments where at least one specimen was found (positive inspections). Using the parameter estimates presented in Table A.79 (p.136–137), the infestation rate of the positively inspected consignments from Kenya (the country with by far the highest number of imported cut roses and interceptions) is:

$$r_{positively\ inspected\ consignments} = q_{1\,spec} \times r_{1\,spec} + q_{2\,spec} \times r_{2\,spec} \times q_{3\,spec} \times r_{3\,spec}$$

$$= 0.77 \times 0.0025 + 0.15 \times 0.005 \times 0.08 \times 0.0075 = 0.003275,$$

which is the weighted average infestation rate of the samples from the positively inspected consignments. The infestation rate of the negatively inspected consignments from Kenya is:

$$r_{negatively\ inspected\ consignments} = r_{0\,specimens}$$

$$= (0 + 0.00746)/2 = 0.00373,$$

which is the median value calculated for the Uniform distribution with input values '0' and '0.00746' from Table A.79 on p. 136 in the qPRA. Thus, the Panel estimated the infestation rate of the positively inspected consignments (0.003275) to be lower than the infestation rate of the negatively inspected consignments (0.00373). However, the Panel did not provide an explanation for the higher infestation level of the negatively inspected consignments. Logically, if there would be a difference between these groups, one would assume that the positively inspected consignments would have a higher infestation rate.

The Panel estimated the infestation rate for all inspected consignments ($r_{inspected}$) from Kenya at 0.00395 by simulation (median value, Table A.79, p. 136–137). For calculation of the infestation rate of the total import (inspected and non-inspected consignments), it was assumed "*that intercepted consignments are not imported, but the [consignments] not inspected have the same infestation level as the inspected one*" (p. 135). For Kenya, the Panel estimated this infestation rate ($r_{total\ import}$) at 0.0394 also by simulation (median value, Table A.79, p. 136–137). BuRO considers these estimates too high. If the infestation rate (p) within the inspected consignments would truly be 0.00395, the pest would have been expected to be detected in approximately 79% of the samples given a sample size (n) of 400 cut roses and using formula 5 in Appendix 3 in FAO (2008):

$$P(k > 0) = 1 - (1-p)^n = 1 - (1 - 0.00395)^{400} \approx 0.79$$ (formula 5 in Appendix 3 in FAO (2008)).

However, the interception rate ($p_{intercepted}$) observed in practice only amounts to 0.69% (136 interceptions in the Netherlands out of 19,779 inspected consignments from Kenya):

$$p_{intercepted} = 136/19{,}779 \approx 0.0069.$$

Another approach to check whether the infestation rate has a realistic value is to calculate the detection probability (% infested cut roses detected during import inspections) assuming that the infestation rate was indeed 0.00395 for the inspected consignments:

- the total number of cut roses inspected was: 19,779 consignments × 400 cut roses/consignment = 7,911,600 (Table 4 in the present evaluation),
- the total number of infested cut roses was: 7,911,600 × 0.00395 ≈ 31,251,
- the number of infested cut roses detected during inspections was (assuming 1, 2 and 3 infested cut roses found in 77, 15 and 8% of the samples; same percentages as in the qPRA) = 0.77 × 136 + 0.15 × 2 x 136 + 0.08 × 3 × 136 × 2 = 178.16,
- the detection probability would be: 178.16/31,251 × 100 ≈ 0.57%.

This detection probability (0.57%), i.e. the sensitivity of inspection, is unrealistically low for trained inspectors. Thus, both approaches to check whether the model output is realistic indicate that the infestation rate is strongly overestimated by the model used in the qPRA.

3.4.3.1 Expert knowledge elicitation

Across all countries with interceptions on cut roses (Ethiopia, Kenya, Tanzania, and Zambia), the Panel estimated the infestation rate (proportion of infested cut roses) at 0.00319 (median value) based on interception data from 2018 – 2021 (Table A.79, p. 137). Finally, the Panel estimated the proportion of infested cut roses from these African countries at 0.0021 by EKE (90% uncertainty range 0.0003–0.0054) (p. 139). This EKE estimate (0.0021) is lower than the simulated infestation rate (0.00319) for the period 2018–2021. The Panel does not provide a justification for this adjustment. While it is indicated that information from the 'Kenyan Systems Approach and working instruction' including the inspection of 700 cut roses before export was considered during the EKE, it is not clear from the qPRA how it decreases the infestation rate as compared to the period 2018 – 2021. The 'Kenyan Systems Approach' may have been implemented only after 2021 which could be an explanation for the lower infestation rate. However, the time of implementation of the 'Approach' is not discussed in the qPRA. On the other hand, the detection probability may be less than 100% at import especially when only eggs are present. Thus, the actual infestation rate could actually be higher than infestation rates calculated from the interception data.

3.4.3.2 Alternative methods

BuRO used two alternative methods to estimate the infestation rate of cut roses imported from Kenya during 2018–2021 based on the interception data provided in the qPRA (Table 2, p. 9). Both of these methods assume that the infestation rate of positively and negatively inspected consignments is the same. This is because samples may be positive or negative just by chance.

Therefore, BuRO considers these alternative methods to provide better estimates of the actual infestation rate than the one used in the qPRA (see also section 6.2).

Proportion of consignments found infested
The first method derives the infestation rate or proportion of infested units (p)[3] from the proportion of consignments found infested and has also been used in the qPRA of *E. lignosellus* (p. 52):

$$p = -\ln(1 - i/N)/n, \text{ where}$$

p = the proportion of infested units (in this case the proportion of infested cut roses),
i = the number of intercepted consignments,
N = the number of consignments inspected, and
n = the sample size.

Using this formula, the infestation rate for cut roses from Kenya would be:

$$p = -\frac{\ln\left(1 - \frac{136}{19{,}779}\right)}{400} = 0.00001725.$$

This value for the infestation rate of cut roses is more than a factor 100 lower than the estimate (p = 0.00395) in the qPRA.

Proportion of cut roses found infested
The method presented above does not take into account that more than one unit (a cut rose) may be infested in a sample while in some samples 2 or 3 cut roses were found infested with *T. leucotreta*. Therefore, the second method estimates the proportion (p) of infested cut roses by dividing the total number of cut roses found infested by the total number of cut roses inspected during the period 2018–2021. BuRO considers this method to give the best estimate for the proportion of infested cut roses.

For Kenya:

- the average sample size was assumed to be 400 based on the average consignment size (as in the qPRA);
- 136 out of 19,779 consignments that had been inspected were found infested during the period 2018 – 2021 (data from the qPRA, Table 2, p. 9);
- the total number of infested cut roses in these 136 samples is not known but using the same percentages for 1, 2 and 3 infested cut roses as in the qPRA based on Dutch interception data from all countries during the period 2019 - 2022 (77, 15 and 8%, respectively), the total number of infested cut roses was calculated as:

$$0.77 \times 136 + 0.15 \times 2 \times 136 + 0.08 \times 3 \times 136 = 178.16;$$

- then, the proportion of infested cut roses (p) can be calculated as:

$$178.16/(19{,}779 \times 400) \approx 0.0000225.$$

This proportion of infested cut roses is higher than the one based on the interception rate (see above) but still more than a factor 100 lower than in the qPRA. For all four African countries, the proportion of infested cut roses would be approximately 0.0000327 following this method (Appendix B) which is 98 times lower than the infestation rate calculated in the qPRA.

3.4.3.3 Clustering of infested cut roses

BuRO argues that the percentage of samples (400 cut roses) with more than one infested cut rose (15% + 8% = 23%) is higher than one would expect if the sample of cut roses that is inspected at import would be truly random. This is illustrated by the inspection results of cut roses from Kenya

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[3] Note that from now on, the infestation rate (proportion of infested units) is indicated by p and not by r to be consistent with the symbols used in the other two qPRAs which are discussed in Chapters 4 and 5.

(Table 6). Cut roses are packed in boxes (with usually several hundreds of stems per box) and during an import inspection cut roses are taken from a limited number of boxes (usually 2–6) which is therefore not a truly random sample. It is likely that cut roses from the same box were grown closer to each other in the field or greenhouse than cut roses from different boxes. Since most pests have an aggregated distribution in the field (FAO, 2008), infested cut roses are more likely to be clustered in boxes. Thus, the percentage of samples with more than one infested cut rose can be expected to be higher than one would expect under true random sampling.

Table 6. Observed and expected percentages of samples of 400 cut roses (n) from Kenya with one, two or three cut roses infested with *Thaumatotibia leucotreta* (k); expected percentages calculated for two different infestation rates (*p*) in case of truly random sampling (binomial distribution: $P(k) = p^k \times (1-p)^{(n-k)} \times (n!/((n-k)! \times k!)$

No. of infested cut roses per sample	**Percentages of samples**		
	Observed (%)^1	**Expected (%)**	
		***p*=0.00001725**	***p*= 0.0000225**
0	99.312	99.312	99.104
1	0.530	0.685	0.892
2	0.103	0.002	0.004
3	0.055	0.000	0.000

[1] Assuming 1, 2 and 3 infested cut roses found in 77, 15 and 8% of the samples; same percentages as in the qPRA (19,779 samples inspected with 136 interceptions)

3.4.4 Vase life

In the qPRA, it is stated (referring to various sources) that the "*Vase life at the consumer is aimed at a period of 7.0–10.0 days for imported cut roses (…) and 2 weeks for locally produced cut roses (…), but can vary between 4.0 and 14.0 days (Yakimova et al., 1996; Ichimura et al., 2006)*". Next, a vase life of 7 to 14 days (with a most likely value of 10.5) is assumed for cut roses imported from countries where *T. leucotreta* is present (p. 19). However, the research of Yakimova et al. (1996) and Ichimura et al. (2006) concerns locally produced cut roses. Apparently, the assessors have chosen for a worst-case scenario (a minimum of 7 days instead of 4 days, and a most likely value of more than 10 days instead of a value between 7 and 10 days for imported cut roses). No justification is given for this choice but overestimating vase life leads to an overestimate of the number of emerging adults.

3.4.5 Development rate

The Panel estimated the proportions of infested cut roses with eggs, young larvae (L1 and L2) and old larvae (L3, L4 and L5) by EKE informed by interception data from the Netherlands (p. 120-129). Pupae and adults were unlikely to be associated with the cut roses. Development rates of the different life stages at different temperatures were retrieved from literature (Table 7 on p. 20-21).

3.4.6 Survival rate during waste treatment

The Panel estimated the proportions of different types of waste treatments (landfill, composting or incineration/ anaerobic digestion) of commercial waste (cut roses rejected for quality reasons directly after import) using EU statistics (p. 154). The proportion of cut roses in household waste that entered home composting was estimated by EKE informed by percentages of households that apply home composting in several EU Member States (p. 152-153). It was assumed that 100% of specimens survive and escape home composting (indicated as a conservative assumption in Table 8, p. 23). For cut roses from households that were going to a communal waste treatment, the proportions going to each of three different kinds of waste treatments (landfill, composting or incineration/anaerobic digestion) were estimated using EU statistics (p. 154).

The proportion or percentage of specimens that survive and escape the different waste treatments other than private composting was estimated by EKE (p. 155 – 160). The estimated survival percentages ranged between 0.0001% and 0.01% for composting and between 0.001% and 0.1% for landfill (98% uncertainty range, Uniform distributions). Probably, these percentages are mainly based on expert judgement. The qPRA refers to four publications in 'the summary of the evidence' as examples of literature on effects of waste treatments on insects. It is not indicated specifically which information from these publications substantiates the estimates. An exception is the reasoning of the upper limit (99th percentile) of the proportion of specimen that will survive and escape ‘landfill’ where ‘no effect on compaction’ is mentioned referring to Love et al. (2019). However, in the experiments of Love et al. (2019) mature larvae of *T. leucotreta* were placed on the soil surface and were not buried. The results of the experiments do not indicate whether larvae will still pupate after burial and whether emerging adults will be able to escape. It is, therefore, unclear how the results of Love et al. (2019) can be used as a justification of the upper limit for the percentage of survivors in ‘landfill’.

No survivors were expected during incineration/anaerobic digestion. Reasoning was the closed process in which all the material is burned or fermented. BuRO agrees with this conclusion.

3.4.7 Natural developmental mortality

The natural mortality factor in the overall model was derived from reported mortality of larvae in citrus fruit and the assumption that natural mortality of the pupal stage would be similar (44–66%, Uniform distribution, p. 161).

3.4.8 Final output

As stated in the qPRA (p. 72), the model does not estimate the number of founder populations. Instead, the proportion of mated females was calculated based on the probability/likelihood of two or more specimens occurring in a bunch of ten cut roses (see section 3.3.6). The total number of mated females of *T. leucotreta* per year was subsequently estimated for four scenarios with different numbers of days between the initial disposal of the cut roses and waste treatment (3, 7, 14 and 28 days). The lowest estimate (3-days-scenario) amounted to 115 (90% uncertainty range between 12 and 538) and the highest estimate (28-days-scenario) to 330 (90% uncertainty range between 49 and 923) mated females in the suitable EU regions.

BuRO argues that if the number of mated females of *T. leucotreta* per year is indeed as high as the Panel estimated, the ‘average’ probability of oviposition and establishment in the suitable regions must be very low, e.g. less than 1% or even less than 0.1%. This probability would be much lower than the probability of oviposition and establishment of 30% (90% uncertainty between 7.6 and 48.0%) estimated for *E. lignosellus* although the presence of host plants is not considered a limiting factor for either species and a single female of each species can lay many eggs (see section 5.4.4.4 for the Panel’s estimation of the probability of oviposition and establishment of *E. lignosellus*). Cut roses have been imported from countries where *T. leucotreta* is present in large numbers since at least 2011 (import data in Appendix 4 and 5 of the qPRA). Thus, if the model output would be correct, there must have been hundreds or even more than a thousand mated females already in suitable regions. In contrast, no outbreaks (including incursions) had been detected in any of these regions at the time the qPRA was adopted (and still have not been reported). Two incursions were known from glasshouses in the Netherlands, but these have been linked to the import of infested *Capsicum* fruits (BuRO, 2025). Both incursions were also outside the area that was assessed suitable for establishment. The finding of a single male in a glasshouse producing sweet pepper in Germany in 2018 is mentioned in the qPRA as a third incursion (p. 12). However, BuRO does not consider a single observed adult without further evidence for presence of the pest as an incursion (i.e. an ‘isolated population’; see section 2.1 for the definition of an incursion from FAO (2024)). In addition, this finding was linked to fruit and vegetable waste from a nearby supermarket and not to cut roses (EPPO, 2018). It was also outside the area that was assessed suitable for establishment.

The Panel provided two possible explanations for the discrepancy between the lack of outbreaks and the expected number of mated females: (i) “*the relatively recent shift of pest pressure in Africa towards cut roses*” and (ii) “*much of the consumption of cut roses in the EU occurs in regions with lower climate suitability*”. BuRO considers both of these explanations insufficient to resolve the discrepancy between the lack of incursions and the high estimate for the number of mated females. Concerning the first explanation: the Panel did not provide any data or references that indicate a ‘recent shift of pest pressure towards cut roses’. In fact, *T. leucotreta* had been intercepted on cut roses for many years at the time of the adoption of the qPRA which is illustrated by the interception data from 2015–2018 (Table A.63; p. 120) in the qPRA. In addition, interceptions had already been reported before 2015 (EPPO, 2013). Concerning the second explanation: the Panel indeed estimated most of the mated females in regions with suitability classes 1 or 2, being the two lowest suitability classes out of four classes (Fig 19, p 40, Fig. 20, p. 41). BuRO agrees that in such regions the probability of oviposition and establishment is expected to be lower than in more suitable regions. The regions with suitability class 3 or 4 with the highest estimated number of mated females were Andalucia, Attica, Sicily and Valencia (Fig. 20, p. 41). In Andalucia and Attica, the estimated numbers of mated females per year were 0.7 – 2.3 mated females in the scenarios of 3 - 14 days between the time of initial disposal and the waste treatment and 2.3 – 7.3 mated females in the '28-days-scenario'. In Sicily, these figures were 2.3-7.3 and 7.2 – 23.0, respectively. In Valencia, the estimated numbers of mated females per year were 0.2 – 0.7 in the '3-7- days-scenarios' and 0.7 – 2.3 in the '14-28-days-scenario'. Based on these estimates and the fact that cut roses had already been imported from infested countries for many years when the qPRA was adopted, the probability of oviposition and establishment would on average still be less than 10% for the most suitable regions (classes 3 and 4). This probability is still considerably lower than the estimated 'average' probability of oviposition and establishment of *E. lignosellus* for the entire EU area that was assessed suitable for establishment of this species (see section 5.4.4.4 and the paragraph above).

3.5 Summary and conclusions

The Panel estimated the number of adults of *T. leucotreta* that emerge every year from cut roses imported from Ethiopia, Kenya, Tanzania and Zambia in climatically suitable NUTS 2 regions using an entry pathway model. The Panel also estimated the proportion of mated females for every emerging adult and finally calculated the number of mated females per year per region. The pest arrives as immature stages (eggs and larvae) on/in the cut roses. First, the number of adults that develop from these stages and emerge (emerging adults) before the cut roses are destroyed by waste treatments was estimated. The number was calculated as the sum of the number of adults that emerge from cut roses used at consumer level including cut roses in household waste and those that emerge from commercial waste corrected for natural developmental mortality. The number of emerging adults from waste treatments was also estimated. Then, the proportion of mated females was calculated based on the following information and assumptions:

- in samples of 400 cut roses taken at import 41% of the *T. leucotreta* specimens intercepted were present with at least one other conspecific specimen,
- a sex ratio of 2:1 (two females per one male),
- no more than one *T. leucotreta* specimen is present per cut rose,
- cut roses are distributed in bunches of 10 cut roses,
- specimens are uniformly distributed among the bunches, and
- if a male and female are present in a bunch mating will take place.

This resulted in the following calculation: 0.41 × 2/3 × 1/3 × 0.025 × 100 = 0.23% (one mated female for every 435 adults).

Conclusions of the evaluation

Structure of the model (estimating the number of emerging adults):

- The model to estimate the number of adults that emerges from imported cut roses was considered accurate.

Uncertainties

- Uncertainties were addressed and clearly expressed in the parameter estimates and final output of the model. However, uncertainty concerning the proportion of mated females for every emerging adult was not accounted for.

Parameter estimates

- The parameter estimates were generally considered to be sufficiently justified taking into account that the available information is generally limited. However, the following errors or inconsistencies were found:
    - The estimated infestation rate of cut roses (proportion of infested roses), based on the interception data, was considered too high leading to a considerable overestimation of the number of emerging adults. This overestimation was mainly

    due to the method used to calculate the infestation rate of inspected consignments using interception data, which was deemed inaccurate. The Panel calculated a higher infestation rate for consignments of which samples had been found non-infested than for consignments that had been found infested. Assuming the same infestation rate for all consignments BuRO calculated an infestation rate that was 98 times lower and considered this a better estimate of the actual infestation rate.
    - A longer vase life was assumed for the imported cut roses than could be expected based on information provided in the qPRA. Using an overestimate of vase life leads to an overestimate of the number of emerging adults.
    - Trade data: a few outliers were identified, which may have been clerical errors but may have led to an overestimation of the number of emerging adults in Portugal and Spain.

Proportion of mated females

- The calculation method in the qPRA overestimates the number of mated females for every escaping adult because it does not take into account a decrease in pest density in a bunch of cut roses due to natural mortality, a factor that the Panel did take into account in the estimation of the number of emerging females. Using the same data and assumptions as in the qPRA but making a correction for this natural mortality and also taking into account that a bunch of 10 cut roses may include three specimens, BuRO estimated by simulation that there will be one mated female for every 690 adults instead of one for every 435 adults.
- The number of mated females for every escaping adult may also be overestimated due the assumption that specimens present in the same bunch of flowers always have similar life stages and develop in parallel.
- For the calculation of the proportion of mated females, the Panel used different data or estimates for the infestation rate of cut roses than for the calculation of the number of emerging adults but did not give an explanation for this. The proportion of infested samples of 400 cut roses with two or more specimens was directly derived from interception data. However, the infestation rate to calculate the number of emerging adults was estimated by EKE informed by interception data. This infestation rate was lower (median value 0.0021) than the infestation rate calculated from the interception data (0.00319). A lower infestation rate would logically result in a lower number of specimens per sample of 400 cut roses and hence not only a lower number of emerging adults but also a lower proportion of mated females.

Comparison of the final output with the number of known outbreaks

- Lack of outbreaks of *T. leucotreta* reported in suitable regions suggests that either the estimated number of mated females per year is too high or the ‘average’ probability of oviposition and establishment, two parameters which have not been taken into account in the qPRA, after mating is very low (less than 0.01 or even less than 0.001).

Other comments

- The model calculates the number of mated females in suitable regions but not the number of founder (established) populations. Therefore, the title of the qPRA ‘Assessment of the probability of introduction of Thaumatotibia leucotreta into the European Union with import of cut roses’ is not fully consistent with its contents because ‘establishment’ is part of ‘introduction’.

4 *Citripestis sagittiferella*

4.1 Biology

Citripestis sagittiferella (Lepidoptera: Pyralidae, EPPO code: CITPSA), commonly known as the citrus fruit borer, is a pest that feeds on *Citrus* spp. After mating, female adults lay eggs on fruit (singly or in small clusters), larvae develop in the fruits, mature larvae pupate in the soil, adults emerge from the pupae in the soil (EFSA Panel on Plant Health et al., 2021). Several eggs are usually laid on one fruit (Khoo et al. 1991 as cited in CABI (2019)) and several larvae can be present in one fruit (EFSA Panel on Plant Health et al., 2023c).

4.2 Description of the model

The qPRA describes a pathway model that calculates the number of founder (established) populations of *C. sagittiferella* per year due to the import of citrus fruit.

The pathway unit is not explicitly defined in the qPRA but would be one ton of fruit according to the description of the parameters (Table 7). The Panel did not estimate the number of fruits per ton but BuRO estimated that one ton may contain 500 to many thousands of fruits depending on the citrus species (see section 4.3.2). A 'disaggregation factor' is included in the model and the transfer unit is one ton of fruit divided by this disaggregation factor (although not explicitly defined as such).

Three models are used in the qPRA to assess the probability of introduction of *C. sagittiferella*. One model calculates the number of founder populations (N_{inf}):

$$N_{inf} = N_{trade} \times p_{prevalence} \times (1 - p_{sorting}) \times (1 - RRO_{effectivenes}) \times d \times p_{transfer} \text{ (p. 8).}$$

Another model calculates the proportion of infested fruit that is being removed in the exporting country ($p_{sorting}$):

$$p_{sorting} = 1 - (1 - p_{sorting\,packing}) \times (1 - p_{sorting\,border}) \text{ (p. 15),}$$

and the last model calculates the number of established populations (N_{est}):

$$N_{est} = N_{inf} \times p_{estab} \text{ (p. 27).}$$

Descriptions of the parameters are presented in Table 7 (amended from Table 1 on p. 8 in the qPRA).

The qPRA considers two scenarios: A0 (current practice) and A2 (additional post-harvest cold treatment) in which an additional input factor is included to account for the effectiveness of a post-harvest cold treatment (1-$RRO_{\text{effectivenes}}$). A scenario A1 (deregulation) was not considered because the organism was not regulated at the time the qPRA was made (p. 12). BuRO only evaluated the models for scenario A0 ($RRO_{effectivenes} = 0$). The inclusion of a parameter that reduces the number of infested pathway units does not change the model structure and an evaluation of the assessment of the effectiveness of risk reduction options was not part of the present study.

4.3 Evaluation of the model

4.3.1 Founder populations

The purpose of the pathway model was to estimate the number of established or founder populations. However, the terminology used in the qPRA is not completely in line with EFSA's guidance (EFSA Panel on Plant Health et al., 2018). According to this guidance, '*founder populations assessed in the entry step are potential founder populations*' and '*founder populations assessed in the establishment step are realised (actual) founder populations'.* See also section 2.1 for the definition of a 'founder population'. According to these definitions, N_{inf} should be the number of 'potential founder populations' and N_{est} the number of 'founder' or 'established populations'.

Table 7. Descriptions of the output variable (N_{inf}) and input parameters used in the pathway model '*Citripestis sagittiferella* - citrus fruit' (EFSA Panel on Plant Health et al., 2023c)

Parameter	**Description**	**Units**
N_{inf}	Number of founder populations of *C. sagittiferella*	Number of founder populations per year
N_{trade}	Total quantity of citrus fruit (infested or not) imported by the EU from Indonesia, Malaysia, Thailand and Vietnam	Tons (1,000 kg) per year
$p_{prevalence}$	Prevalence of *C. sagittiferella* at the origin where citrus fruit is harvested for export to the EU (expressed as the proportion of infested citrus fruit to all citrus fruit harvested in the areas considered)	Proportion of fruit
$p_{sorting\ packing}$	Proportion of infested citrus fruit removed following inspection and culling at the packinghouse	Proportion of fruit
$p_{sorting\ border}$	Proportion of infested citrus fruit removed following inspection at the border in the exporting country	Proportion of fruit
$p_{sorting}$	Proportion of infested citrus fruit removed following pre-import inspection (identification and removal of infested fruits before entry in the EU)	Proportion of fruit
$RRO_{effectivenes}$	Reduction in the proportion of infested citrus fruit with postharvest cold treatment	Proportion of fruit
d	Disaggregation factor, reflecting the distribution of one ton of infested citrus fruit to several locations in the risk assessment area	Number of disaggregated batches of citrus fruit/ton
$p_{transfer}$	Probability that the pest in one disaggregated batch of citrus fruit is transferred to suitable hosts, thus leading to a founder population (transfer includes mating and oviposition according to the text on p. 18-19)	Probability
N_{est}	Number of *C. sagittiferella* populations established in the EU	Number of established populations per year
p_{estab}	Probability that one founder population (from a successful entry) will establish. Once transfer occurs, the probability of establishment is the same for all founder populations	Probability

4.3.2 Pathway and transfer units

The model calculates the number of founder populations by multiplying the trade volume in tons of fruit per year by the proportion of infested fruits, the number of disaggregated batches of fruit (in number per ton fruit), the probability of transfer from one disaggregated batch of fruit and the probability of establishment (see 4.2). Below the following parts of the model are discussed:

- the calculation of the number of founder population as affected by the choice to use one ton of fruit as pathway unit,
- the calculation of the number of infested pathway units, and
- the transfer unit.

4.3.2.1 Pathway units and number of potential founder populations

The unit of the trade volume (N_{trade}) is 'tons per year' while the infestation rate ($p_{prevalence} \times (1-p_{sorting})$) is the proportion of fruits infested (and not the probability that one ton of fruit is infested) (Table 7). Since the pathway unit is one ton of fruit, the product of the trade volume and the infestation rate does not yield the number of infested pathway units, i.e. the number of tons that contain at least one infested fruit. Instead, it yields (roughly) the total tons of infested fruits imported. For the same reason the product of trade volume, infestation rate and disaggregation factor does not yield the number of infested transfer units, i.e. the number of disaggregated batches that contain at least one infested fruit. Instead, it yields the product of the total number of disaggregated batches and the proportion of infested fruits, which does not lead to an accurate estimate of the number of (potential) founder populations. For example, in case of:

- the import of one ton of fruit,
- an infestation rate (proportion of infested fruits) after sorting of 1% ($p_{prevalence} \times (1\text{-}p_{sorting}) = 0.01$),
- no disaggregation (d=1), and
- a 100% chance that the pest will transfer and establish ($p_{transfer} = 1$ and $p_{estab} = 1$),

the number of potential founder populations (N_{inf}) would be:

$$N_{inf} = N_{trade} \times p_{prevalence} \times (1 - p_{sorting}) \times d \times p_{transfer} = 1 \times 0.01 \times 1 \times 1 = 0.01,$$

and the number of founder populations (N_{est}) would be:

$$N_{est} = N_{inf} \times p_{estab} = 0.01 \times 1 = 0.01.$$

However, one ton of fruit may contain 500 to many thousands of fruits. The UK (United Kingdom) has intercepted the pest on fruit of *Citrus aurantifolia* (Key lime) from Malaysia and there were three other suspect findings on citrus fruit in the UK in 2013 (EFSA Panel on Plant Health et al., 2021). The average weight of a single fresh fruit of *Ci. aurantifolia* was approximately 38 g in a study by Onmankhong et al. (2024) in Thailand. Thus, one ton of Key limes may contain 1,000/0.038 ≈ 26,316 fruits. Other citrus fruits can be heavier with pomelo fruit having a weight of usually 1–2 kg (Makkumrai et al., 2021). Thus, when the infestation rate at import is 1%, one ton of fruit is expected to contain 5 to hundreds of infested fruits. Therefore, one founder population per year would be expected instead of only 1 per 100 years in case d=1, $p_{transfer} = 1$ and $p_{estab} = 1$.

Instead of the 'proportion of infested fruit' ($p_{prevalence} \times (1\text{-}p_{sorting})$), a parameter for the probability that a transfer unit (pathway unit divided by the disaggregation factor) is infested could be included in the model (i.e. the probability that a transfer unit contains at least one infested fruit). However, this probability will vary with the disaggregation factor. In addition, there is a dependency between the probability of transfer and the disaggregation factor (see section 4.3.3.3). Therefore, a simpler approach would be to divide the trade volume by the weight of a single fruit and use a single fruit as transfer unit. In that case, the disaggregation factor (d) can be removed from the model because the transfer unit would be the smallest unit possible (a single fruit). A single fruit can contain several specimens and can potentially lead to one founder population (see also section 4.3.2.3).

4.3.2.2 Trade volume and number of infested pathway units

The number of infested pathway units is not correctly calculated in the qPRA because the infestation rate (the proportion of infested fruits) does not correspond with the pathway unit (a ton of fruit) as discussed above (section 4.3.2.1). However, even if the pathway unit would be a single fruit, the first part of the model

$$N_{trade} \times p_{prevalence} \times (1 - p_{sorting})$$

does not accurately calculate the number of infested pathway units. Instead, the product of pest prevalence ($p_{prevalence}$) and the proportion of infested fruit that is not being removed ($1\text{-}p_{sorting}$) should be multiplied by the original volume before sorting ($N_{bef.sorting}$) and not by the trade volume (i.e. the volume after sorting). This is illustrated by the following:

the quantity of fruits imported (N_{trade}) is the quantity of fruits before sorting ($N_{bef.sorting}$) minus the quantity of infested fruits ($N_{bef.sorting} \times p_{prevalence}$) that is removed by sorting ($p_{sorting}$):

$$N_{trade} = N_{bef.sorting} - N_{bef.sorting} \times p_{prevalence} \times p_{sorting}.$$

The quantity of infested fruits that is not removed ($N_{inf.fruits}$) is:

$$N_{inf.fruits} = N_{bef.sorting} \times p_{prevalence} \times (1 - p_{sorting}).$$

Thus, the infestation rate on arrival ($p_{inf\text{-}arrival}$) would be:

$$p_{inf-arrival} = \frac{N_{inf.fruits}}{N_{trade}} = \frac{N_{bef.sorting} \times p_{prevalence} \times (1 - p_{sorting})}{(N_{bef.sorting} - N_{bef.sorting} \times p_{prevalence} \times p_{sorting})}$$

$$= \frac{p_{prevalence} \times (1 - p_{sorting})}{(1 - p_{prevalence} \times p_{sorting})}.$$

The number of infested pathway units ($N_{\text{pathway-units-inf}}$) would be:

$$N_{pathway-units-inf} = N_{trade} \times p_{inf-arrival} = N_{trade} \times \frac{p_{prevalence} \times (1 - p_{sorting})}{(1 - p_{prevalence} \times p_{sorting})},$$

which will result in higher values than the formula used in the qPRA on p. 8 unless no fruits are removed by sorting. For example, if 20% of the harvested fruits (elicited value for the median value, p. 12) is infested and 97,7% of the infested fruit is removed (median value, p. 15), then the actual infestation rate ($p_{\text{inf-arrival}}$) would be:

$$p_{inf-arrival} = \frac{0.20 \times (1 - 0.975)}{(1 - 0.20 \times 0.975)} \approx 0.0057,$$

which is approximately 24% higher than the product of the proportion of infested fruit at origin and the proportion of infested fruit removed by sorting ($p_{\text{prevalence}} \times (1\text{-}p_{\text{sorting}})) \approx 0.0046$) which is used in the model in the qPRA.

4.3.2.3 Transfer units

According to the model in the qPRA, the transfer unit is one ton of fruit (the pathway unit) divided by a disaggregation factor (*d*) (section 4.2). The Panel considered '10' to be the most likely value for this disaggregation factor and hence a batch of 100 kg of fruit to be the most likely volume of a transfer unit (p. 19). BuRO argues that the qPRA lacks critical information on the trade chain in order to accurately assess the size of the transfer unit. Fruit can be moved and stored in large batches before being sold to the final consumer as single fruits or in small batches (e.g. 10 fruits). However, to maintain the quality of the fruit, movement and storage of large batches typically occur in climatized (cool) conditions. Such conditions will stop or slow down the development of immature stages of the pest that may be present in the fruits and prevent transfer of the pest. Transfer may, however, be possible from fruit discarded as waste. Fruit may be discarded for quality reasons and placed under ambient conditions before they are treated by a waste processor. However, it seems unlikely that all infested fruits from a batch are always discarded at a single location. Instead, infested fruits may be discarded by different operators in the trade chain or end up at a consumer's place. A single fruit can contain several larvae and adults may develop from a single or a few infested fruits at the place of an operator (e.g. a retailer) or a consumer and infest a citrus tree in an orchard but also in public green or a private garden. The model does, however, not account for these possibilities (see sections 6.1.3.1 and 6.1.3.2 for further discussion on the choice of the transfer unit and the probability of transfer from different compartments in a trade chain).

4.3.3 Transfer

The Panel did not include a separate parameter in the model for the proportion of infested fruits that enters a suitable region in the EU. There is only one parameter covering 'transfer' and 'entering a suitable region' is part of this parameter although not explicitly stated in the qPRA. The steps included in transfer are described on p. 18–19 of the qPRA: "*For transfer to occur:*

- *Infested fruit should be discarded under suitable temperatures in the risk assessment area, mainly in summer or warm periods in spring and autumn, also during winter in citrus-growing areas of EU southern MS.*
- *The insect should emerge from the fruits discarded close to a citrus orchard.*
- *Then one male and at least one female have to meet, mate and find a suitable host for the female(s) to oviposit".*

Thus, transfer includes (i) disposal of infested fruit close to a citrus orchard during a period of the year when the weather conditions are suitable for development of the pest (for which the fruit has to enter a region with citrus orchards during a suitable time of the year), (ii) development of immature stages (eggs, larvae) present in the fruit into adults (including the formation of pupae), and (iii) mating and oviposition. The probability that all these subsequent steps will happen is included in a single parameter ($p_{transfer}$). This makes estimation of the parameter by means of EKE difficult because also according to EFSA Panel on Plant Health (2024b) precise questions are required for elicitation of model parameters (see also section 4.4.4).

4.3.4 Dependency between parameters

Several parameters in the model are not independent from each other. Dependencies are also discussed in the qPRA but the Panel does not consider these dependencies to affect the conclusions of the assessment because they were taken into account during elicitation of the parameters (p. 22-23). However, BuRO is of the opinion that at least some of the dependencies have an effect on the model output. Therefore, dependencies between parameters and how they affect the conclusions in the qPRA are discussed in this section.

4.3.4.1 Proportion of infested fruits and proportion of infested fruits removed

The proportion of infested fruits after harvest ($p_{prevalence}$) and the proportion of infested fruits removed by sorting ($p_{sorting}$) are dependent according to the qPRA. It is assumed that the efficacy of sorting increases with the proportion of infested fruits. Thus, the proportion of infested fruits that is not removed by sorting ($1-p_{sorting}$) is expected to increase with decreasing infestation rates. It is stated that this dependency "*was considered during the elicitation of sorting*". Indeed, in the elicitation section it is written: "*for the 99% quantile it was considered that sorting at the packinghouse can in some cases be 100% effective, given the high pest prevalence*" and (for sorting at the border) "*for the 1% quantile, it was considered that if inspection is effective at the packinghouse, then pest prevalence is reduced substantially and, as a consequence, inspection at the border is no longer removing much infested material*". However, the use of more extreme values for the 1st and 99th percentiles cannot account for this dependency. It will increase the uncertainty of the output because in the model high values for pest prevalence can go together with high values for the proportion of fruits that is not removed by sorting and vice versa (while high values of $p_{\text{prevalence}}$ are in fact assumed to go together with low values of $1 - p_{sorting}$). A rough simulation suggests that this does not have a major influence on the median estimate of the infestation rate (i.e. $p_{prevalence} \times (1 - p_{sorting})$), which varies from about 0.036 to 0.040 depending on the simulated correlation between $p_{\text{prevalence}}$ and p_{sorting} (see Appendix C for details). However, for the 5th percentile (the lower boundary of the 90% uncertainty interval), the estimated infestation rate varies from 0.00022 for no correlation to 0.0009 for a perfect positive correlation. The upper boundary of the 90% uncertainty interval (i.e. the 95th percentile) shows a similar but reversed pattern, ranging from 0.0049 for a perfect positive correlation to 0.025 for no correlation. Thus, in case of no correlation the higher boundary of the 90% uncertainty range is approximately $0.025/0.00022 \approx 113.6$ times higher than the lower boundary while in case of a perfect positive correlation this difference is only a factor $0.0049/0.0009 \approx 5.4$ (i.e. the uncertainty range decreases considerably when a positive correlation between pest prevalence and the efficacy of sorting is taken into account).

Whether a dependency in fact exists between the proportion of infested fruits and the efficacy of sorting may strongly depend on the sorting procedures in the country of origin. Lots with 20% of infested fruits (the estimated median value for pest prevalence in the qPRA) may actually not be considered for export at all. If the infestation level of a single fruit (i.e. symptom expression) is independent from the proportion of infested fruits, the percentage of infested fruits with detectable symptoms may be the same for all infested lots and hence the percentage of infested fruits that is removed by sorting may be the same for all infested lots. Removal of infested fruits takes time and when the 'sorting time' per lot is independent of the infestation level, the sorting efficacy may even decrease with an increasing proportion of infested fruit. However, to avoid any dependency, an alternative is to estimate the infestation rate on arrival in the EU based on interception data and sampling protocols used during import inspections (see section 6.1.2).

4.3.4.2 Proportion of infested fruits and trade volume

It is stated in the qPRA (p. 22) that "*increased prevalence at the origin might lead to lower trade, but exporting growers might find areas for production in other regions less affected by the pest,* *thus making the conclusions of this assessment robust to this potential parameter dependency*." Trade volume might indeed be affected by pest prevalence but this dependency may only exist during years of exceptional outbreaks. Pest prevalence (proportion of infested fruits) can already be high (>90%, p. 13) but trade volume has nevertheless increased between 2015 and 2018 and seems to be fairly constant since (see 4.4.2). Hence, BuRO agrees that this dependency will not or hardly affect the conclusions of the assessment.

4.3.4.3 Proportion of infested fruits and probability of transfer

It is stated in the qPRA (p. 22): "*Transfer is likely to be dependent on prevalence, as males and females are needed to mate for transfer to occur"*. Indeed, for estimation of the probability of transfer, the number of adults that is expected to be present a the same time and in the same location (or close enough for a female and male to find each other) needs to be taken into account. This number will not only depend on the proportion of infested units but also on the number of infested units present at the same time and in the same location (or nearby locations) and the probability that adults will emerge from these units. From the justification of the elicited values for the probability of transfer (p. 18-19), it is, however, not clear whether the proportion of infested fruits or the expected number of emerging adults was taken into account.

4.3.4.4 Probability of transfer and disaggregation factor

It is stated in the qPRA (p. 22-23): "*Similarly, for transfer and disaggregation, if the infested ton of citrus fruit is not disaggregated, transfer is going to be more likely, but again this dependency between model parameters was taken into account during the elicitation of the probability of transfer (…) and should thus not affect the conclusions of the assessment*". Indeed, the probability of transfer ($p_{transfer}$) is expected to increase with less disaggregation of the fruits. For estimation of the median value of the probability of transfer ($p_{transfer}$), it was assumed that the disaggregation factor (*d*) is 10 (the median value estimated for *d*), while for the estimation of the 99th percentile, it was assumed that $d = 1$ (p. 19). Large values of the disaggregation factor (*d*) should indeed result in smaller values of the probability of transfer ($p_{transfer}$) and vice versa. Thus, for any value of the disaggregation factor (d), the probability of transfer ($p_{transfer}$) will have its own uncertainty distribution. In the current model, large values for the disaggregation factor (*d*) can, however, go together with large values of the probability of transfer (p_{transfer}) and vice versa. This increases the uncertainty of the model output and, thereby, affects the conclusions of the assessment. The negative dependency between the probability of transfer ($p_{transfer}$) and the disaggregation factor (*d*) does not have a very noticeable effect on the median estimate of the product of the disaggregation factor and the probability of transfer ($d \times p_{transfer}$) which varies from 0.267 to 0.274 (see Appendix C for details). Such a small effect was also described in section 4.3.3.1 for the possible dependency between pest prevalence ($p_{prevalence}$) and the proportion of infested fruit removed by sorting ($p_{sorting}$). However, in this case the effect on the uncertainty of the estimate is even larger, with the 5th percentile ranging from 0.00023 for no correlation to 0.0080 for perfect negative correlation, and the 95th percentile ranging from 0.61 for perfect negative correlation to 19.3 for no correlation. In other words: for no correlation the upper boundary is about 84,000 times larger than the lower boundary, whereas for perfect negative correlation this difference is only about a factor 76. Even in case of a relatively weak negative correlation of -0.3 the difference between the upper and lower boundary is already a factor of about 4.35 smaller. Thus, the uncertainty range decreases considerably when a negative correlation between the probability of transfer and the disaggregation factor is taken into account.

4.3.4.5 Probability of transfer and probability of establishment

It is stated in the qPRA (p.30) "*There is a possible dependency between the probability of transfer and the probability of establishment, as locations more suitable to transfer might tend to be also more suitable to establishment. However, the Panel expects the conclusions of the assessment model not to be modified substantially by this dependency between parameters*". There is, however, no such dependency between the probabilities of transfer and establishment as the probability of establishment (i.e. the probability that a potential founder population becomes a founder population) is estimated given that transfer has happened.

4.4 Uncertainty, estimation of parameter values and final output

4.4.1 Uncertainty

Uncertainty is addressed and clearly expressed in the conclusions and abstract of the qPRA.

The Panel estimated uncertainty distributions for the different parameter values by EKE (Table 8) and used Monte Carlo simulations to estimate the number of founder populations (p. 9). In addition, a sensitivity analysis was performed using the Spearman rank coefficient and the parameters included in the entry model that correlated most with the output variable (N_{inf}) were (p. 21):

- $p_{transfer}$ (R = 0.74)
- d (disaggregation factor) (R = 0.44)
- $p_{sorting}$ (R = -0.31)
- $p_{prevalence}$ (R = 0.22)
- N_{trade} (R = 0.12)

Table 8. Parameter estimates (elicited values) in the pathway model '*Citripestis sagittiferella* – citrus fruit' in EFSA Panel on Plant Health et al. (2023c)

Parameter	Parameter estimation by	Median (1st and 99th percentile)
N_{trade}	EKE informed by import volumes from countries where the pest is present for the period 2012 – 2021 (Eurostat) and the assumption that trade would increase over the 10 years of the PRA time horizon (2023–2032). Unit: ton	13,000 (3,000–20,000)
$p_{prevalence}$	EKE informed by infestation rates in the countries of origin	0.20 (0.01–0.50)
$p_{sorting\ packing}$	EKE informed by information about symptoms caused by the pest and based on assumptions about the efficacy of sorting at high and low prevalence of the pest (less effective at low prevalence)	0.95 (0.80–1.00)
$p_{sorting\ border}$		0.50 (0.05–0.95)
d	EKE based on assumptions about the number of locations to which 1 ton of fruit is allocated	10 (1–500)
$p_{transfer}$	EKE based on assumptions; d = 1 was considered for the 99th percentile, d = 10 for the median value and d = 500 for the 1st percentile	0.01 (0–0.33)
p_{estab}	EKE informed by the presence of pests in the Mediterranean Basin that occur in the same area of distribution as *C. sagittiferella*.	0.7 (0–1)

4.4.2 Trade volume

The average trade volume of citrus fruits for the period 2023– 2032 (time horizon of the qPRA)[4] was estimated at 13,000 tons per year (median value) using 2012–2021 Eurostat data (Fig. 2, p. 14). Based on the reasoning presented below, BuRO considers this estimate not sufficiently substantiated and an overestimate of the actual import volume.

Data on trade volumes presented in Table 2 (p. 12) and Figure 2 (p. 14) in the qPRA differs from each other considerably (approximately tenfold). Trade volumes range from 29,646 to 75,456 tons per year in Table 2 for the years 2016–2020 whereas the trade volumes in Figure 2 vary between approximately 2,000 and 8,000 tons per year for the years 2012–2021. The data in Figure 2 are correct according to Eurostat (accessed on 13-12-2024) and were also used to estimate the trade volume for the period 2023–2032 in the qPRA (in other words, the figures in Table 2 are probably

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[4] In section 2.2.2.5 (p. 9) and in Table 6 (p. 13) in the qPRA, the time horizon period is indicated as '2023–2033' instead of '2023–2032. This may be a clerical error because 2023-2033 covers 11 years and not 10 years.

incorrect). The data presented in Figure 2 show that the trade volume was quite stable from 2012 to 2015 but increased from approximately 2,000 tons in 2015 to over 7,200 tons in 2018 after which it remained more or less constant. The Panel, however, concluded that there was still an increasing (linear) trend in trade volume and that this trend would even be stronger without considering the data points for 2020–2021. Trade of the citrus fruits was thought to have been 'strongly reduced' in 2020 and 2021 due to the COVID-19 pandemic but no evidence was provided for that. In fact, FAO (2021) concluded that the "*world agricultural and food trade remained resilient to COVID-19-related shocks, despite short-term disruptions observed at the beginning of the pandemic".* The trade volumes in 2019 (7,543 tons), 2020 (6,479 tons) and 2021 (8,285 tons) do not clearly indicate an increasing trend since 2018 (7,246 tons) and after a period of growth the trade volume may have stabilized after the year 2018. Thus, BuRO considers that the estimated trade volume is not sufficiently substantiated and recent trade data (data 'citrus fruit, fresh or dried' from Eurostat, accessed on 19-02-2025) from the years 2022 (6,728 tons), 2023 (7,016 tons) and 2024 (2,668 tons) indeed indicate that the trade volume had stabilized at about 7,000 tons between 2018 and 2023. It remains to be seen whether the much lower trade volume in 2024 is an anomaly or whether the trade will also be that low in the coming years.

4.4.3 Infestation rate and removal of infested fruit by sorting

The infestation rate after harvest and the proportion of infested fruits that is removed through subsequent sorting in the countries of origin were estimated in the qPRA. The estimation of the infestation rate after harvest was mainly based on data from literature and personal communications (p. 13).

Due to the absence of data, the efficacy of sorting was based on assumptions. It was argued that the efficacy of sorting decreases with pest prevalence and the proportion of infested citrus fruits removed at the border in the exporting country ($p_{sorting\ border}$) was indeed estimated to be lower than the proportion of infested fruits that was removed at the packinghouse ($p_{sorting\ packinghouse}$) (Table 8 on p. 15).

The proportion of infested fruits removed at the packinghouse was estimated to range between 0.8–1.0 (1st – 99th percentile). Especially the upper limit seems unrealistically high because according to EFSA Panel on Plant Health et al. (2021) "*eggs are minute and may be difficult to detect*" and "*larvae burrow inside fruit; infested fruit might not be detected during inspections of imports*". It is argued in the qPRA that "sorting at the packinghouse can in some cases be 100% effective, given the high pest prevalence". However, it seems unlikely that every fruit is inspected in detail and that always 100% of infested fruits will be removed.

It is not fully clear how the value for the proportion of fruits that is removed by sorting (p_{sorting}) was obtained from the values for the proportions of fruits removed in the packinghouse ($p_{\text{sorting packing}}$) and at the border ($p_{sorting\ border}$) (Table 8, p. 15). Probably, distributions were fitted through the elicited values of the proportions of fruits removed in the packinghouse ($p_{sorting\ packing}$) and at the border ($p_{sorting\ border}$) (distributions not presented in the qPRA). Then, the proportion of fruits that is removed by sorting ($p_{sorting}$) was probably obtained by Monte Carlo simulation as on p. 9 it is stated that "*the pathway model was run using Monte Carlo simulation*".

The infestation rate on arrival ($p_{inf\text{-}arrival}$) is, according to the model, the product of the proportion of infested fruit after harvest and the proportion of infested fruits that are not removed by sorting ($p_{prevalence} \times (1-p_{sorting})$). This calculation method is not fully correct (see section 4.3.2.2), but the output can still be used to evaluate whether the estimate is reasonable in order of magnitude. Using the fitted distribution of the two parameters (Fig. 1 on p. 13 for $p_{\text{prevalence}}$ and Fig. 5 on p. 17 for p_{sorting}), BuRO obtained the following infestation rate after sorting by Monte Carlo simulation (see Appendix D.1):

Percentile	1%	25%	Median	75%	99%
$p_{prevalence} \times (1-p_{sorting})$	4.0 x 10-5	0.0014	0.0038	0.0090	0.044

The sample size taken at import is not mentioned but Commission Implementing Regulation (EU) 2019/2130[5] sets specific rules for inspection of consignments at the border. For consignments with more than 500 units (which will most likely be the case for citrus fruits) the requirement is a "*sampling scheme able to identify with 95 % reliability a level of presence of infected plants of 5% or above*". This would mean a sample size of at least 59 fruits for large lots with sample sizes less than 5% of the lot size (FAO, 2008). In case of a sample size of 59 fruits, an inspection efficacy of 100% and an infestation rate of 0.0038 (median value), the probability of interception (the probability of having at least 1 infested fruit in sample of 59 fruits) would be:

$$P(k > 0) = 1 - P(k = 0) = 1 - (1 - p)^n = 1 - (1 - 0.0038)^{58} \approx 0.20.$$

The inspection efficacy may be lower than 100% but on the other hand sample sizes may be larger. For example, the Netherlands (NL) inspect fruits in 2–15 packaging units depending on the size of the consignment and usually more than 60 fruits are inspected. Thus, if the infestation rate on arrival would be 0.0038, relatively many consignments are expected to be intercepted. There are three interceptions known from the UK but there are no interceptions notified in the EU databases Europhyt and TRACES for the period 1995–2021 as mentioned in the pest categorisation of *C. sagittiferella* (EFSA Panel on Plant Health et al., 2021). The pest has also not been notified in recent years (TRACES database visited on 09.01.2025). The pest is not regulated and EU Member States may have intercepted the pest without notification (eggs and larvae are visually detectable). Indeed, NL has intercepted *Citripestis* (cf.) *sagittiferella* eight times from 2007 to 2023 on citrus fruits from Indonesia, Malaysia and Vietnam including one dead specimen (NVWA 2025, personal communication). The interceptions were on *Citrus* sp. (1 ×), *Ci. hystrix* (4 times), *Ci. reticulata,* (1×), *Citrus* × *limonia* (1×) and ×*Citrofortunella microcarpa* (1×). In 2023, NL intercepted *Citripestis* (cf.) *sagittiferella* in two out of 457 consignments imported from countries where the pest is present, which corresponds with an interception rate of 0.0044 (2/457). This is much lower than an interception rate of 0.20 which would be expected based on the median infestation rate calculated from the parameter estimates in the qPRA. Inspectors may not have sent in each infested sample because *C. sagittiferella* is not a Union quarantine pest but it is expected that at least since 2018 infested samples are sent to the laboratory for identification because of similarities with the Union quarantine pest *T. leucotreta* (another lepidopteran species that also infests citrus fruits). These data indicate that the estimated infestation rate after harvest (pest prevalence) is too high and/or the estimated efficacy of sorting in the country of origin is too low. Also note that USDA (2020) and DAFF (2025) do not consider pomelo fruit (*Ci. maxima*) from Vietnam to be a pathway of *C. sagittiferella,* in part because of a lack of interceptions. While the Panel considered all kinds of citrus fruits in their pathway analysis, the infestation rate of the fruits was mainly based on infestation rates reported for pomelo in Vietnam (p. 11 in the qPRA).

4.4.4 Transfer

The 1st percentile, median and 99th percentile of the probability of transfer ($p_{transfer}$) were estimated at 0, 0.01 and 0.33, respectively (Table 12 in the qPRA) with the following justification (p. 18-19):

"*For transfer to occur:*

- *Infested fruit should be discarded under suitable temperatures in the risk assessment area, mainly in summer or warm periods in spring and autumn, also during winter in citrus-growing areas of EU southern MS.*
- *The insect should emerge from the fruits discarded close to a citrus orchard.*
- *Then one male and at least one female have to meet, mate and find a suitable host for the female(s) to oviposit".*

For the 1% quantile, it was considered that the need for these subsequent steps to take place greatly reduces the probability of transfer. In addition, some sorting will take place also after import, for instance at market and consumer level and the culled fruit with be subjected to

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[5] Commission Implementing Regulation (EU) 2019/2130 of 25 November 2019 establishing detailed rules on the operations to be carried out during and after documentary checks, identity checks and physical checks on animals and goods subject to official controls at border control posts. Official Journal L 321, 12.12.2019, pp. 128–138

composting or burial. For the 99% value, the most favourable conditions were considered, when one ton of infested fruit is delivered to a packinghouse in close proximity to citrus orchards, and then, the fruits are disseminated at a suitable time of the year. Mediterranean climate can be warm enough to allow the adult insects flying all year round to find suitable hosts. The median was set considering the most frequent situation, with about 100 kg of infested fruit (median of the disaggregation factor). This bulk quantity would favour transfer, as several infested fruits are likely to be in the same lot."

In the qPRA, qualitative information is provided about the flight capacity of adults of *C. sagittiferella* and it is stated that one fruit with several larvae is theoretically 'enough to provide the founder population' (p. 12): *"Adults of C. sagittiferella are strong flyers, particularly in the evening. It is possible that wind could disperse the moths over relatively longer distances (…). Consequently, transfer is not likely to be difficult, as citrus packinghouses in the risk assessment area are often close to citrus orchards. As C. sagittiferella is not a parthenogenic species, at least one female and one male are needed to start a new infestation. Theoretically, one fruit with several larvae could be enough to provide the founder population."*

Neither the proportion of infested fruits entering a suitable NUTS 2 region nor the proportion of infested fruits discarded near citrus orchards during a season favourable to pest development was estimated separately. It is stated that citrus packinghouses are often close to citrus orchards (p. 12). However, no estimate was made of the proportion of the imported fruits that is going to these packinghouses. In fact, many of the fruits may go to EU Member States that do not grow citrus fruits. In addition, no details are provided about the trade chain after arrival of the fruits in the EU. The fruits may be sorted at the border in regions that are unsuitable for establishment and subsequently transported and stored under cool conditions before going to retail and being sold to the final consumer. During 2019–2021, approximately 99.6% of the citrus fruit imported from Vietnam, Indonesia, Thailand and Malaysia was imported through EU Member States which have no commercial citrus production (Eurostat, EU trade since 1988 by HS2-4-6 and CN8, CN 0805, data extracted on 11 March 2025).

Fruit found infested during sorting/packing will probably be discarded but may be processed before adults can emerge. The possibility of burial or composting of infested fruit is mentioned in the justification of the 1st percentile but may also play a role in an 'average situation'.

The development times of eggs and larvae in fruit are not mentioned. The development time may be unknown but without that information and information about the trade chain, the probability that an adult will emerge from an infested fruit before it is consumed or processed remains highly uncertain.

The statement that adults are strong fliers has been taken from a factsheet from Australia (Anonymous, 2024). However, this factsheet provides neither data nor references to justify that statement, which makes the assessment of adult flight behaviour highly uncertain.

From the text in the qPRA, it is unclear whether all of the aspects discussed above have been taken into account for the estimation of the probability of transfer (p_{transfer}). For example, for the 99th percentile it was considered that "*one ton of infested fruits is delivered to a packinghouse in close proximity to citrus orchards*" (p. 19). However, this assumes that all imported citrus fruits enter a NUTS 2 region suitable for establishment while most NUTS 2 regions in the EU are not suitable for establishment. This seems an unrealistic scenario. Fundamentally, when estimating a percentile for a parameter involving multiple steps, it cannot be assumed that one or more steps have already been completed unless this approach is consistently applied to all percentiles. The need for several consecutive steps will generally reduce the probability of transfer of a pest from produce and this probability can easily be overestimated without considering separately each of the steps needed for transfer to take place.

4.4.5 Establishment

Citripestis sagittiferella is only known to occur in tropical climates which are not present in Europe (p.25). The qPRA refers to a study of Rossi et al. (2023) for more details about the climatic suitability in the EU for this pest. All occurrence records of *C. sagittiferella* with coordinates are located in tropical climates. However, when larger administrative units are considered in which the pest is present, the Cfb climate type (temperate oceanic climate, which is primarily found in western Europe) is present but only in 0.60 to 1.04% of the pixels in three units (see Rossi et al. (2023) for details). Therefore, the Panel considered it uncertain whether the pest could establish in a Cfb climate because "*no report of pest presence was found in the specific area with Cfb climate type*" (p. 25).

In the EU, citrus is mainly grown in areas with Mediterranean climate types (Csa and Csb) (EFSA Panel on Plant Health et al., 2021; EFSA Panel on Plant Health et al., 2023c). It is stated in the qPRA that a large proportion of citrus-growing areas in the EU with Mediterranean climate types (Csa and Csb) would be classified as Cfa and Cfb when considering the average monthly irrigation volumes for citrus (p. 26). However, the Panel did not discuss the effect of the irrigation system on climate. Drip irrigation is the main irrigation system used in citrus orchards at least in Spain (Poveda-Bautista et al., 2021). It is questionable whether such a sub-surface irrigation method (unlike overhead irrigation which is more comparable with natural rainfall) can change the climate in a citrus orchard into a Cfa or Cfb climate type.

The Panel estimated the probability of establishment by EKE because of the uncertainties discussed above. The 1st percentile, median and 99th percentile were estimated at 0, 0.7 and 1, respectively, with the following justification (p. 26):

> "*For the 1% quantile, the value was set considering that C. sagittiferella is not currently present in areas with Cfb climate and that the entire EU territory is considered unsuitable for pest establishment based on the Köppen–Geiger comparison. For the 99% quantile, it was assumed that wherever citrus is present in the EU (…), the pest can establish. The median was set closer to the 99% value, as other citrus pests (e.g. A. aurantii, P. citrella, D. citri; …) occurring in the same area of distribution of C. sagittiferella were able to establish in the Mediterranean Basin. Some natural enemies could hamper establishment, but in most cases, founder populations would be able to reproduce and establish. Establishment might not be similarly probable in different Citrus species and cultivars, as there is uncertainty about their different susceptibility to C. sagittiferella. However, this factor is likely to affect more impact and spread, rather than establishment.*
>
> *No thermal studies and specific temperature thresholds are available for C. sagittiferella, so it is difficult to build appropriate maps of accumulated degrees. Frost-free day map could be suitable, but there is no evidence showing that the pest can survive a certain number of frost days. Irrigation-based Köppen–Geiger maps were explored, but there is high uncertainty on the climate type where the pest is reported, so this approach did not reduce the uncertainty of the elicitation on the probability of establishment*."

From this justification, it appears that the estimated probability of establishment (p_{estab}) is the probability that citrus growing areas in the EU are suitable for establishment rather than the "*probability that one [potential] founder population (from a successful entry) will establish*" as defined in Table 15 in the qPRA. For establishment to occur, the area not only needs to be suitable for establishment but the pest also needs to actually persist. After entry, establishment may not happen, for example due to application of pesticides, presence of natural enemies, Allee effects etc. Suboptimal climatic conditions may also decrease the probability of establishment of a potential founder population. Indeed, EFSA's guidance states that "*The potential founder populations derive from encounters between propagules and hosts. However, few encounters may result in an established population, for instance because the weather conditions are not suitable, or the initial population size is too small to be successful due to demographic stochasticity. Hence, there will be (much) fewer actual founder populations than potential founder populations."* Natural enemies are mentioned in the qPRA but it remains unclear what $\mathrm{p}_{\mathrm{estab}}$ exactly stands for. Either the conditions are suitable for establishment (though possibly suboptimal) and the probability of establishment (p_{estab}) represents the probability that a potential founder population becomes established, or the conditions are unsuitable, in which case the number of founder populations is expected to be zero. Considering that the conditions in the citrus growing areas in the EU seem at best suboptimal for establishment, BuRO argues that the median value for the probability of establishment (0.7) but also the 99th percentile (1.0) are too high.

Additional comment: the Panel justifies a median value > 0.5 for the probability of establishment (p_{estab}) based on the fact that citrus pests that are native to the same tropical area as *C. sagittiferella* have been able to establish in the Mediterranean Basin (p. 26: "*The median was set closer to the 99% value as other citrus pests (e.g. A. aurantii, P. citrella, D. citri; …) occurring in the same area of distribution of C. sagittiferella were able to establish in the Mediterranean Basin*"). However, organisms that originate from the same area may have different abilities to adjust to conditions in other climate zones. In fact, the opposite could also be argued: while other citrus pests from the same region have been able to spread to other regions and establish in non-tropical regions, *C. sagittiferella* has not and may, therefore, not be able to adapt to dry Mediterranean conditions.

4.4.6 Final output

The Panel assessed the number of potential founder populations (indicated as 'founder populations', see section 4.3.1) as 9.5 per year with a 90%-uncertainty range between about one potential founder population per 180 years and about 1,300 potential founder populations per year for the period 2023–2032. The number of established populations was estimated to be 4.8 per year with a 90%-uncertainty range between about one established population every 400 years and about 800 established populations per year. Below, BuRO discusses how likely this estimate is considering the absence of outbreaks in the EU when the qPRA was adopted on 26 January 2023.

Citrus fruit has been imported from countries where the pest is present for many years. In the qPRA, it is estimated that about one year after establishment (median value 12.9 months, 90%-uncertainty interval between 2 and 33 months), the pest will start spreading to neighbouring orchards and the pest will spread by natural means and transport of infested fruit from orchards to packinghouses at a rate of about 100 km/year (median value, 90%-uncertainty interval between 40 and 500 km/year). Using these estimates, it is considered that the time to detection of an outbreak is less than 3 years (36 months). At the time the qPRA was adopted (26 January 2023) no outbreaks were known in the EU (they are currently not known either). Thus, the number of founder populations (N_{est}) until at least 2019 can be considered to be zero. The probability of introduction may have increased over time due to an increase in pest prevalence in the countries of origin or an increase in the probability of transfer in the EU, which is discussed below.

Among the countries where the pest is present, Vietnam is by far the largest exporter of citrus fruit to the EU (Eurostat, accessed January 2025) (EFSA Panel on Plant Health et al., 2021). The pest prevalence (proportion of infested fruit) may have increased in Vietnam but an infestation rate of 20-40% of pomelo fruit was already reported from the Mekong delta in 2013 (Le Quoc et al., 2021)[6]. In addition, there were several (suspect) findings of the pest in citrus fruit from Malaysia in the UK during 2011–2013 (EFSA Panel on Plant Health et al., 2021). Therefore, it can be assumed that the infestation rate in the countries of origin has been high since at least 2013 and the proportion of infested fruits on arrival has not changed much since 2013.

The probability of transfer may increase with an increasing citrus production area in the EU. However, there has been no significant increase in the citrus production area in the EU since 2013. Eurostat provide figures for 2012 and 2017 with a total crop area of citrus fruit trees of 464,369 ha in 2012 and 455,227 ha in 2017. More recent figures are not available in Eurostat but the production area of oranges has not changed much since 2013 according to EC (2025). It decreased from 292,500 ha to 272,000 ha in 2019 after which it increased to 280,000 ha in 2023. A possible increase in the probability of transfer due to an increase in citrus crop area in the period 2023–2032 is also not mentioned in the qPRA. Thus, like the proportion of infested fruit the probability of transfer (p_{transfer}) may not have changed much since 2013 (assuming that there have been no changes in the trade chain that may have affected the probability of transfer; such changes are not discussed in the qPRA either). Thus, using the parameter estimates from the qPRA and the total import volume for the period 2013–2019 (27,289 tons, Eurostat, accessed January 2025), a total number of about 10 founder populations (27,289/13,000 × 4.8) could have been expected at the

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[6] In the qPRA an infestation rate of 40-70% is mentioned referring to the same publication but these figures could not be found in .

time the qPRA was adopted (or even more because citrus fruit had also been imported before 2013). However, no outbreaks are known in the EU and, therefore, the qPRA appears to overestimate the number of founder populations of *C. sagittiferella* that can be expected. Especially, the upper limit of the 90% uncertainty range (800 populations per year) appears unrealistically high.

The observation of zero founder populations can be used to update the model (Bayesian updating). The lack of founder populations until 2019 is not truly new evidence but this information does not seem to have been taken into account in the qPRA. Using the model as a prior and using the information of zero founder population during 2013–2019 as data, a posterior probability can be calculated. This calculation results in an expected number of about one founder population per 30 years with a 90%-uncertainty range between one founder population per 35,000 years and 0.61 founder populations per year for the period 2023–2032 assuming the uncertainty distribution elicited in the qPRA (see Appendix E for details). Using a trade volume of 7,500 tons per year, which seems a more likely volume (see section 4.4.2), the number of expected founder populations would be approximately one per 45 years. This calculation should not be considered as an accurate estimate of the number of founder populations because several shortcomings of the model and parameter estimates has been identified (see sections 4.3 and 4.4). However, the difference between these estimates and those provided in the qPRA emphasize the importance of critical reflection on the output of any model.

4.5 Summary and conclusions

The Panel estimated the number of founder populations of *C. sagittiferella* introduced each year through the import of citrus fruit from Indonesia, Malaysia, Thailand, and Vietnam. The pest arrives as immature stages (eggs and larvae) in the fruit. It was estimated how many adults emerge from the fruit and establish a founder population. The estimate was made using a model with the following components:

- the import volume of fruits (in tons),
- the proportion of infested fruit after harvest,
- the proportion of infested fruit that is not removed by sorting in the country of origin,
- the proportion of fruits that is not removed by risk reduction options,
- a disaggregation factor reflecting the distribution of one ton of infested citrus fruit to several locations in the risk assessment area,
- the probability of transfer, and
- the probability of establishment.

<u>Conclusions of the evaluation</u>

Structure of the model

- The model does not calculate the number of founder populations accurately:
    - The product of the infestation rate after harvest and the proportion of infested fruit that is not removed by subsequent sorting in the country of origin is multiplied by the import volume in the EU but should instead be multiplied by the volume of citrus fruit before sorting to calculate the volume of infested fruit on arrival in the EU accurately.
    - The product of the number of pathway units (tons of fruit), infestation rate (proportion of fruits infested) and a disaggregation factor does not yield the number of infested transfer units, i.e. the number of disaggregated batches that contain at least one infested fruit. Instead, it yields the product of the total number of disaggregated batches and the proportion of infested fruit, which does not lead to an accurate estimate of the number of (potential) founder populations.
    - It is likely that dependencies exist between some parameters. The Panel assumed a negative correlation between the proportion of infested fruit after harvest and the proportion of infested fruit that is not removed by sorting but the model does not account for this dependency. In addition, the probability of transfer and the disaggregation factor are negatively correlated. When these negative correlations are taken into account, the uncertainty range of the model output decreases.

    - Transfer to citrus trees outside orchards (e.g. transfer from fruit at consumer's places to citrus trees in private gardens) was not taken into account.

Uncertainties

- Uncertainties were addressed and clearly expressed in the conclusions and abstract of the qPRA.

Parameter estimates

- Trade volume: the Panel made the assumption that the import volume would increase linearly in the next ten years but no convincing evidence was provided for that. The evidence that was provided could also be used to argue that the import volume had stabilized after some years of increase.
- Infestation rate: the Panel made no comparison between the number of infested fruits on arrival in the EU (i.e. the number of infested fruits after sorting) and interceptions. No interceptions have been notified in EU-databases but BuRO made a comparison between the estimated infestation rate and the number of interceptions (not notified) in the Netherlands. This interception rate was much lower than would be expected based on the estimated infestation rate, which was, therefore, considered too high.
- Transfer: from the justification in the qPRA it is not clear whether all consecutive steps that need to take place for transfer to occur, including the distribution of units into suitable regions, the development of immature stages into adults, mating and oviposition, have sufficiently been taken into account. The probability of transfer may, therefore, have been overestimated.
- Establishment: the justification of the estimate for the probability of establishment suggests that this estimate reflects the probability that the climate in the citrus-growing areas in the EU is suitable for establishment rather than the probability that a potential founder population becomes a founder populations in an area suitable for establishment (which are different probabilities). Therefore, the probability of establishment may have been overestimated.

Comparison of the final output with the number of known outbreaks

- BuRO considers the calculated median number of founder populations (4.8 per year) a considerable overestimate of the probability of introduction of *C. sagittiferella* into the EU taking into account the volume of citrus fruit that had been imported and the lack of known outbreaks (at the time the qPRA was adopted). Using the model as a prior and using the information of zero founder population during 2013–2019, BuRO calculated a posterior probability. This calculation resulted in one founder population expected per 30 years with a 90%-uncertainty range between one founder population per 35,000 years and 0.61 founder populations per year for the period 2023–2032 using an average trade volume of 13,000 tons per year as estimated in the qPRA. Using a trade volume of 7,500 tons per year, which BuRO considers more likely, the number of expected founder populations would be approximately one per 45 years.

Other comments

- The terminology is not completely in line with EFSA's guidance: the term 'founder populations' is used instead of 'potential founder populations' before establishment has actually occurred.

5 *Elasmopalpus lignosellus*

5.1 Biology

Elasmopalpus lignosellus (Lepidoptera: Pyralidae, EPPO code: ELASLI), commonly known as the lesser cornstalk borer, is a pest that feeds on many different plant species including *Asparagus.* After mating, female adults usually lay eggs singly or in small clutches in the soil; occasionally eggs are laid on stems and leaves of host plants. After hatching, larvae move towards the roots of their host plants. Larvae feed on young roots, vegetative buds in the root-hypocotyl region or leaves that touch the soil. Later instars can bore into the plant stalk. Mature larvae pupate in the soil. Adults hide in low parts of plants and in soil clods during the day, whereas they are active at night, flying short distances at low altitude (EFSA Panel on Plant Health et al., 2021).

5.2 Description of the model

The qPRA describes a pathway model which estimates the number of founder populations in the EU per year due to the import of asparagus spears from Peru in NUTS 2 regions that are suitable for establishment (suitable regions) of *E. lignosellus*. This was the only relevant pathway that was identified for introduction of the species.

The pathway unit is a single asparagus spear although not explicitly stated in the qPRA. The assumption in the qPRA is that an infested asparagus spear carries no more than one *E. lignosellus* larva. The transfer unit is also a single asparagus spear (indicated in Fig. 2 on p. 14 in the qPRA) although at least two infested asparagus spears are needed for transfer (which includes mating) to occur.

The model in the qPRA is described as follows (p. 13):

"*The pathway model for introduction is a product of the following components:*
- *Import quantity of asparagus from Peru into the EU.*
- *Inverse weight of a single asparagus spear (to calculate the number of imported spears as the volume of trade (kg) divided by the weight of a single spear).*
- *Proportion of infested spears entering the EU.*
- *Proportion of infested spears imported to suitable NUTS 2 regions (two scenarios: current climate and climate change).*
- *Proportion of asparagus disposed of as waste.*
- *Probability of a discarded larva surviving to become an adult.*
- *Probability of a female mating*
- *Probability of a mated female initiating a persisting founder population*."

No formula is presented in the qPRA, but the model could be presented by:

$$N_{established} = V \times 1/W_{unit} \times p_{inf} \times p_{clim} \times p_{waste} \times p_{adult} \times p_{female} \times p_{mate} \times p_{est},$$

with parameter descriptions presented in Table 9.

A parameter for the proportion of females (p_{female}) is not included in the description of the model on p. 13–14 in the qPRA. On p. 62 it is indicated that 'sex ratio' is included in the model but no sex ratio is given. The number of founder populations would indeed be overestimated without a parameter for the proportion of females (p_{female}) (Appendix F).

Table 9: Descriptions of the output variable ($N_{established}$) and input parameters in the pathway model '*Elasmopalpus lignosellus* - asparagus spear' in EFSA Panel on Plant Health et al. (2023d)

Parameter	Description	Units
$N_{established}$	Number of founder populations of *E. lignosellus*	Number of founder populations per year
V	Imported quantity of asparagus from Peru into the EU	Kg per year
W_{unit}	Weight of a single asparagus spear	Kg
p_{inf}	Proportion of asparagus spears that is infested	Proportion
p_{clim}	Proportion of infested spears entering an area where the climate is suitable for establishment of *E. lignosellus* (defined as NUTS 2 regions where EI ≥ 30)	Proportion
p_{waste}	Proportion of asparagus spears disposed of as waste	Proportion
p_{adult}	Probability that a larva develops to adulthood and escapes from a discarded asparagus	Probability
p_{female}	Proportion of females	Proportion
p_{mate}	Probability that a female will mate	Probability
p_{est}	Probability that a mated female will oviposit and establish a founder population	Probability

5.3 Evaluation of the model

The model estimates the number of founder populations. BuRO considers the structure of the model to be accurate (with the inclusion of a parameter for the proportion of females). However, the parameters in the model are not fully independent because the probability that a female will mate will depend on the number of adults that will be present at the same time and in the same location. Thus, the probability of mating (p_{mate}) will increase with the infestation rate (p_{inf}) and the probability that a larva develops to adulthood and escapes from a discarded asparagus spear (p_{adult}). The probability that a female will mate can, however, be estimated for a given number of adults ($N_{\mathrm{adults}} = V \times 1/W_{\mathrm{unit}} \times p_{inf} \times p_{\mathrm{clim}} \times p_{\mathrm{waste}} \times p_{\mathrm{adult}}$; see also section 5.4.4.3). This dependency between parameters is not addressed in the qPRA.

The term 'transfer' is not explicitly defined in the qPRA and the qPRA is inconsistent concerning the steps that are involved in 'transfer'. On p. 33 (under 'uncertainty decomposition'), the following steps are considered to be part of transfer including the establishment of a founder population:

- development of a larva into an adult which subsequently escapes from the waste,
- mating,
- establishment of a founder population by a mated female.

However, in other parts of the qPRA, a distinction is made between 'transfer' and the 'initiation of a founder population', e.g. on p. 13: "*The process of transfer and initiation of a founder population was broken down into four steps*:

- *Estimating the proportion of imported asparagus discarded by commercial stakeholders in the supply chain due to e.g. infestation, physical damage, substandard quality or oversupply,*
- *The proportion of larvae that develop to adulthood and escape from discarded material,*
- *The proportion of females that find a mating partner and lay eggs,*
- *The likelihood that adults develop from the eggs to reproduce and initiate a founder population*."

However, it is not made clear which of these four steps are part of 'transfer' and which are part of 'establishment'. Looking at the description of the model parameters, 'establishment' includes oviposition by the mated female and the subsequent development of a persistent population after mating (p_{est}, see section 5.2). This would mean that 'transfer' ends after mating.

5.4 Uncertainty, estimation of parameter values and final output

5.4.1 Uncertainty

Uncertainty is addressed and clearly expressed in the conclusions and abstract of the qPRA (indicated by a 90% confidence range for the number of founder populations).

Uncertainty distributions for import volume, infestation rate and the probabilities of adult emergence, mating, and establishment of a founder population were estimated using EKE (Table 10). Constant values were used for the weight of a single asparagus spear, the proportion of spears entering a suitable NUTS 2 region and the proportion of spears disposed of as waste (Table 10). Monte Carlo simulations were used to estimate the number of founder populations (p. 29 in the qPRA).

The overall uncertainty is discussed in a separate chapter of the qPRA (Chapter 4, p. 32-34). The largest uncertainty is within the estimate of the infestation rate of the asparagus spears accounting for 69.8% of model uncertainty, followed by the estimates of the probability that larvae develop into adults (18.0%), the probability of mating (7.5%), the probability that founder populations are initiated by a mated female (4.7%), and the trade volume (0.1%) (p. 33). It was noted that the 'infestation rate' is often the largest uncertainty in qPRAs and that lack of empirical data adds to uncertainty about the parameter estimates of the steps involved in transfer.

5.4.2 Trade volume

Trade data were retrieved from Eurostat. It was assumed that trade over the next five years would be similar to trade in recent years (2018–2022) (p. 48). However, the estimated mean annual import of asparagus from Peru (21.4 million kg) is 1.31 times higher than the mean annual import during 2018–2022 (16.3 million kg) (Tables C.1 and C.2 on pp. 47-48). On p. 47, it is mentioned that the estimate is based on imports from Peru 2017–2022 (instead of 2018–2022). However, the import volume in 2017 was similar to the volumes in 2018–2022 (data shown in Figure C.1 on p. 47). Possibly, the Panel has unintentionally used the mean annual import volume from all American countries which was 21.4 million kg during 2018-2022, a value that is also shown in Table C.1 (p. 47). This may have led to an overestimation of the number of founder populations by roughly 30%.

5.4.3 Infestation rate

The proportion of infested spears (the infestation rate) was calculated using UK interception data from the winter of 2019–2020. The infestation rate was calculated by a formula derived from formula 9 in ISPM No. 31 assuming a 100% chance of detection (FAO, 2008) (p. 52):

$$p = -ln(1 - i/N)/n,$$

where:
p = the proportion of infested units,
i = the number of intercepted consignments,
N = the total number of consignments inspected, and
n = the sample size.

The Panel made several assumptions to calculate the infestation rate from the UK interception data. The consignment size in the UK was assumed to vary from 800 to 3,200 kg (p. 52). It is, however, not clear what this assumption was based on. It was furthermore assumed that 1, 5 or 10% of the consignments were inspected in the UK. In 2019–2020, phytosanitary import inspections were not required for asparagus spears imported into the EU and the percentage of inspected consignments was unknown (phytosanitary inspection of asparagus spears has only been required since approximately mid-June 2023)[7]. An inspection percentage of 5 or 10% may be more likely than 1%. In the Netherlands, a 5% or 10% inspection (to check for marketable quality based on

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[7] Commission implementing regulation (EU) 2023/1134 of 8 June 2023 on measures to prevent the introduction into, establishment and spread within the Union territory of Spodoptera frugiperda (Smith), amending Implementing Regulation (EU) 2019/2072 and repealing Implementing Decision (EU) 2018/638. Official Journal L149, pp. 62-79.

Regulation (EU) 1308/2013)[8] was for example required for *Asparagus* from Peru during most months in 2024 (KCB, 2025). Another assumption was a sample size of 300 spears. No reasoning was provided for this assumption either, although the sample size had a large effect on the calculated infestation rate (e.g. assuming a sample size of 60 spears results in a five times higher infestation rate).

Table 10. Parameter estimates in the pathway model '*Elasmopalpus lignosellus* – asparagus spears' (median value and 90% confidence range (CR)) according to EFSA Panel on Plant Health et al. (2023d))

Parameter	Description (unit)	Parameter estimation by	Median (90% CR)
V	Imported quantity of asparagus from Peru into the EU (kg per year)	EKE informed by EU imports from Peru in recent years	21,339,494 (17,395,737–25,283,332)
W_{unit}	Weight of a single asparagus spear (kg)	Constant (standard weight from database: 0.026 kg)	Not estimated
p_{inf}	Proportion of asparagus spears that is infested (infestation rate)	EKE informed by pest status in Peru and UK interceptions	0.106 (per 10,000 spears) (0.016–0.716)
p_{clim}	Proportion of infested spears entering an area where the climate is suitable for establishment of *E. lignosellus* (defined as NUTS 2 regions where EI ≥ 30)	Constant (% EU population in NUTS 2 regions where EI ≥ 30)	0.1643
p_{waste}	Proportion of asparagus spears disposed of as waste	Constant based on figures from a study on asparagus in the US	0.1
p_{adult}	Probability that a larva develops to adulthood and escapes from a discarded asparagus	EKE informed by development time of larvae (27 days at 21°C) and pupae (12 days at 21°C)	0.012 (0.0012–0.042)
p_{mate}	Probability of mating	EKE informed by the estimated number of discarded infested asparagus spears in the NUTS 2 region of Andalucia (16; 90% CR 2-110), most likely in the time frame June to January and the lifespan of adults (10-20 days)	0.00081 (0.00018–0.0017)
p_{est}	Probability that a mated female will establish a founder population	EKE informed by the wide host range of the pest, a female carrying many eggs, not susceptible to predators and parasitoids.	0.303 (0.0764–0.4796)

Calculated infestation rates (based on the UK data) varied from 0.47 to 27.0 infested spears per 10,000 spears depending on the assumed sample size and inspection percentage (Table C.4 on p. 53). The infestation rate varied from 0.47 to 3.9 assuming that 5–10% of the consignments were inspected. The infestation rate estimated by EKE was much lower than the calculated rate with a median value of 0.1 and a 90% confidence range between 0.016 and 0.72 infested spears per

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[8] Regulation (EU) 1308/2013 of 17 December 2013 establishing a common organisation of the markets in agricultural products and repealing Council Regulations (EEC) No 922/72, (EEC) No 234/79, (EC) No 1037/2001 and (EC) No 1234/2007. Official Journal L 347, pp. 671–854

10,000 spears (fitted distribution, p. 51). The reasoning for the much lower infestation rate estimated by EKE was that the UK interception data of 2019–2020 "*represent a worst case with fewer detections per year having been reported since, and no interceptions having been reported before 2019/2020*" (p. 52). However, the inspection efficacy may have increased after the first interception in the UK in 2019. UK inspectors may have looked more specifically for the presence of *E. lignosellus* since the first interception which could explain the strong increase of interceptions in 2019 (Fig. 4 on p. 18). The reduction in notifications after 2019–2020 may be due to the withdrawal of the UK from the EU in 2020. Ireland had the highest number of notified interceptions from the current EU Member States with four records until 7 March 2023, two in 2019 and two in the beginning of 2023 (Fig. 4 on p. 18). These numbers are much lower than from the UK, but Ireland imported much less asparagus from Peru than the UK (on average 199 tons per year during 2019–2023 while the UK imported 8,880 tons in 2019 (Eurostat, dataset: EU trade since 1988 by HS2-4-6 and CN8 [ds-045409 custom 16258421], Fresh or chilled asparagus). Ireland imported 857 tons of asparagus spears from Peru from January 2019 to March 2023 and intercepted the pest four times during this period (Fig. 4 on p. 18). Four interceptions per 857 tons would even mean a higher infestation rate than the 20 UK interceptions per 11,500 tons (the import volume used for the calculations in the qPRA) assuming the same consignment size, inspection percentage and sample size. For example, assuming a consignment size of 3,200 kg and 10% of the consignments being inspected, the calculated number of infested spears per 10,000 spears would be 5.3 which is 2.8 times higher than calculated for the UK for the same consignment size and inspection percentage (Table C4 on p. 53 in the qPRA). Other Member States may have inspected a lower percentage of consignments and/or may not have notified their interceptions because the pest had no quarantine status. In the Netherlands for example, the first registered (but not notified) interception or finding of *E. lignosellus* (dead and living specimens but most specimen being alive) on asparagus spears from Peru dates back to 2010. From 2010 to 2023, 45 interceptions/findings have been registered with most (25) in the years 2021 and 2022. In four samples more than one specimen (up to 4) have been registered. The Netherlands intercepted/found *E. lignosellus* during import inspections (for quality), during export inspections and during surveys on imported products that do not require a phytosanitary import inspection.

In the qPRA, an import volume of 11,500 tons per year is noted for the UK with reference to Eurostat (Table C.4, p. 53), but BuRO extracted a lower import volume of 8,880 tons for 2019 (Eurostat does not show import data for the UK after 2019; the import volume for 2018 was 9,323 tons). Calculations were made using 20 interceptions from the UK (p. 52). However, 23 UK interceptions are mentioned between 12 August 2019 and 1 March 2020 on p. 17 and in Fig. 4 on p. 18. A lower import volume and a higher number of interceptions results in a higher calculated infestation rate. Using an import volume of 8880 tons and 23 consignments found infested (instead of 11,500 tons and 20 consignments found infested) and for example a consignment size of 3,200 kg and 10% of consignments inspected, the number of infested spears per 10,000 spears would be 2.9 instead of 1.9 (see Table C.4 on p. 53 in the qPRA).

In the qPRA, it is noted that "*the NPPO of Peru published export procedures indicating a 0% tolerance for E. lignosellus in December 2022*" (p. 17). This may have led to a lower infestation rate, but the decrease in notified interceptions had already begun after the last notification by the UK on 1 March 2020 (Fig. 20, p. 18). Given that the decrease does not correspond closely to the amended export procedures as well as other reasons mentioned previously, BuRO considers that the infestation rate is highly uncertain and may actually be higher than the estimate of 0.106 per 10,000 spears. In fact, the infestation rate may well be a factor 10 or more higher. It may be closer to the higher rates calculated in Table C.4 in p 53 of the qPRA, which lie outside the 90% confidence range of the estimated infestation rate in the qPRA (Table 10).

5.4.4 Transfer and establishment

In the model, transfer includes development of a larva into an adult, emergence of the adult and mating (see section 5.3.1). The probability of development into an adult and the probability of mating were estimated separately. Establishment included one parameter: the establishment of a founder population by a mated female. The estimations of the different parameters for transfer and establishment are discussed below (sections 5.4.4.1 to 5.4.4.4).

5.4.4.1 Probability of larvae developing to adulthood

The Panel estimated the 1st percentile, the median and the 99th percentile of the probability of "*larvae surviving to develop to adulthood then escape from discarded waste*" at 0.0010, 0.012 and 0.05, respectively (fitted values) but did not provide a justification for these estimates. The development time of larvae (approximately 27 days at 21°C) is given, but no explanation is given how this would affect the probability of development (p. 55). Older larval stages will need shorter times to complete their development into adults than younger ones, but no information is provided about the larval stages that have been intercepted in the EU. The waste may be processed (e.g. by composting or incineration) before larvae and pupae have been able to complete their development. No information is, however, provided about the time between disposal of the waste and its processing. Asparagus spears will deteriorate at temperatures that allow development of the larvae, but whether this may affect development is not discussed. Under natural circumstances pupation takes place in the soil. No information is provided on whether pupation is possible in the waste itself, or whether it is more likely that a larva will leave the waste bin to enter the soil or another site to pupate and how this may affect the probability that a larva develops to adulthood. In summary, because no justification or scenario description is given, it is not clear whether all of these aspects have been taken into account during the EKE.

5.4.4.2 Proportion of females

As discussed in section 5.2, a parameter for the proportion of females (p_{female}) is not mentioned in the qPRA. The sex ratio is also not indicated. When running the model using the parameter estimates given in the qPRA but without a parameter for the proportion of females, the calculated number of founder populations per year was twice as high (0.000265 instead of 0.000133, Appendix F). Thus, probably a sex ratio of 1:1 was used in the model calculations ($p_{female} = 0.5$).

5.4.4.3 Proportion of adults mating

The 1st percentile, the median and the 99th percentile of the 'proportion of adults mating' were estimated at 0.00018, 0.00081 and 0.0017, respectively (fitted values). Justification for these low proportions were the low number of discarded spears, each with a single larva, in suitable NUTS 2 regions. It is stated on p. 65: "*At this point in the model, there is a median of approximately 16 discarded asparagus spears, each with a single live larva in the NUTS2 region of Andalucia (90% CI 2–110), most likely in the time frame of June to January. The probability of mate finding is likely to be low at such low numbers, that are spread out in space as well as time. Adults live for 10–20 days*". It is, however, not clear how this information leads to an overall probability of 0.00081. Andalucía is the region with the highest expected number of infested spears from all regions where conditions were assessed as suitable for establishment (Table D.2, p. 63). The probability that a larva will develop to adulthood and escape is estimated to be 0.012 (median value, p. 65). Thus, the expected number of adults will be roughly 16 x 0.012 ≈ 0.2 per year in Andalucía and the probability of having a female and male in the same year would be 0.2 × 0.2 × 0.5 = 0.02. Assuming that the probability that a female will mate is 0.00081, the probability that a male and female adult are present at the same time and close enough to find each other in Andalucía would be 0.00081/0.02 = 0.0405. This seems fairly high considering that 70% of the discarded spears are located at retailers (p. 64), the likely large number of retailers (>100) selling asparagus spears that can be expected in a region with more than 8.6 million citizens (Wikipedia) and import of asparagus spears throughout the year (In 2019–2021, spears were imported every month into the EU, with most spears (86%) from June to January; data from Eurostat). Therefore, the probability that a female will find a mate may even be lower than 0.00081. On the other hand, the Netherlands has found more than one specimen (up to four) of *E. lignosellus* in samples from consignments originating in Peru (see section 5.4.3). Clustering of specimens in a consignment will increase the probability that a female adult will find a mate. The possibility that specimens are clustered is, however, not addressed in the qPRA. Also note that the infestation may have been underestimated (see section 5.4.3). With a higher infestation rate the probability of mating will also increase (see also section 5.3).

5.4.4.4 Probability of establishment

The 1st percentile, the median and the 99th percentile of the 'probability that a founder population will be initiated following successful mating' (fitted values) were estimated at 0.0302, 0.303 and

0.501, respectively. The wide host range, the many eggs that a female is carrying and a relatively low probability of being killed by natural enemies due its hidden life stage and the absence of specialised predators and parasitoids justified a relatively high probability (p. 66).

5.4.5 Final output

The median number of founder populations was estimated to be 0.0001 per year (90% CR 0.000005–0.002). No outbreaks are known from the EU. Thus, field observations do not contradict the low number of populations expected.

5.5 Summary and conclusions

The Panel estimated the number of founder populations of *E. lignosellus* introduced each year through the import of asparagus spears from Peru. The pest arrives as larvae on the asparagus spears. It was estimated how many adults emerge from the spears and establish a founder population. The estimate was made using a model with the following components:

- import quantity of asparagus spears from Peru into the EU (in kg),
- inverse weight of a single asparagus spear (to calculate the number of imported spears as the volume of trade (in kg) divided by the weight of a single spear),
- proportion of infested spears entering the EU,
- proportion of infested spears imported to suitable NUTS 2 regions (two scenarios: current climate and climate change),
- proportion of asparagus spears disposed of as waste,
- probability of a discarded larva surviving to become an adult,
- probability that a female mates,
- probability of a mated female initiating a persisting founder population.

Conclusions of the evaluation

Structure of the model

- The model is considered accurate. The model probably includes a parameter for the proportion of females, which is correct but is not explicitly indicated in the qPRA.

Parameter estimations

- The Panel provided justifications for the different parameter estimates except for the "*probability of larvae surviving to develop to adulthood*".
- The infestation rate of asparagus (proportion of infested spears) from Peru may have been underestimated by more than a factor of 10. The estimate by the Panel was partly based on notified interceptions by EU Member States. Interceptions had mainly been notified by the UK, which notified the last interception on 1 March 2020. Therefore, the sharp decline in the number interceptions after 1 March 2020 may have (partly) been due to the withdrawal of the UK from the EU instead of the presumed decrease in infestation rate.
- BuRO considers the justification of the probability of mating to be incomplete. The model estimated a very low number of escaped adults per region per year, roughly less than 0.2. With such low numbers, the probability that a female will find a mate may even be lower than the value estimated in the qPRA (p=0.00081). The presence of more than one specimen in a consignment (clustering of specimens) may, however, increase the probability of mating. This possibility is not addressed in the qPRA. The probability of mating may also be higher due to a higher infestation rate than estimated in the qPRA.
- The trade volume of asparagus spears from Peru appears to have been (unintentionally) overestimated. This may have led to an overestimate of the number of founder populations by roughly 30%.

Uncertainties

- Uncertainties are addressed and clearly expressed in the conclusions and abstract of the qPRA.

Comparison of the final output with the number of known outbreaks

- The final output (median value of one founder population per 10,000 years) was not in contradiction to field observations in the EU (no outbreaks detected).

Other comments

- There are contradictory statements about the steps involved in 'transfer' and those involved in 'establishment', but this does not affect the output of the model.

6 Discussion and recommendations

6.1 Model structure and parameters

6.1.1 Number of infested units

An important difference between the three pathway models evaluated in the present study was the method used to estimate the number of infested (pathway) units arriving in the EU. In the qPRAs of *T. leucotreta* and *E. lignosellus*, this number was the product of the import volume (N_{trade}) and the estimated infestation rate (proportion of infested units) on arrival in the EU. However, the model in the qPRA of *C. sagittiferella* has a parameter for the infestation rate after harvest and another one for the proportion of infested units being removed by sorting in the exporting country. In this model, the number of infested pathway units at import is calculated as the product of the estimated infestation rate after harvest ($p_{prevalence}$), the estimated proportion of infested units that is not removed by sorting ($1-p_{sorting}$), and the import volume (N_{trade}). However, the product of the infestation rate after harvest and the proportion of infested units that is not removed by sorting should be multiplied by the number of units before sorting and not by the import volume to yield the number of infested pathway units at import. Alternatively, the number of infested units at import ($N_{pathways\text{-}units\text{-}inf}$) can be obtained by the formula (see section 4.3.2.2):

$$N_{pathway-units-inf} = N_{trade} \times \frac{p_{prevalence} \times (1 - p_{sorting})}{(1 - p_{prevalence} \times p_{sorting})}.$$

However, there may be a dependency between the infestation rate after harvest and the proportion of infested fruit that is removed in the country of origin as discussed in section 4.3.4.1. This dependency cannot be accounted for during elicitation of the parameter values like it has been done in qPRA of *C. sagittiferella* (see section 4.3.4.1). In addition, information on the infestation rate in the country of origin and the efficacy of sorting after harvest may be difficult to obtain. Without any solid data, estimates of infestation rates are highly uncertain and may vary considerably between risk assessors. For example, USDA (2020) and DAFF (2025) assumed that pomelo fruit (*Ci. maxima*) infested with *C. sagittiferella* is unlikely to be harvested. This assumption is supported by the lack of *C. sagittiferella* interceptions on pomelo fruits. Consequently, USDA (2020) and DAFF (2025) did not consider pomelo fruits from Vietnam as a pathway for *C. sagittiferella*. However, the Panel estimated the infestation rate of harvested citrus fruit to be 20% (median value). This infestation rate concerned all *Citrus* species but was mainly based on infestation rates of pomelo before harvest in Vietnam (p. 11 in the qPRA). For these reasons, the infestation rate can probably be more accurately estimated using interception data like in the qPRAs of *T. leucotreta* and *E. lignosellus* (see section 6.1.2).

6.1.2 Infestation rate based on interceptions

Interception data – including the lack of interceptions – may give the best indication for the infestation rate of the pathway units on arrival in the EU for pests that can be visually detected (see also section 6.1.1). Interception data were indeed used to inform the EKE in the qPRAs of *T. leucotreta* and *E. lignosellus*. However, different methods were used to calculate the infestation rate, which can yield significant differences in the results. (i.e. more than a factor 100, see section 3.4.3). BuRO examined other qPRAs of the Panel published in 2023 and 2024 (five in total) for calculation methods of infestation rates from interception data. The qPRAs of *Phlyctinus callosus, Resseliella citrifugis* and *Retithrips syriacus* did not include such calculations (no interception records were available for *P. callosus* and only one for *R. syriacus* on cuttings dating back to 1998) (EFSA Panel on Plant Health et al., 2023b; EFSA Panel on Plant Health et al., 2024a; EFSA Panel on Plant Health et al., 2024b). In the qPRA of *Leucinodes orbonalis,* the same method was used as in the qPRA of *E. lignosellus* (p. 67), whereas in the qPRA of African *Leucinodes* species a similar approach was used as in the qPRA of *T. leucotreta*. In the qPRA of African *Leucinodes* species, different infestation rates were also estimated for positively inspected consignments (256 out of

20,905 consignments inspected) and negatively inspected consignments[9] (Table C10 on p. 49). An important difference with the qPRA of *T. leucotreta* was that a Beta distribution (instead of a Uniform distribution) was used to describe the uncertainty for the infestation rate of the negatively inspected consignments. This Beta distribution assigned a higher probability to lower infestation rates which resulted in a lower infestation rate for the negatively inspected consignments than for the positively inspected consignments:

$$p_{\text{negatively inspected consignments}} = 27.8/10{,}000 = 0.00278,$$

$$p_{\text{positively inspected consignments}} = 67.3/10{,}000 = 0.00673.$$

The uncertainty distributions of both infestations rates were combined to one Beta distribution by 'weighted averaging compounding', which resulted in an overall infestation rate (median value) of:

$$p = 28.2/20{,}000 = 0.00282 \text{ (p. 51–52).}$$

However, this method still results in a much higher infestation rate than using the method applied in the qPRAs of *E. lignosellus* and *L. orbonalis*. Using that method, the infestation rate would be (256 interceptions out of 20,905 inspected consignments and a sample size of 248; p. 49–50):

$$p = -\ln(1-256/20{,}905)/248 \approx 0.0000497.$$

If the infestation rate (p) would be 0.00282 (calculated in the qPRA), you would expect an interception rate of:

$$P(k \geq 1) = 1 - (1-p)^n = 1 - (1 - 0.00282)^{248} \approx 0.504,$$

while the actual interception rate was only 0.0122. The actual interception rate may be lower than calculated from the infestation rate due to clustering of specimen in consignments (see section 3.4.3.2). However, the actual interception rate was so much lower that the infestation rate seems to be considerably overestimated.

BuRO is of the opinion that no difference should be made between positively and negatively inspected consignments to assess the average infestation rate unless there are good arguments to do so. Infestation rates of imported commodities will generally be low because of quality and/or phytosanitary reasons and samples may be positive or negative just by chance. Infested units may, however, be clustered in import samples which should be taken into account (see sections 3.4.3.2 and 3.4.3.3).

A total lack of interceptions can also be useful information for the estimation of the infestation rate. From information of the total number of consignments inspected (in recent years) and the sampling protocol (i.e. the number of units inspected per consignment), the total number of units inspected (n) (for a certain period) can be calculated. Subsequently, the detection limit (p) could be derived from the equation:

$$P(k = 0) = (1 - \phi p)^n \text{ (formula 4 in Appendix 3 of ISPM No. 31),}$$

where $P(k=0)$ is the probability of observing zero infested units and ϕ is the inspection or detection efficacy.

This binomial distribution equation can be approximated by the Poisson distribution equation to calculate the infestation rate:

$$P(k = 0) = e^{-n\phi p} \text{ (formula 8 in Appendix 3 of ISPM No. 31),}$$

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[9] Positively inspected consignments are consignments that after inspection were found to be infested with the relevant organism. Negatively inspected consignments are consignments that were also inspected but not found to be infested

which can be rewritten as:

$$p = -ln(P(k = 0))/n\phi.$$

Assuming that the detection efficacy is 100% or lower (e.g. 80%), the detection limit can be calculated (the infestation level above which the pest would be detected with a probability of for example more than 99%: P(k=0) = 0.01). The median value would be subsequently between zero and the detection limit. There may be reason to believe that the infestation rate will increase or decrease and in that case the infestation rate could be argued to be higher or lower than calculated based on historical data.

Interceptions may not have been notified (and not present in EU databases) because the pest was not a regulated pest (at that time). For example, the Netherlands has interception records of *C. sagittiferella* but did not notify them (see section 4.4.3). Thus, for non-regulated pests, Member States could be asked whether they have interception data that have not been notified.

6.1.3 Transfer

In EFSA's guidance, transfer is defined as "*the movement of a pest from an imported commodity to a place where the pest can establish*" referring to ISPM 11 (FAO, 2017). In the case of arthropod pests, it is not stated whether 'transfer' also includes mating and oviposition following escape of the pest from a transfer unit. In the qPRA of *C. sagittiferella*, transfer included mating and oviposition, while in the qPRA of *E. lignosellus* oviposition was part of establishment (although not in a consistent way throughout the document, see section 5.3). In the qPRA of *T. leucotreta* mating was part of transfer (p. 45-46). The probability of oviposition and establishment was not estimated for *T. leucotreta* and it was not explicitly indicated whether oviposition was part of 'entry' or 'establishment'. In a qPRA (and in PRAs in general), 'transfer' needs a clear definition that explicitly indicates which processes or steps are part of 'transfer' and which are part of 'establishment'. For the present discussion, 'transfer of an arthropod pest' is defined as the entire process from pest arrival to first egg laying following the definition in Van der Gaag et al. (2019). Thus, for non-viviparous arthropod pests arriving as immature stages, 'transfer' includes:

- the distribution of pathway/transfer units into suitable regions,
- the development into a mobile stage and escape from the pathway/transfer units,
- the movement to a host, mating (if needed for oviposition) and egg laying.

The probability that all of the subsequent steps described above will take place starting from a single transfer unit of cut flowers, fruits or vegetables may often be very low (i.e. less than 0.1%). This will especially be the case for pests where only a limited area within the EU has a suitable climate (with presence of host plants) and where the presence of a male and female are required before oviposition can take place. It may be very difficult to estimate such low probabilities without considering each 'transfer-step' separately. In the qPRA of C. *sagittiferella*, all steps are included in a single parameter and the estimated probability of transfer was relatively high compared to the estimated probabilities in the qPRAs of *T. leucotreta* and *E. lignosellus.* In these qPRAs, the probability of transfer was not calculated as such but the estimated probability of at least one of the 'transfer-steps' was already much lower than the probability of transfer estimated for *C. sagittiferella* (Table 11). A somewhat higher transfer rate may be expected for *C. sagittiferella* because of the larger transfer unit: a – potentially large – batch of fruit instead of a bunch of ten cut roses for *T. leucotreta* and only a single asparagus spear for *E. lignosellus*. However, the estimate was orders of magnitude higher than in the other qPRAs and Bayesian updating indeed suggests that the probability of transfer of C. *sagittiferella* has been considerably overestimated (Appendix E).

In the qPRAs of *T. leucotreta* and *E. lignosellus*, probabilities were estimated for different 'transfer-steps'. These steps are discussed below (sections 6.1.3.3 – 6.1.3.5) and estimates for the probabilities of the different 'steps' in each of the models are shown in Table 11. The importance of knowledge on the trade chain and the choice of the transfer unit (fixed or variable) are also discussed (sections 6.1.3.1 and 6.1.3.2).

6.1.3.1 Trade chain

Details on the trade chain of the commodity on which the pest may arrive in the PRA area are needed to estimate the probability of transfer. The commodity may for example be stored and transported under cooled conditions to maintain the quality of the product. Such conditions may not allow the development of the pest and hence transfer may only be possible from units that are discarded for quality reasons. Details on the temperatures during storage and transport of the commodity and the proportion of units that is discarded are indeed provided in the qPRA of *T. leucotreta* (p. 18-19). In the qPRA of *E. lignosellus*, transfer is assumed to be possible only from asparagus spears that are discarded by commercial operators (p. 64). In the qPRA of *C. sagittiferella* details on the trade chain are, however, lacking. It is stated for example that citrus packinghouses are often close to citrus orchards (p. 12). However, no evidence was provided that the imported fruit is going to such packinghouses. In fact, nearly all the fruits from countries where the pest is present are imported via EU Member States that do not grow citrus (section 4.4.4). Thus, detailed information on the trade chain is important to identify the compartments from which transfer may be possible and to estimate the probability of transfer as accurately as possible.

6.1.3.2 Transfer unit and disaggregation factor

The transfer units in the qPRAs of *T. leucotreta* (a bunch of 10 cut roses) and *E. lignosellus* (a single asparagus spear) were fixed whereas the transfer unit in the qPRA of *C. sagittiferella* was variable by the inclusion of a disaggregation factor (see section 4.2). This 'disaggregation factor' led to an inaccurate estimate of the number of (potential) founder populations. The product of the trade volume (expressed in number of pathway units) and the infestation rate provides the number of infested pathway units. When a pathway unit is divided into several subunits that can each act as a transfer unit, the infestation rate does not match anymore with the transfer unit and the model will not accurately estimate the number of founder populations (see section 4.3.2). In addition, the probability of transfer and the disaggregation factor are not independent. On average, larger transfer units will carry more specimens than smaller units, increasing the likelihood that at least one female and one male emerge at the same time and in the same location and mate. Thus, a disaggregation factor should not be included in the model as was done for *C. sagittiferella.* The same model has also been used in a qPRA for another citrus pest, *Resseliella citrifrugis* (EFSA Panel on Plant Health et al., 2023b), and this qPRA may also need reconsideration. Instead, the smallest possible unit, e.g. a single fruit, could be used as transfer unit. However, different situations may occur in the trade chain. For example, several infested units may end up in waste at locations where many units are sorted and packed while at a consumer's place not more than one or a few infested units may be present at the same time. Estimates of the proportions of infested units that end up in different compartments of a trade chain from which transfer is possible (e.g. from waste at packinghouses and retailers and from consumer's places) could be made based on data from literature as has been done in the qPRA of *E. lignosellus* or (if no such data are available) on expert judgement. Then, the probability that adults will emerge and mate may be estimated for each compartment. Some situations may be considered nonsignificant. For example, in the qPRA of *E. lignosellus* the probability of a male and female emerging from the same pack of asparagus at a consumer's place was considered to be 'unmeasurable' by the Panel and was not included in the model (p. 64). BuRO agrees with that choice.

6.1.3.3 Distribution of units into suitable regions

In the qPRA of *T. leucotreta*, the number of infested pathway units (cut roses) was calculated for each suitable region and the estimated number of escapes (adults) is presented per region (Fig. 20 on p. 41). The climatic suitability may differ between regions and this approach makes it possible to use different estimates for the probability of establishment (i.e. the probability that a potential founder population becomes a founder population (see also 6.1.4)). In the qPRA of *E. lignosellus* 'the proportion of spears that enter an area where the climate is suitable for establishment' is estimated but no difference is made between regions that are more suitable than others.

Table 11. Comparison of parameter estimates (median values) between three quantitative pathway models from the Panel on Plant Health of EFSA in which the number of mated females of *Thaumatotibia leucotreta* and the numbers of founder populations of *Citripestis sagittiferella* and *Elasmopalpus lignosellus* were estimated through the import of cut roses, citrus fruit and asparagus spears, respectively

Parameter	**Description**	***Thaumatotibia leucotreta* – cut roses**	***Citripestis sagittiferella* – citrus fruit**	***Elasmopalpus lignosellus* – asparagus spears**
$p_{prevalence\ at\ origin}$	Proportion of infested units after harvest	Not estimated	0.2	Not estimated
$1\text{-}p_{sorting}$	Proportion of infested units that is not removed in the country of origin	Not estimated	0.023	Not estimated
$p_{inf\text{-}at\text{-}import}$	Proportion of infested units on arrival in the risk assessment area	0.0021	0.0038[1,2]	0.000011
p_{clim}	Proportion of infested units entering an area where the climate is suitable for establishment	Not included[3]	0.01	0.164
p_{waste}	Proportion of units disposed of as waste	Not relevant (all cut roses are finally disposed of as waste)		0.1
$p_{mortality\ immature\ stages}$	Proportion of immature stages that survive	0.48		Not included
p_{adult}	Probability that a larva develops to adulthood and escapes	0.0005 – 1.00[4]		0.01
p_{mate}	Probability of mating	0.0023		0.0008
$p_{oviposition}$	Probability that a mated female will lay eggs (potential founder population)	Not estimated		0.3
$p_{establish}$	Probability that a potential founder population establishes (becomes a founder population)	Not estimated	0.7	
$p_{transfer+establish}$		Not estimated	0.011[2]	0.000000033[2]

[1] Calculated using the formula $p_{prevalence} \times (1\text{-}p_{sorting})$ as in the qPRA but the correct formula would be $p_{prevalence} \times (1\text{-}p_{sorting})/(1\text{-}p_{prevalence} \times p_{sorting})$ (see section 4.3.2.2).

[2] Calculated from the parameter estimates in the qPRAs (Appendices D.2 and F)

[3] Number of cut roses entering (a cluster of) countries climatically suitable was directly estimated from import and EU-internal trade data

[4] Depending on climate suitability, season and time between initial disposal and waste treatment (3–28 days) with the highest probabilities during summer and 28 days between disposal and waste treatment (excluding specimens that survive and escape the waste treatments).

6.1.3.4 Development into mobile stages

In general, the probability that an immature stage that is present on a pathway unit (cut flower, fruit or vegetable) develops into an adult is highly uncertain because of lack of empirical evidence as also stated in the qPRA of *E. lignosellus*. Factors that will affect the probability of development are:

- the development rate of the immature stages of the pest,
- the shelf life of the product,
- the ambient temperature during storage (and vase life of cut flowers) and after disposal (taking into account seasonal differences),
- the time between initial disposal and waste treatment.

These factors are explicitly taken into account in the qPRA of *T. leucotreta*. In the qPRA of *E. lignosellus* it is not clear whether all of these factors have been taken into account. In fact, it is not clear on which data or considerations the estimated '1%' for the probability that a larvae will develop into adulthood is based (see section 5.4.4).

6.1.3.5 Movement to a host, mating and oviposition

Both, *T. leucotreta* and *E. lignosellus* have a wide host range which increases the probability that the pest will find a host plant after it has escaped from the commodity on which it has arrived in the PRA area. *Citripestis sagittiferella* has a much smaller host range and is only known to infest *Citrus* spp. (EFSA Panel on Plant Health et al., 2021). The probability that the pest will escape from an infested citrus fruit close enough to a citrus tree was, however, not estimated separately but was part of the single parameter for transfer as discussed before.

Each of the three pests first needs to mate before oviposition can take place after arrival in the EU. The probability of the presence of a female and male at the same time may be lower for *T. leucotreta* and *E. lignosellus* than for *C. sagittiferella* because only one specimen is (likely) to be present per infested unit (a single cut rose or asparagus spear). Low probabilities have indeed been estimated for both species (Table 11) but the pathway model used for *C. sagittiferella* has no parameter for the probability of mating which makes comparison of parameter estimates not possible. For pests that can reproduce without mating the probability of transfer is generally considered higher than for pests that first need to find a mating partner.

The probability that a female will mate will depend on the number of adults that are present at the same time and in the same or nearby locations. A higher infestation rate and a higher probability that a larva develops into an adult will result in a higher number of adults and therefore a higher probability of mating. Hence, the probability of mating can only be estimated given the number of adults (see also sections 4.3.4.3 and 5.3). After mating the probability of oviposition is assessed to be relatively high provided that host plants are nearby (see also section 6.1.4).

6.1.4 Establishment

Once transfer has taken place, i.e. the pest has laid eggs on a host plant in a suitable region, the probability of establishment may be relatively high compared to the probability of transfer. On produce, arthropod pests usually arrive as immature stages. After arrival, the most critical steps (steps with the lowest probabilities) for introduction to occur are probably the development of these stages into adults and subsequent mating between males and females (for which at least one female and male adult need to emerge close to each other). This is also expressed by the relatively high probability for oviposition and establishment in the qPRA of *E. lignosellus* (Tabel 11).

Major uncertainties may exist about the suitability of the environmental conditions for establishment like in the qPRA of *C. sagittiferella.* However, a clear distinction should be made between the probability that the climate is suitable and the probability that a potential founder population becomes a founder population in a climatically suitable area (see section 4.4.5). The suitability of the environmental conditions may vary among regions as assessed in the qPRA of *T. leucotreta*. In such a case, different probabilities of establishment can be estimated depending on the climate suitability of the region. This approach has indeed been followed by the Panel in more recent qPRAs of the weevil *Phlyctinus callosus* and the thrips species *Retrithrips syriacus* (EFSA Panel on Plant Health et al., 2024a; EFSA Panel on Plant Health et al., 2024b).

6.2 Comparison with actual number of known outbreaks

A quantitative assessment of the probability of introduction has the great advantage over a qualitative assessment that the assessment is very clear about the number of outbreaks that can be expected. In fact, the present detailed evaluation was only possible because of the transparency that such a quantitative assessment provides. However, parameter values can be difficult to estimate due to lack of data. Therefore, it is important to perform what in statistics is usually referred to as *model checking* (Gelman et al., 2013). This process involves checking whether the final results - and where possible also intermediate results - present reasonable numbers. For example, the expected number of founder populations of *C. sagittiferella* due to the import of citrus fruit appeared to be very high considering the lack of known outbreaks and the volume of fruit that had already been imported at the time the qPRA was adopted (section 4.4.6). Apparently, this kind of information was not (sufficiently) taken into account. Also, the expected number of mated females of *T. leucotreta* seems very high (section 3.4.8). While unexpected model results may yet be correct, any model whose predictions have practical consequences should be subject to a detailed evaluation of how the predictions were generated. Roughly, the question is then whether it is more likely that the model – and hence any extreme predictions - are correct, or whether there is some kind of mistake in the model or its parameter estimates that leads to unjustified predictions. Therefore, it is recommended to always compare the expected number of founder populations calculated by the model with the number of outbreaks reported in the EU and also to compare the parameter estimates with those from other existing qPRAs.

6.3 Other statistical considerations

It was observed that some of the fitted distributions in the qPRAs show some undesirable behaviour (Appendix G). In addition, all of the models in the qPRAs evaluated here include parameters that are described as probabilities. In all of these models, these probabilities are multiplied with other model parameters to obtain the final estimated number of events (and uncertainties). In general, this approach is valid for proportions but not for probabilities. However, these issues had little impact on the final model output of the three qPRAs and are discussed in Appendix G.

6.4 Recommendations

The recommendations listed below are based on the evaluation of three quantitative pathway assessments (*T. leucotreta* – cut roses, *C. sagittiferella* – citrus fruit and *E. lignosellus* – asparagus spears). These assessments only include insect pests that arrive as immature stages on produce (cut flowers, fruits & vegetables) in the PRA area, need a mating partner for reproduction and can be visibly detected. Therefore, the recommendations are specifically aimed at such pest-pathway combinations. However, many of the recommendations may also be useful for other pests and pathways.

Definitions

- Clearly define the pathway unit and transfer unit and do not include a disaggregation factor like in the qPRA of *C. sagittiferella*, which causes a mismatch between the infestation rate and the transfer unit.
- Clearly define ‘transfer’ to make clear which steps are involved in transfer and which in establishment.

Infestation rate

- The infestation rate of pathway units may best be estimated on arrival in the EU based on interception data because of a potential dependency between the infestation rate at harvest and the percentage of units being removed before export to the EU. In addition, data on infestation rates in the country of origin may be difficult to get.
- Request interception data from EU Member States for non-regulated pests and for pests that have only recently been regulated, because these pests may have been intercepted without notification before they were regulated.
- A lack of interceptions can also be used to estimate the infestation rate for pests that can be visually detected, especially when this is based on data from EU Member States directly (rather than a lack of notifications).

- No difference should be made in infestation rate between positively and negatively inspected consignments unless there are good arguments to do so. Even then, the estimated infestation rate of positively inspected consignments should be at least as high as that of negatively inspected consignments.

Transfer

- Include a detailed description of the trade chain in the EU in qPRAs to identify those compartments from which transfer may be possible and to estimate the probability of transfer as accurately as possible.
- Take into account that the probability of transfer may differ between compartments in the trade chain depending on the number of adults that are expected to emerge at the same time and in the same location (or close enough for a female and male to find each other).
- Also take into account that the probability of mating (considered here to be part of 'transfer') for sexually reproducing insects may depend on the infestation rate.
- Estimate the probability of each 'transfer-step' (e.g. development into an adult, mating and oviposition) separately.

Establishment

- Make a clear distinction between the probability that a potential founder population becomes a founder population in an area suitable for establishment and the probability that an area is suitable for establishment.
- Different estimates of the probability of establishment could be made for different EU regions depending on the suitability of the environmental conditions in a region.

Final output

- Always compare the expected number of founder populations calculated by the model with the number of outbreaks reported in the EU and also compare the parameter estimates with those from other existing qPRAs.

General

- Use consistent methods aligned with EFSA guidance for qPRAs, and clearly indicate in the qPRA if any steps are omitted or assessed differently than outlined in the guidance.
- To avoid potential errors and the use of inappropriate methods, submit draft reports for external peer review by experts in PRA and statistics before publication. This is especially important given that EFSA outputs directly influence the EU Plant Health legislation.

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Appendix A *Thaumatotibia leucotreta*: number of mated females

A conceptual description of the simulation process was provided in the main text of the assessment (section 3.4.3). This appendix only contains the R code that was used to run the simulation. This code was run using R 3.4.3 and uses no additional packages.

```
# This notebook estimates the probability of a female Thaumatotibia moth being
# mated given the assumed (lack of) clustering, the NVWA interception data,
# the sex ratio and the estimated mortality.

# define random seed for reproducible results
roseseed <- 86928

# NVWA data and implied probabilities
ntot <- 217
n1 <- 167
n2 <- 32
n3 <- 18
p1 <- n1/ntot
p2 <- n2/ntot
p3 <- n3/ntot

# The simulation proper starts here

# Set random seed for reproducible results
# Please note that for reproducibility it is necessary to run all
# blocks in order and only once.
set.seed(roseseed)

# Generate the numbers of specimens in a sample of 400 flowers
samps <- runif(1e7)
simframe <- data.frame(rand = samps)
# at least one specimen (assumed)
simframe$nspec <- 1 * (simframe$rand > 0)
# two or more specimens
simframe$nspec <- simframe$nspec + 1 * (simframe$rand > p1)
# three specimens
simframe$nspec <- simframe$nspec + 1 * (simframe$rand > (p1 + p2))

# Simulate gender for each specimen, p_female = 2/3, p_male = 1 - 2/3 = 1/3
simframe$gen1 <- ifelse(runif(1e7) > (2/3), "m", "f")
simframe$gen2 <- ifelse(runif(1e7) > (2/3), "m", "f")
simframe$gen2[simframe$nspec == 1] <- NA
simframe$gen3 <- ifelse(runif(1e7) > (2/3), "m", "f")
simframe$gen3[simframe$nspec <= 2] <- NA
# for control purposes
head(simframe)

# Simulate mortality
s1 <- runif(1e7) < 0.48
simframe$surv1 <- NA
simframe$surv1[s1] <- simframe$gen1[s1]
s2 <- runif(1e7) < 0.48
simframe$surv2 <- NA
simframe$surv2[s2] <- simframe$gen2[s2]
s3 <- runif(1e7) < 0.48
simframe$surv3 <- NA
simframe$surv3[s3] <- simframe$gen3[s3]
```

```
# Check for presence of surviving males and females in the sample
simframe$malepresent <- apply(simframe[,c("surv1", "surv2", "surv3")] == "m",
                              1, any)
simframe$malepresent[is.na(simframe$malepresent)] <- FALSE
simframe$femalepresent <- apply(simframe[,c("surv1", "surv2", "surv3")] == "f",
                                1, any)
simframe$femalepresent[is.na(simframe$femalepresent)] <- FALSE

# Save simulation result (simulation takes a few minutes to run)
save('simframe', file = "simframe.rdata")

# Select only those samples with at least one surviving male AND
# at least one surviving female
subframe <- simframe[simframe$malepresent & simframe$femalepresent,]

# This function simulates drawing bunches of _size_ flowers from
# a sample of _x_ flowers, where tars contains the presence of surviving
# Thaumatotibia specimens in the sample.
# The function throws an error if the sample is not a multiple of the
# bunch size.
simbouquet <- function(x, size = 10, tars){
  if((x %% size) != 0){
    errorCondition("vector length is not a multiple of set size")
  } else {
    # Randomly distribute all roses over 10 columns
    mat <- matrix(sample(x, x), ncol = 10)
    # Count the number of Thaumatotibia specimens in each bunch
    res <- apply(matrix(mat %in% tars, ncol = 10), 1, sum)
    # Select only those bunches with more than one speciment
    res <- mat[res > 1,]
    # This is inelegant coding. The goal is just to return a vector
    # with the indices (1-3) of the individuals in any bunches
    # with more than one surviving Thaumatotibia specimen.
    res <- res[res <= 3]
    return(res)
  }
}

# Set up variables to contain the individuals in any bunch with
# more than one surviving Thaumatotibia specimen.
subframe$bunch1 <- NA
subframe$bunch2 <- NA
subframe$bunch3 <- NA

# Loop through all the remaining lines (i.e. all samples with at least one
# surviving male and at least one surviving female). This is not efficient
# but since this simulation shouldn't need to run often it would have taken
# more time than it's worth to write more efficient code.
for(k in 1:nrow(subframe)){
  tmp <- simbouquet(400, 10, which(!is.na(subframe[k,c("surv1", "surv2",
"surv3")])))
  subframe$bunch1[k] <- ifelse(1 %in% tmp, subframe$surv1[k],NA)
  subframe$bunch2[k] <- ifelse(2 %in% tmp, subframe$surv2[k],NA)
  subframe$bunch3[k] <- ifelse(3 %in% tmp, subframe$surv3[k],NA)
  if((k %% 1e4) == 0){
    print(k)
  }
}
```

```
# Check for presence of surviving males and females in _bunches_ from
# previously selected samples.
subframe$malepresent <- apply(subframe[,c("bunch1", "bunch2", "bunch3")] == "m",
1, any)
subframe$malepresent[is.na(subframe$malepresent)] <- FALSE
subframe$femalepresent <- apply(subframe[,c("bunch1", "bunch2", "bunch3")] ==
"f", 1, any)
subframe$femalepresent[is.na(subframe$femalepresent)] <- FALSE

# Save results (simulation takes a while to run, i.e. > 10 minutes)
save('subframe', file = "subframe.rdata")

# Select only bunches with at least one male and at least one female present
mateframe <- subframe[subframe$malepresent & subframe$femalepresent,]
# Count the total number of mated females (we assume all females in bunches
# which also contain a male are mated).
mateframe$sumfemales <- apply(mateframe[,c("bunch1", "bunch2", "bunch3")] == "f",
1, sum, na.rm = TRUE)

# Save results again
save('mateframe', file = "mateframe.rdata")

# Count the total number of moths in the simulation
totalmoths <- sum(!is.na(simframe$gen1)) + sum(!is.na(simframe$gen2)) +
sum(!is.na(simframe$gen3))

# Count the number of moths surviving to reproductive maturity
survmoths <- sum(!is.na(simframe$surv1)) + sum(!is.na(simframe$surv2)) +
sum(!is.na(simframe$surv3))

# Calculate the rate of mated females per total number of specimens
rate <- sum(mateframe$sumfemales)/totalmoths
rate
1/rate

# Calculate the rate of mated females per number of surviving moths
ratepersurv <- sum(mateframe$sumfemales)/survmoths
ratepersurv
1/ratepersurv
```

Appendix B *Thaumatotibia leucotreta*: percentage of infested roses

See section 3.4.3.1 for explanation of the calculation method

Parameter	Country					Source[1]
	Ethiopia	Kenya	Tanzania	Zambia	All countries	
Total number or imported roses (2018-2021)	3,131,614,781	8,102,745,879	100,421,039	369,129,734		Table A.71, qPRA
Number of inspected consignments (a)	175	19,779	767	246		Table A.76, qPRA
Sample size/consignment (b)	1,200	400	400	1,000		Table A.79, qPRA
Number of roses inspected (a × b)	210,000	7,911,600	306,800	246,000		Calculated (present evaluation)
Number of intercepted consignments (c)	8	136	30	16	190	Table A.76, qPRA
Proportion of interceptions with 1 specimen	77%	77%	77%	77%		Table A.73, qPRA
Proportion of interceptions with 2 specimens	15%	15%	15%	15%		Table A.73, qPRA
Proportion of interceptions with 3 specimens	8%	8%	8%	8%		Table A.73, qPRA
Total number of infested roses intercepted (d = 0.77 × c + 0.15 × 2 × c + 0.08 × 3 × c)[2]	10.48	178.16	39.3	20.96		Calculated (present evaluation)
Infestation rate within total import (× = d/(a×b) × 100%)	0.00499%	0.00225%	0.0128%	0.0085%	0.00327%[3]	Calculated (present evaluation)
Infestation rate within total import (y = median value in qPRA)	0.136%	0.394%	0.400%	0.164%	0.319%[3]	Table A.79, qPRA
Factor difference (y/x)	27	175	31	19	98	Calculated (present evaluation)

[1] qPRA: EFSA Panel on Plant Health et al. (2023a)

[2] assuming one specimen per rose like in the qPRA

[3] trade-weighted average

Appendix C *Citripestis sagittiferella*: dependency between parameters

C.1 Methods

To simulate dependencies between parameters, we first set up a covariance matrix. To this end, we start with a diagonal covariance matrix, i.e. a matrix with ones on the first diagonal and zeros for all other entries. The simulation in this section replaces the pair of zeros corresponding to the covariance between the variables of interest with a particular value of the correlation, e.g. -0.5 for a negative correlation of 0.5.

The covariance matrix is then used to generate random draws from a multivariate standard normal distribution (i.e. a multivariate normal distribution with mean 0 and standard deviation 1). This generates a set of variables with the desired correlations between each pair of parameters (i.e. 0 except for the pair of interest). These normally distributed values are then transformed into the target distribution by replacing each value with the value from the target distribution that has the same percentile rank. For example, for $p_{prevalence}$ a value of 1 corresponds to the 84.13th percentile. This would yield a value of 0.3604 for $p_{prevalence}$, i.e. the 84.13th percentile of a beta distribution with parameters $\alpha = 1.6517$ and $\beta = 5.9871$. Note that this transformation does not conserve the linear (Pearson) correlation between pairs of parameters, and therefore is not generally suitable for modeling a specific dependency between parameters. Here, however, the aim is just to demonstrate the effects of different levels of dependency on the model results and for this purpose the somewhat rough approximation suffices.

All simulations were performed using R 4.2.3 and the packages *tidyverse* (2.0.0), *ggplot2* (3.4.3), *PearsonDS* (1.2.2) and *mvtnorm* (1.2-3).

C.2 Proportion of infested fruit ($p_{prevalence}$) and proportion of infested fruit that is not removed by sorting ($1 - p_{sorting}$)

Random but correlated samples were drawn from the beta(1.6517, 5.9871) and the beta(31.328, 1.0500) distributions for $p_{prevalence}$ and $p_{sorting}$, respectively. For each draw, the value of $p_{prevalence}$ was multiplied with ($1 - p_{sorting}$), yielding the estimated proportion of infested fruit at import to the EU (Table C1). If there is no correlation between $p_{prevalence}$ and $p_{sorting}$ then the upper boundary of the 90%-uncertainty interval is about 100 times larger than the lower boundary. However, the text of the qPRA (p.22) suggests that there may be a positive correlation between $p_{prevalence}$ and $p_{sorting}$, with more effective sorting for higher prevalence. This implies a negative correlation between $p_{prevalence}$ and $1 - p_{sorting}$. As can be seen from Table C1, a positive correlation between $p_{prevalence}$ and $p_{sorting}$ is associated with decreased width of the uncertainty interval.

Table C1. Estimated proportion of infested fruit at import into the EU for different levels of correlation between $p_{prevalence}$ and $p_{sorting}$. Note that a negative correlation between $p_{prevalence}$ and $p_{sorting}$ implies a positive correlation between $p_{prevalence}$ and 1 - $p_{sorting}$, and vice versa.

Correlation	Median	5th percentile	95th percentile	Factor (95th/5th percentile)
-1	0.0045	0.000068	0.04544	667
-0.9	0.0044	0.000076	0.0432	570
-0.8	0.0043	0.000085	0.0410	485
-0.7	0.0043	0.000094	0.0388	411
-0.6	0.0042	0.000105	0.0366	348
-0.5	0.0041	0.000118	0.0345	293
-0.4	0.0041	0.000132	0.0325	246
-0.3	0.0040	0.000148	0.0304	206
-0.2	0.0039	0.000167	0.0284	171
-0.1	0.0039	0.000188	0.0265	141
0	0.0038	0.000213	0.0246	115
0.1	0.0038	0.000242	0.0227	94
0.2	0.0037	0.000275	0.0208	75
0.3	0.0037	0.000315	0.0190	60
0.4	0.0036	0.000362	0.0171	47
0.5	0.0036	0.000419	0.0153	37
0.6	0.0036	0.000487	0.0135	28
0.7	0.0036	0.000572	0.0117	21
0.8	0.0036	0.000673	0.0099	15
0.9	0.0036	0.000788	0.0079	10
1	0.0040	0.000900	0.0049	5

C.3 Probability of transfer and disaggregation factor

Random but correlated samples were drawn from the Pearson V(0.70603, 5.0632) and the beta(0.33251, 4.6503) distributions for d and $p_{transfer}$, respectively. For each draw, the value of d was multiplied with $p_{transfer}$, conceptually yielding the expected number of transfers from one ton of infested fruit (Table C2). If there is no correlation between d and $p_{transfer}$ then the upper boundary of the 90% uncertainty interval is almost 100,000 times larger than the lower boundary. The text of the qPRA (p.22-23) suggests that there might be a negative correlation between the disagreggation d and the probability of transfer $p_{transfer}$, so that a low disagreggation factor implies a higher probability of transfer. As can be seen from Table C2, such a negative correlation significantly decreases the width of the 90% uncertainty interval.

Table C2. Estimated proportion of infested fruit at import into the EU for different levels of correlation between $p_{prevalence}$ and $p_{sorting}$. Note that a negative correlation between $p_{prevalence}$ and $p_{sorting}$ implies a positive correlation between $p_{prevalence}$ and $1 - p_{sorting}$, and vice versa.

Correlation	Median	5th percentile	95th percentile	Factor (95th/5th percentile)
-1	0.267	0.00802	0.6	76
-0.9	0.271	0.00433	1.1	245
-0.8	0.272	0.00264	1.7	637
-0.7	0.274	0.00174	2.5	1459
-0.6	0.274	0.00120	3.6	3048
-0.5	0.274	0.00086	5.1	5918
-0.4	0.274	0.00063	6.9	10952
-0.3	0.274	0.00048	9.2	19118
-0.2	0.274	0.00037	11.9	32170
-0.1	0.274	0.00029	15.3	52592
0	0.273	0.00023	19.3	83200
0.1	0.273	0.00019	24.1	128155
0.2	0.272	0.00015	29.8	194770
0.3	0.272	0.00013	36.3	287620
0.4	0.271	0.00011	43.9	415912
0.5	0.271	0.00009	52.5	593146
0.6	0.270	0.00008	62.3	825791
0.7	0.269	0.00006	73.3	1139761
0.8	0.268	0.00006	85.9	1547489
0.9	0.267	0.00005	99.7	2061317
1	0.261	0.00004	115.9	2862224

C.4 Code to simulate from the qPRA model

This section provides the R code that was used to simulate from the qPRA model. Note that this code is also used for the simulations in appendix D.

```
# Load required packages.
library(tidyverse)
library(mvtnorm)
library(PearsonDS)
library(ggplot2)

# Define a single random seed for the simulations for reproducible results.
lemonseed <- 921084

# Set the number of simulations to run.
# This applies to each estimate, as it is used in the
# sim_from_qpramodel function.
nsim <- 1e6

# Functions

# Convenience function to insert the selected dependencies into the covariance
# matrix.
setup_covmat <- function(cp){
  covmat[2,1] <- cp$prevbytrade
  covmat[1,2] <- cp$prevbytrade
```

```
  covmat[1,3] <- cp$prevbysort
  covmat[3,1] <- cp$prevbysort

  covmat[4,5] <- cp$dbytrans
  covmat[5,4] <- cp$dbytrans

  covmat[5,6] <- cp$transbyest
  covmat[6,5] <- cp$transbyest
  return(covmat)
}


# Distribution parameters
# The values of these parameters come from the Citripestis qPRA.

# prevalence = beta distribution
prevpar1 <- 1.6517
prevpar2 <- 5.9871

# ntrade = scaled beta distribution
tradepar1 <- 2.3853
tradepar2 <- 1.5285
tradescale <- 20411

# psort = beta distribution
sortpar1 <- 31.328
sortpar2 <- 1.0500

# d = disaggregation = Pearson V distribution
dpar1 <- 0.70603
dpar2 <- 5.0632

# ptransfer = beta distribution
transpar1 <- 0.33251
transpar2 <- 4.6503

# pestablishment = beta distribution
estpar1 <- 1.0809
estpar2 <- 0.62036

# Set up the covariance matrix for simulation.

# Generate diagonal covariance matrix = no dependencies.
covmat <- diag(6)

nodependence <- list(prevbytrade = 0, prevbysort = 0, dbytrans = 0,
                     transbyest = 0)

covmat <- setup_covmat(cp = nodependence)

# This function does the actual simulation.
# Note that there are several different estimates which can be returned.
# Of course these estimates can also be calculated outside the function.
sim_from_qpramodel <- function(cx = covmat, estimate = NA){
  wingnut <- 9346
  set.seed(wingnut)
    # We first generate a multivariate normal distribution with the correct
```

```
    # covariance structure.
  y <- rmvnorm(nsim, sigma = cx)
  y <- data.frame(y)
  names(y) <- c("prevalence", "trade", "sorting", "disaggregation", "transfer",
"establishment")
    # This section transforms each of the normal distributions composing
    # the multivariate normal by assigning a value from the target distribution
    # that corresponds to the same percentile.
    # Note that given the non-linearity of the transformation this does not
    # retain the same (Pearson) correlations between variables, but since the
    # transformations are monotonic the direction of the relation is
    # still consistent.
  y$prevalence <- qbeta(pnorm(y$prevalence), prevpar1, prevpar2)
  y$trade <- tradescale * qbeta(pnorm(y$trade), tradepar1, tradepar2)
  y$sorting <- qbeta(pnorm(y$sorting), sortpar1, sortpar2)
  y$disaggregation <- qpearsonV(pnorm(y$disaggregation), shape = dpar1, location
= 0, scale = dpar2)
  y$disaggregation <- round(y$disaggregation)
  y$transfer <- qbeta(pnorm(y$transfer), transpar1, transpar2)
  y$establishment <- qbeta(pnorm(y$establishment), estpar1, estpar2)
  if(is.na(estimate)){
      y$estimate <- y$trade * y$prevalence * (1-y$sorting) * y$disaggregation *
y$transfer * y$establishment
  } else if(estimate == "prevbysort"){
      y$estimate <- y$prevalence * (1-y$sorting)
  } else if(estimate == "dbytrans"){
      y$estimate <- y$disaggregation * y$transfer
  }
  return(y)
}

# Simulate from the model without any dependencies.
set.seed(lemonseed)
y <- sim_from_qpramodel(cx = diag(6))

# Plot the distributions of the individual parameters and the estimate.
z <- reshape2::melt(y)
ggplot(data = z, aes(x = 1, y = value, fill = variable)) +
  geom_violin() + facet_wrap(. ~ variable, scales = "free_y")
```

C.5 Code to introduce dependency between parameters and evaluate results

This section provides the additional code that was used to simulate the effects of dependency between prevalence and sorting and between disaggregation and probability of transfer. Please refer to the previous section (C.4) for the code that was used to simulate the model in general, in particular the sim_from_qpramodel function that performs the simulation itself.

```
# This code simulates the estimates of combinations of parameters
# depending on the dependency (correlation) between those parameters
# in steps of 0.1 from perfect negative to perfect positive correlation.

# set dep2est to "prevbysort" to simulate the effects of dependency between
# prevalence and sorting, or to "dbytrans" to simulate the effects of
# dependency by the disaggregation factor d and p_transfer
dep2est <- "dbytrans"

corsteps <- seq(from = -1, to = 1, by = 0.1)
ra <- array(NA, c(length(corsteps), nsim))
set.seed(lemonseed)
for(k in 1:length(corsteps)){
```

```
  deppars <- nodependence
  if(dep2est == "prevbysort"){
      deppars$prevbysort <- corsteps[k]
      covmat <- setup_covmat(deppars)
  } else if(dep2est == "dbytrans"){
      deppars$dbytrans <- corsteps[k]
      covmat <- setup_covmat(deppars)
  }
  #print(covmat)
  tmp <- sim_from_qpramodel(cx = covmat, estimate = dep2est)
  ra[k, ] <- tmp$estimate
}

# Summarize the results
ps.df <- data.frame(cor = corsteps, yest = apply(ra, 1, quantile, 0.5),
                    ymin = apply(ra, 1, quantile, 0.05), ymax = apply(ra, 1,
quantile, 0.95))
ps.df$rangefactor <- ps.df$ymax/ps.df$ymin
#ps.df$rangefactor[11]/ps.df$rangefactor[8] # difference between correlation = 0
and correlation = -0.3
ps.df

# Plot the results
ggplot(data = ps.df, aes(x = cor, y = yest, ymin = ymin, ymax = ymax)) +
  geom_ribbon(alpha = 0.3) + geom_line() + scale_y_log10()
```

Appendix D *Citripestis sagittiferella*: infestation rate, probability of transfer and establishment

D.1 Calculation of the infestation rate at import

The estimated infestation rate at import $p_{\text{inf-at-import}}$ was obtained by Monte Carlo simulation using R 4.3.3. Independent samples from the fitted distributions for $p_{\text{prevalence}}$ (Fig.1 on p. 13) and p_{sorting} (Fig. 5 on p. 17) were generated using the method and code reported in appendix C. The values of $p_{\text{prevalence}}$ and p_{sorting} were pairwise multiplied according to the formula $p_{\text{inf-at-import}} = p_{\text{prevalence}} \times (1-p_{\text{sorting}})$ to obtain the estimated infestation rate at import. Note that this is the calculation used in the qPRA but the correct formula would be $p_{\text{inf-at-import}} = p_{\text{prevalence}} \times (1-p_{\text{sorting}})/(1-p_{\text{prevalence}} \times p_{\text{sorting}})$ (see section 4.3.2.2). Using the formula from the qPRA yields a median infestation rate of just under 0.4%, whereas the correct formula yields a median infestation rate of just under 0.5% (Table D1).

Table D1. Estimated proportion of infested fruit at import into the EU ($p_{\text{inf-at-import}}$).

Percentile	**1%**	**5%**	**25%**	**Median**	**75%**	**95%**	**99%**
$p_{\text{prevalence}} \times (1-p_{\text{sorting}})$	4.0×10^{-5}	2.1×10^{-4}	0.0014	0.0038	0.0090	0.025	0.044
$p_{\text{prevalence}} \times (1-p_{\text{sorting}})/(1-p_{\text{prevalence}} \times p_{\text{sorting}})$	4.5×10^{-5}	2.4×10^{-4}	0.0016	0.0048	0.0123	0.039	0.077

D.2 Calculation of the probability of transfer and establishment

The estimated probability that an infested batch leads to a founder population $p_{\text{transfer+establish}}$ was obtained by Monte Carlo simulation using R 4.3.3. Independent samples from the fitted distributions for p_{transfer} (Fig.7 on p. 19) and $p_{\text{establish}}$ (Fig. 14 on p. 27) were generated using the method and code reported in appendix C. The values of p_{transfer} and $p_{\text{establish}}$ were pairwise multiplied according to the formula $p_{\text{transfer+establish}} = p_{\text{transfer}} \times p_{\text{establish}}$ to obtain the estimated infestation rate at import. This yields a median of approximately one founder population per 100 batches and a 90% uncertainty interval of one founder population per 100,000 batches to one founder population per five batches (Table D2).

Table D2. Estimated probability of transfer and establishment from a single infested batch ($p_{\text{transfer+establish}}$).

Percentile	**1%**	**5%**	**25%**	**Median**	**75%**	**95%**	**99%**
$p_{\text{transfer}} \times p_{\text{establish}}$	7.3×10^{-8}	9.0×10^{-6}	0.0012	0.011	0.049	0.197	0.360

Appendix E *Citripestis sagittiferella*: Bayesian updating

E.1 Methods

The model – including the uncertainty distributions for each of the parameters – for the qPRA provides an uncertainty distribution for the total number of founder populations. Given (new) data regarding the number of founder populations, this uncertainty distribution can be used as a *prior estimate* which is then updated through the well-established procedure of Bayesian updating (McElreath, 2020) to provide a *posterior estimate*. This posterior estimate represents the new uncertainty distribution given both the prior estimate and the data.

Given the estimates of the lag period between establishment and spread and the spread rate in the qPRA itself (p. 30), an infestation prior to the year 2020 should have become manifest by the time the qPRA was performed. In other words, despite a total import of 27,289 tons of citrus fruit from the affected region in the years 2013-2019 (see section 4.4.6 of the report), no infestations occurred. BuRO uses this data point to update prior estimate and obtain a posterior estimate.[10]

Since both this Bayesian update and the evaluation of the effects of dependencies between parameters (appendix C) require simulation from the qPRA model, the Bayesian update also uses much of the same code. In particular, it uses the sim_from_qpramodel function defined in section C.4 and all of the preceding setup code. The difference between the simulations for appendix C and the simulations here lies in the covariance matrix used in the simulation step. All simulations in this appendix are based on a diagonal covariance matrix, i.e. a matrix with ones on the main diagonal and zeros for all other entries.

To obtain this posterior estimate, a slight modification to the model was made. While the text of the assessment describes $p_{transfer}$ and $p_{establishment}$ as probabilities, by multiplying them with the total number of (disaggregated) batches, it essentially treats them as proportions. This method works adequately for obtaining the *expectation*, i.e. the number of infestations that is expected on average, but it is not appropriate for assessing the *realization*, i.e. the actual number of infestations that may be expected to occur in a single year. In particular, by treating these probabilities as proportions the outcome of zero infestations is possible only if any of the parameters in the model is itself equal to 0 (or to 1, in the case of $p_{sorting}$). Therefore, the number of disaggregated batches was rounded up to an integer, and $p_{transfer}$ and $p_{establishment}$ were applied as probabilities to obtain the binomial likelihood of 0 infestations given

$$n = N_{trade} \times p_{prevalence} \times \left(1 - p_{sorting}\right) \times d$$

and

$$p = p_{transfer} \times p_{establishment},$$

where *n* is the total number of infested batches (i.e. the number of trials for the binomial distribution) and *p* is the probability of success for each trial (i.e. the probability that a single infested batch results in a founder population).

One million (1,000,000 or 1e6) draws were taken from the prior (i.e. for each parameter of the model) based on the distributions fitted in the qPRA. For each draw, the likelihood of 0 infestations was calculated as described above. Then, the sum of these likelihoods were normalized to 1 to bring them back to probability scale. Finally, the draws were ordered with respect to the estimate (or parameter) of interest and the cumulative probability was calculated. This allows to

---

[10] A strict interpretation may suggest that this lack of outbreaks over the period 2013–2019 is not in fact *new* data: the observation that there were no known outbreaks of *Citripestis sagittiferella* at the time the qPRA was performed could have been taken into account – implicitly or explicitly – in the estimates of each of the model parameters. However, if this observation *was* already taken into account in the estimates from the qPRA (again, implicitly or explicitly), then the implication is that the estimates would have been several orders of magnitude higher *without* this information. In other words, prior to consideration of the lack of observed outbreaks, the *median* estimate would have been in the order of thousands if not millions of founder populations per year.

(approximately[11]) determine any quantiles of interest of the cumulative probability function. These quantiles can then be compared to quantiles of the prior distribution. A large difference between the quantiles of the prior and those of the posterior distribution suggests that the prior estimate was not very accurate (though see footnote 3).

E.2 Results

When the posterior distribution evaluated with respect to the resulting estimate for a single year within the 2023–2033 temporal horizon of the assessment, very little agreement is observed between the model estimates and the posterior estimates (Table E1). The posterior estimates of the lower quantiles (including the median) are approximately two orders of magnitude smaller than the prior estimates. For the highest quantiles the difference is more than three orders of magnitude.

Table E1. Comparison of prior and posterior estimates of the number of founder populations for a single year within the 2023-2033 temporal horizon of the assessment.

Quantile:	**1%**	**5%**	**25%**	**Median**	**75%**	**95%**	**99%**
Prior estimate[12]	1.7×10^{-5}	2.3×10^{-3}	0.36	4.8	41	770	7,900
Posterior estimate	2.3×10^{-7}	2.8×10^{-5}	3.6×10^{-3}	3.3×10^{-2}	0.14	0.61	1.26

In addition to the total estimate, the same procedure can be performed with regard to each of the model parameters (except for N_{trade} because this is set to a fixed value in the simulation). For the prevalence *of C. sagittiferella* at the origin no major differences are observed between the prior and the posterior (Table E2).

Table E2. Comparison of elicited and posterior estimates of the prevalence at origin ($p_{prevalence}$).

Quantile:	**1%**	**25%**	**Median**	**75%**	**99%**
Elicited estimate	1%	10%	20%	30%	50%
Posterior estimate	0.7%	8.0%	15.6%	26.1%	58.3%

The posterior estimates of the effectiveness of sorting of infected fruit before import into the EU (at the packinghouse or at the border suggest a slightly more optimistic value for this parameter than the elicited estimates, but the differences are not large (Table E3).

Table E3. Comparison of elicited and posterior estimates proportion of infested citrus fruit removed from trade due to sorting.

	Quantile:	**1%**	**25%**	**Median**	**75%**	**99%**
$p_{sorting}$	Elicited estimate	0.838	0.954	0.977	0.990	0.999
	Posterior estimate	0.880	0.968	0.985	0.995	1.000
$1 - p_{sorting}$	Elicited estimate	0.162	0.046	0.023	0.01	0.001
	Posterior estimate	0.120	0.033	0.015	0.005	1×10^{-4}

The disaggregation factor is the first model parameter for which a systematic shift is observed between the elicited quantiles and the posterior quantiles (Table E4). All quantiles are of the posterior are lower than the corresponding elicited quantiles. Note also that the 95th percentile of the posterior (not given in Table E4) is only 92, which is less than twice as much as the elicited 75th percentile, while the 75th percentile of the posterior is 17 or about one third of the elicited 75th percentile.

Table E4. Comparison of elicited and posterior estimates of the disaggregation factor (*d*) for citrus fruit.

Quantile:	**1%**	**25%**	**Median**	**75%**	**99%**
Elicited estimate	1	6	10	50	500
Posterior estimate	0	3	7	17	435

---

[11] In this implementation the cumulative probability distribution is discrete and therefore does not allow determination of the exact quantiles. However, given the number of samples the discretization steps are small enough that this should not lead to meaningful distortions of the quantile estimates.

[12] Taken from Table 18 on p. 27 of the qPRA, as well as Figure 15 on p. 28 of the qPRA.

For the probability of transfer ($p_{transfer}$), the difference between the elicited quantiles and the posterior quantiles is particularly large (Table E5). Note in particular the median of the posterior is 25 times smaller than the elicited median and also smaller than the elicited 25th percentile. Similarly, the 75th percentile of the posterior is approximately 30 times smaller than the elicited 75th percentile and smaller than the elicited median.

Table E5. Comparison of elicited and posterior estimates of the probability of transfer ($p_{transfer}$) for citrus fruit.

Quantile:	1%	25%	Median	75%	99%
Elicited estimate	0	0.007	0.01	0.10	0.33
Posterior estimate	0	0	4×10^{-4}	0.003	0.14

Finally, for the probability of establishment the posterior quantiles are systematically lower than the elicited quantiles but the difference is not large (Table E6). The exception is the first percentile but this is due to the fact that the elicited value is 0, whereas the beta-distribution that was fit to the elicited quantiles does not allow an exact value of 0.

Table E6. Comparison of elicited and posterior estimates of the probability of establishment ($p_{establishment}$) for citrus fruit.

Quantile:	1%	25%	Median	75%	99%
Elicited estimate	0	0.4	0.7	0.9	1
Posterior estimate	0.008	0.28	0.60	0.86	1.000

In summary, the posterior estimates suggest that the model overestimates the number of founder populations by (at least) two orders of magnitude. The updated posterior suggests that the major cause of the overestimate is that the elicited quantiles of the probability of transfer ($p_{transfer}$) are too high.

E.3 Code for Bayesian updating

This section provides the R code that was used to perform the actual Bayesian updating. Note that this code assumes that model simulations are already available in a data frame called "y" as produced by the code in section C.4.

```r
# Bayesian updating of the qPRA estimate with the datapoint that there
# have been no infestations in the period from 2013-2018.

# Functions

# Function to calculate the cumulative log sum of a vector of small (log)
# probabilities with improved precision (log(cumsum(exp(x))) is imprecise
# for very small values in x.
log_cumsum_exp <- function(x){
  max.x <- max(x)
  return(max.x + log(cumsum(exp(x - max.x))))
}

# Set trade volume 2013-2018.
tradevolume2018 <- 27289

# Simulate batches for the 2013-2018 total trade volumes
# (using model parameters).
y$batches2018 <- tradevolume2018 * y$prevalence * (1 - y$sorting) *
    y$disaggregation

# Simulate the probability of infestation from p_transfer and p_establishment.
# This code actually implements this as a single probability rather than
# the proportions used in the report (note that the report actually defines
```

```
# p_transfer and p_establishment as probabilities but treats them as
# proportions in the model formula).
# This is required to allow for a substantial possibility of 0 infestations,
# since otherwise N_est == 0 only if:
# N_batches == 0 | p_transfer == 0 | p_establishment == 0
# Given that p_transfer and p_establishment are drawn from a beta distribution
# which has support 0 < x < 1, this means that the model effectively only
# allows N_est == 0 for disaggregation d == 0.
y$pinf <- y$transfer * y$establishment

# Calculate the log probability of ZERO infestations given the number of
# batches and the total probability of infestation per batch.
# Note that this probability is (1-p_inf)^N_batches =
# N_batches * log(1-p_inf)
y$log_pnoinf2018 <- y$batches2018 * log1p(-y$pinf)

# Calculate the expected number of infestations for 2013-2018 given the number
# of batches
# and p_inf
y$est2018 <- y$batches2018 * y$pinf

# Order all simulations (= sets of draws from the parameter uncertainty
# distributions) by their predicted number of infestations for the
# period 2013-2018.
y <- y[order(y$est2018, y$batches2018),]

# Calculate the cumulative (log) sum of the log probabilities.
y$cumlogsum <- log_cumsum_exp(y$log_pnoinf2018)
# Normalize and revert to raw probability scale.
y$cumprob <- exp(y$cumlogsum - max(y$cumlogsum))

# Calculate the estimated number of infestations for a year in 2023-2032
# period at which the qPRA is aimed.
y$est2028 <- y$trade * y$prevalence * (1-y$sorting) * y$disaggregation *
    y$transfer * y$establishment

# This function calculates the marginal posterior distribution based on the
# single data point "ZERO infestations in the period 2013-2018 with
# trade volume of 27,289 tons".
# The calculations relating directly to this data point are in the main
# code and not inside this function. The function therefore assumes that
# the dataframe supplied as _dx_ contains a variable "log_pnoinf2018".
calc_posterior <- function(dx = y, var = "est2028", supvar = "trade",
                           minval = 0, maxval = 1, prob = c(0.05, 0.5, 0.95)){
    # Correct the ends of the support of the probability distribution.
    # This assumes a support to -Inf respectively +Inf if the values in
    # dx[,var] are outside the given range.
    if(minval > min(dx[,var])){
        minval <- -Inf
    }
    if(maxval < max(dx[,var])){
        maxval <- Inf
    }

    # Check that var and supvar refer to different columns
    # Then sort by var (ascending) with supvar as tiebreaker
    if(var != supvar){
        dx <- dx[order(dx[,var], dx[,supvar]), ]
```

```
    }
    dx$index <- 1:nrow(dx)

    # Calculate the cumulative (log) sum of the log probabilities.
    dx$cumlogsum <- log_cumsum_exp(dx$log_pnoinf2018)
    # Normalize and revert to raw probability scale.
    dx$cumprob <- exp(dx$cumlogsum - max(dx$cumlogsum))

    # Remove duplicates in the CDF (dx$cumprob), retaining the max value.
    dx <- dx[order(dx$cumprob, dx[,var], dx[, supvar], decreasing = TRUE),]
    dx <- dx[!duplicated(dx[,var]),]

    # Resort in ascending order
    dx <- dx[order(dx[,var], dx[,supvar]), ]

    dz <- c()
    for(k in 1:length(prob)){
        if(prob[k] < 0.5){
            dz <- c(dz, max(dx[dx$cumprob < prob[k],var]))
        } else {
            dz <- c(dz, min(dx[dx$cumprob >= prob[k], var]))
        }
    }
    names(dz) <- as.character(prob)

    return(list(dx = dx, dz = dz))
}

set.seed(lemonseed)
z <- y
#z[order(z$est2028),]
posterior_est2028 <- calc_posterior(dx = z, var = "est2028", prob = c(0.01, 0.05,
0.25, 0.5, 0.75, 0.95, 0.99))
posterior_est2028$dz

posterior_prevalence <- calc_posterior(dx = z, var = "prevalence", supvar =
"trade", prob = c(0.01, 0.05, 0.25, 0.5, 0.75, 0.95, 0.99))
round(posterior_prevalence$dz, 4)

posterior_trade <- calc_posterior(dx = z, var = "trade", supvar = "est2028", prob
= c(0.01, 0.05, 0.25, 0.5, 0.75, 0.95, 0.99))
round(posterior_trade$dz)

posterior_sorting <- calc_posterior(dx = z, var = "sorting", supvar = "est2028",
prob = c(0.01, 0.05, 0.25, 0.5, 0.75, 0.95, 0.99))
round(posterior_sorting$dz, 4)
round(1-posterior_sorting$dz, 4)
1-c(0.838, 0.954, 0.977, 0.990, 0.999)

posterior_disaggregation <- calc_posterior(dx = z, var = "disaggregation", supvar
= "est2028", prob = c(0.01, 0.05, 0.25, 0.5, 0.75, 0.95, 0.99))
posterior_disaggregation$dz

posterior_transfer <- calc_posterior(dx = z, var = "transfer", supvar =
"est2028", prob = c(0.01, 0.05, 0.25, 0.5, 0.75, 0.95, 0.99))
round(posterior_transfer$dz, 4)
```

```
posterior_establishment <- calc_posterior(dx = z, var = "establishment", supvar =
"est2028", prob = c(0.01, 0.05, 0.25, 0.5, 0.75, 0.95, 0.99))
round(posterior_establishment$dz, 4)

ggplot(data = posterior_est2028$dx, aes(x = est2028, y = 1-cumprob)) +
    geom_line(color = 4) +
    geom_line(aes(y = 1-index/nsim), color = 5) +
    scale_x_log10(limits = c(1e-10,1e6))
```

Appendix F *Elasmopalpus lignosellus*: probability of transfer and establishment

F.1 Sex ratio

BuRO attempted to replicate the results shown in Table 4 on p. 29 of the qPRA of *Elasmopalpus lignosellus*. The replicated estimates were obtained by Monte Carlo simulation using R 4.2.3. Independent samples were drawn from the fitted distributions for each of the model parameters. For each draw the resulting values were multiplied according to the model structure to calculate the respective quantity of interest, using the fixed values of p_{clim} and p_{waste} as given in Table F1 where appropriate.

Table F1. Data source of the parameter estimates in the qPRA of *Elasmopalpus lignosellus* (qPRA).

Parameter	Description	Data source in the qPRA
V_{trade}	Mean annual import of fresh asparagus from Peru into the EU (kg)	Table C.2, p. 48
W_{spear}	Mean weight of an asparagus spear (kg)	0.026 (constant value, Paragraph C.2, p. 48)
P_{inf}	Estimated mean number of asparagus spears infested with *E. lignosellus* when entering the EU (per 10,000 spears)	Table C.3, p. 51
p_{clim}	Proportion of infested spears entering an area where the climate is suitable for establishment (defined as NUTS 2 regions where EI ≥ 30)	0.1643 (constant value, Table D.2, p. 63)
p_{waste}	Proportion of asparagus spears disposed of as waste	0.1 (constant value, p. 64)
p_{adult}	Probability that a larva developes to adulthood and escapes from discarded waste	Table D.4, p. 65
p_{female}	The probability that an adult is a female	0.5 (constant value, imputed by BuRO)
p_{mate}	Probability of mating	Table D.5, p. 66
$P_{founder}$	Probability that a mated female will establish a founder population	Table D.6, p. 66

Tables F2 to F10 compare the results from the BuRO simulation to the results in Table 4 on p. 29 of the qPRA. As can be seen from Tables F2-F5, the results of the BuRO simulation for number of infested spears entering the EU; number of infested spears in suitable climatic regions; number of discarded infested spears in areas suitable for establishment[13]; and number of emerged adults in risk areas closely match the results reported in Table 4 of the qPRA. However, the BuRO simulation results for number of mated females in risk areas (Table F6) and number of founder populations in EU per year (Table F7) are systematically about 100% higher than those reported in Table 4 of the qPRA. This is almost certainly due to the inclusion of an unreported parameter p_{female} (the probability that an adult is a female) in the qPRA model, as demonstrated by the fact that including such a parameter in the BuRO simulations again produces results that closely matches the results reported in Table 4 of the qPRA (Tables F8 and F9).

Table F2. Comparison of BuRO simulation results with results reported in Table 4 on p. 29 of the qPRA for the number of infested spears entering the EU.

Percentile	1%	5%	25%	50%	75%	95%	99%
qPRA	567	1259	3919	8606	18839	58486	127605
BuRO simulation	572	1267	3931	8643	19017	58688	129620
Difference (%)	0.9%	0.6%	0.3%	0.4%	0.9%	0.3%	1.6%

---

[13] There is a large difference in 50th percentile for this quantity, but this is clearly due to a clerical error in Table 4, since the value reported there is smaller than the value reported for the 25th percentile. The correct value would be 141 (0.1 * 1414, as reported for the previous step) which is nearly identical to the value of 142 obtained by BuRO.

Table F3. Comparison of BuRO simulation results with results reported in Table 4 on p. 29 of the qPRA for the number of infested spears in suitable climatic regions[14].

Percentile	**1%**	**5%**	**25%**	**50%**	**75%**	**95%**	**99%**
qPRA	93	207	644	1414	3096	9611	20969
BuRO simulation	94	208	646	1420	3124	9642	21297
Difference (%)	1.1%	0.5%	0.3%	0.4%	0.9%	0.3%	1.6%

Table F4. Comparison of BuRO simulation results with results reported in Table 4 on p. 29 of the qPRA for the number of discarded infested spears in areas suitable for establishment.

Percentile	**1%**	**5%**	**25%**	**50%**	**75%**	**95%**	**99%**
qPRA	9.3	20.7	64.4	141[15]	309.6	961.1	2096.9
BuRO simulation	9.4	20.8	64.6	142	312.4	964.2	2129.7
Difference (%)	1.1%	0.5%	0.3%	0.7%	0.9%	0.3%	1.6%

Table F5. Comparison of BuRO simulation results with results reported in Table 4 on p. 29 of the qPRA for the number of emerged adults in risk areas.

Percentile	**1%**	**5%**	**25%**	**50%**	**75%**	**95%**	**99%**
qPRA	0.03	0.09	0.45	1.43	4.21	16.7	40.6
BuRO simulation	0.03	0.09	0.46	1.44	4.2	17.12	43.15
Difference (%)	0.0%	0.0%	2.2%	0.7%	-0.2%	2.5%	6.3%

Table F6. Comparison of BuRO simulation results with results reported in Table 4 on p. 29 of the qPRA for the number of mated females in risk areas.

Percentile	1%	5%	25%	50%	75%	95%	99%
qPRA	0.00001	0.00002	0.00015	0.00052	0.00163	0.0075	0.01982
BuRO simulation	0.00001	0.00005	0.00030	0.00103	0.00330	0.01520	0.04143
Difference (%)	0.0%	150.0%	100.0%	98.1%	102.5%	102.7%	109.0%

Table F7. Comparison of BuRO simulation results with results reported in Table 4 on p. 29 of the qPRA for the number of founder populations in the EU per year.

Percentile	**1%**	**5%**	**25%**	**50%**	**75%**	**95%**	**99%**
qPRA	0.000001	0.000005	0.000036	0.000133	0.000447	0.002219	0.006242
BuRO simulation	0.000003	0.000010	0.000072	0.000265	0.000904	0.004519	0.012893
Difference (%)	200.0%	100.0%	100.0%	99.2%	102.2%	103.7%	106.6%

Table F8. Comparison of adjusted BuRO simulation results after inclusion of a p_{female} parameter with results reported in Table 4 on p. 29 of the qPRA for the number of mated females in risk areas.

Percentile	**1%**	**5%**	**25%**	**50%**	**75%**	**95%**	**99%**
qPRA	0.00001	0.00002	0.00015	0.00052	0.00163	0.0075	0.01982
Adjusted BuRO simulation	0.00001	0.00002	0.00015	0.00051	0.00165	0.00760	0.02071
Difference (%)	0.0%	0.0%	0.0%	-1.9%	1.2%	1.3%	4.5%

---

[14] In Table 4 on p. 29 of the qPRA, three different terms are used to indicate areas/regions that are suitable for establishment of the pest ('suitable climatic regions', 'areas suitable for establishment' and 'risk areas'); for ease of comparison of the results in Table 4 (p. 29 in the qPRA) and the BuRO simulation results, the terms used Tables F3 – F11 correspond to their use in Table 4 in the qPRA.

[15] The qPRA lists this number as 14.1 but this must be a clerical error because this value is inconsistent with the other numbers in the table.

Table F9. Comparison of adjusted BuRO simulation results after inclusion of a p_{female} parameter with results reported in Table 4 on p. 29 of the qPRA for the number of founder populations in the EU per year.

Percentile	**1%**	**5%**	**25%**	**50%**	**75%**	**95%**	**99%**
qPRA	0.000001	0.000005	0.000036	0.000133	0.000447	0.002219	0.006242
BuRO simulation	0.000001	0.000005	0.000036	0.000133	0.000452	0.00226	0.006447
Difference (%)	0.0%	0.0%	0.0%	0.0%	1.1%	1.8%	3.3%

In addition, the method used in the qPRA effectively treats the probabilities p_{adult}, p_{mate}, p_{mate} and $p_{founder}$ as proportions (see appendix G for a more extensive discussion). If we simulate from the model using these parameters as true probabilities rather than proportions, we obtain somewhat different results (Table F10–F12). In particular, we see that for an individual year the 90% uncertainty interval for the number of founder populations in the EU becomes 0 to 0.[16]

Table F10. Comparison of BuRO simulation results using probabilistic simulation with results reported in Table 4 on p. 29 of the qPRA for number of emerged adults in risk areas.

Percentile	**1%**	**5%**	**25%**	**50%**	**75%**	**95%**	**99%**
qPRA	0.03	0.09	0.45	1.43	4.21	16.7	40.6
BuRO with probabilities	0	0	0	1	4	18	44
Difference (%)	-100.0%	-100.0%	-100.0%	-30.1%	-5.0%	7.8%	8.4%

Table F11. Comparison of BuRO simulation results using probabilistic simulation with results reported in Table 4 on p. 29 of the qPRA for number of mated females in risk areas.

Percentile	**1%**	**5%**	**25%**	**50%**	**75%**	**95%**	**99%**
qPRA	0.00001	0.00002	0.00015	0.00052	0.00163	0.0075	0.01982
BuRO with probabilities	0	0	0	0	0	0	0
Difference (%)	-100.0%	-100.0%	-100.0%	-100.0%	-100.0%	-100.0%	-100.0%

Table F12. Comparison of BuRO simulation results using probabilistic simulation with results reported in Table 4 on p. 29 of the qPRA for number of founder populations in the EU per year.

Percentile	**1%**	**5%**	**25%**	**50%**	**75%**	**95%**	**99%**
qPRA	0.000001	0.000005	0.000036	0.000133	0.000447	0.002219	0.006242
BuRO with probabilities	0	0	0	0	0	0	0
Difference (%)	-100.0%	-100.0%	-100.0%	-100.0%	-100.0%	-100.0%	-100.0%

F.2 Probability of transfer and establishment

The probability of transfer and establishment ($p_{transfer+establish} = p_{clim} \times p_{waste} \times p_{adult} \times p_{mate} \times p_{founder}$) was calculated using the simulations performed section F.1 above. Please refer to Table F.1 for the sources of these distributions.

We find a median estimate for $p_{transfer+establish}$ of 3.3×10^{-8} with a 90% uncertainty range of 2.3×10^{-9} to 2.3×10^{-7} (Table F13).

---

[16] In fact this remains the case if we extend the simulation to the 17-year time horizon of the qPRA with current climate.

Table F13. Estimated probability of transfer and establishment from a single infested asparagus spear imported into the EU ($p_{transfer}+_{establish}$).

Percentile	1%	5%	25%	Median	75%	95%	99%
$p_{transfer}$ x $p_{establish}$	6.8×10^{-10}	2.3×10^{-9}	1.1×10^{-8}	3.3×10^{-8}	8.5×10^{-8}	2.3×10^{-7}	3.9×10^{-7}

F.3 Simulation code

This section provides the code used to simulate from the fitted distributions for all parameters and to calculate both the quantities of interest reported in section F.1 as well as the estimated value of $p_{transfer}+_{establish}$ Reported in section F.2.

```
# Define a single random seed for the simulations for reproducible results.
maizecorn <- 86750

# Set the number of simulations to run.
nsim <- 1e6

# Define quantiles of interest
qoi <- c(0.01, 0.05, 0.25, 0.5, 0.75, 0.95, 0.99)

# reference quantiles from fitted distributions
refqoi <- data.frame(quantile = qoi,
    ntrade = c(15760241, 1739 # reference quantiles from fitted distributions
refqoi <- data.frame(quantile = qoi,
    ntrade = c(15760241, 17394737, 19722267, 21339494, 22956942, 25283332,
               26916988),
    pinf = c(0.0071, 0.016, 0.049, 0.11, 0.23, 0.72, 1.6),
    padult = c(0.10, 0.12, 0.42, 1.2, 2.4, 4.2, 5.0),
    pmate = c(0.0071, 0.018, 0.049, 0.081, 0.12, 0.17, 0.20),
    pfounder = c(3.02, 7.64, 19.7, 30.3, 39.8, 48.0, 50.1)) 4737, 19722267,
21339494, 22956942, 25283332,
               26916988),
    pinf = c(0.0071, 0.016, 0.049, 0.11, 0.23, 0.72, 1.6),
    padult = c(0.10, 0.12, 0.42, 1.2, 2.4, 4.2, 5.0),
    pmate = c(0.0071, 0.018, 0.049, 0.081, 0.12, 0.17, 0.20),
    pfounder = c(3.02, 7.64, 19.7, 30.3, 39.8, 48.0, 50.1))

# Distribution parameters
# The values of these parameters come from the Elasmopalpus qPRA.

# Mean annual import of fresh asparagus from Peru into EU (kg)
# ntrade = normal distribution
tradepar1 <- 21339712
tradepar2 <- 2398003

# (average) weight of a single asparagus spear, in kg
spearweight <- 0.026

# Estimated mean number of asparagus spears infested with E. lignosellus when
# entering the EU (per 10,000 spears).
# pinf = lognormal distribution
infraw1 <- 0.20823
infraw2 <- 0.35138
# the qPRA uses an uncommon parametrization of the lognormal distribution,
# i.e. parametrized by the mean and standard deviation on the response scale,
# as opposed to e.g. the more commonly used parametrization by mean and
# standard deviation on the log scale used by rlnorm in R.
```

```
# We recalculate the parameters to match the parametrization in rlnorm:
infpar1 <- log(infraw1^2 / (sqrt(infraw1^2 + infraw2^2)))
infpar2 <- sqrt(log(1 + infraw2^2 / infraw1^2))
round(infpar1, 6) # should be -2.242827
round(infpar2, 6) # should be 1.160789

# Proportion of infested spears entering an area where the climate is suitable
# for establishment (defined as NUTS 2 regions where EI ≥ 30)
# A constant value is chosen for this proportion (Table D.2 on p.63)
pclim <- 0.1643

# Proportion of asparagus spears disposed of as waste
# A constant value is chosen for this proportion (p.64)
pwaste <- 0.1

# Probability that a larva developes to adulthood and escapes from
# discarded waste
# padult = scaled beta distribution
adultpar1 <- 0.62255
adultpar2 <- 1.7287
adultmin <- 0.00099
adultmax <- 0.0555

# Probability that an adult is a female
# A constant value of 0.5 is imputed for this probability
pfemale <- 0.5

# Probability of mating
# pmate = scaled beta distribution
matepar1 <- 1.8097
matepar2 <- 3.2291
matemin <- 0
matemax <- 0.0024

# Probability that a mated female will establish a founder population
# pfounder = scaled beta distribution
founderpar1 <- 1.7529
founderpar2 <- 1.2895
foundermin <- 0
foundermax <- 0.51

set.seed(maizecorn)
ntrade <- rnorm(nsim, tradepar1, tradepar2)
pinf <- rlnorm(nsim, infpar1, infpar2)
padult <- adultmin + rbeta(nsim, adultpar1, adultpar2) * (adultmax - adultmin)
pmate <- matemin + rbeta(nsim, matepar1, matepar2) * (matemax - matemin)
pfounder <- foundermin + rbeta(nsim, founderpar1, founderpar2) *
    (foundermax - foundermin)

# Check that distribution percentiles match the fitted values from the qPRA.
# In all cases deviations are minor, with the largest deviations showing
# up for pinf. However, those deviations appear to be due to the limited
# number of significant digits reported in the qPRA, as all percentiles except
# the 75th exactly match those in the qPRA when rounded to the same number
# of digits (the 75th percentile is 0.72 in the qPRA but 0.714 here when
# rounded to three significant digits).
# deviations are expressed as a percentage of the value reported in the qPRA
round(100 * (refqoi$ntrade - quantile(ntrade, qoi))/refqoi$ntrade, 3)
```

```
round(100 * (refqoi$pinf - quantile(pinf, qoi))/refqoi$pinf, 3)
round(100 * (refqoi$padult - 100 * quantile(padult, qoi))/refqoi$padult, 3)
round(100 * (refqoi$pmate - 100 * quantile(pmate, qoi))/refqoi$pmate, 3)
round(100 * (refqoi$pfounder - 100 * quantile(pfounder, qoi))/refqoi$pfounder, 3)

set.seed(maizecorn)
res <- data.frame(modelstep = NA, X1 = NA, X5 = NA, X25 = NA, X50 = NA,
                  X75 = NA, X95 = NA, X99 = NA)

ninf_EU <- (ntrade / spearweight) * (pinf / 1e4)
res[1, ] <- c("ninf_EU", round(quantile(ninf_EU, qoi)))

ninf_climreg <- ninf_EU * 0.1643
res[2, ] <- c("ninf_climreg", round(quantile(ninf_climreg, qoi)))

ninf_waste <- ninf_climreg * 0.1
res[3, ] <- c("ninf_waste", round(quantile(ninf_waste, qoi), 1))

nadult <- ninf_waste * padult
res[4, ] <- c("nadult", round(quantile(nadult, qoi), 2))

nmate <- nadult * pmate
res[5, ] <- c("nmate", round(quantile(nmate, qoi), 5))

nmate_adj <- nadult * pfemale * pmate
res[6, ] <- c("nmate_adj", round(quantile(nmate_adj, qoi), 5))

nfounder <- nmate * pfounder
res[7, ] <- c("nfounder", round(quantile(nfounder, qoi), 6))

nfounder_adj <- nmate_adj * pfounder
res[8, ] <- c("nfounder_adj", round(quantile(nfounder_adj, qoi), 6))

binadult <- rbinom(nsim, ceiling(ninf_waste), prob = padult)
res[9, ] <- c("binadult", quantile(binadult, qoi))

binfemale <- rbinom(nsim, binadult, prob = pfemale)
res[10, ] <- c("binfemale", quantile(binfemale, qoi))

binmate <- rbinom(nsim, binfemale, prob = pmate)
res[11, ] <- c("binmate", quantile(binmate, qoi))

binfounder <- rbinom(nsim, binmate, prob = pfounder)
res[12, ] <- c("binfounder", quantile(binfounder, qoi))
res

ptransest <- pclim * pwaste * padult * pmate * pfounder
quantile(ptransest, qoi)
```

Appendix G Other statistical considerations

G.1 Choice of fitted distributions

At some places in the three qPRAs evaluated in this document, the fitted distributions show some undesirable behaviour, which manifests itself in two ways:

1. insufficiently bounded distributions,
2. overly strict bounds on distributions.

Regarding 'insufficiently bounded distributions', the best (and perhaps only) example of this in the three qPRAs is the PearsonV(0.70603, 5.0632) distribution used for the disaggregation factor d in the *Citripestis* qPRA (p.18). As shown in the legend for Figure 6 on p. 18, this distribution has a minimum of 0 and no maximum (or equivalently, a maximum of +infinity). The meaning of the parameter d differs slightly between the model description (p. 8), where it is given as a *"[d]isaggregation factor, reflecting the distribution of one ton of infested citrus fruit to several locations in the risk assessment area"* and section 3.2.2.4, where it is described as a *"[d]isaggregation factor for one ton (1,000 kg) of infested citrus fruit, to take into account the number of* ***suitable*** *locations for transfer to which one ton of infested citrus fruit is delivered"* (Table 9 on p. 17 – our emphasis) or "*number of* ***suitable*** *locations for transfer to which one ton of infested citrus fruit is delivered*" (caption to Figure 6 on p. 18 – our emphasis). According to the description given on p.8 the value of 0 should be impossible when applied to the entire import in a single year (as done in the model), because it implies that the entire import ends up in zero (0) locations. Under the interpretation given in section 3.2.2.4 a value of 0 is possible, but this seems inappropriate since the suitability of the location is also taken into account in the parameter p_{transfer} (section 3.2.2.5 on p. 18). On the other hand, the lack of maximum for this distribution also leads to physical impossible estimates: approximately 0.26% of draws from the PearsonV(0.70603, 5.0632) distribution will be higher than 26,000, which is roughly the upper bound for the number of single fruits in a ton of key limes (see section 4.3.2.1 of this evaluation). This would require that each single fruit in this ton of key limes ends up in a different location in the EU. Approximately one in 10,000 draws would be higher than one hundred times this value (i.e. 2,600,000), which would require each fruit to be split into an average of one hundred parts that then each end up in different locations in the EU. While in this case the inclusion of 0 and the lack of a maximum probably does not materially affect the results of the qPRA (in terms of the resulting 90% uncertainty interval) this cannot be ascertained in general. One solution would be to discard physically impossible simulation runs, but in general it would be better to use a distribution with the appropriate bounds.

Regarding 'overly strict bounds on distributions', there are several examples where a scaled beta distribution (BetaGeneral) is used to fit a parameter which does not have strict bounds (or where the actual bounds are much wider than those of the fitted distribution). Perhaps the best example of this the BetaGeneral (1.7529, 1.2895, 0, 0.51) distribution used for the probability of a founder population after successful mating in the *Elasmopalpus* qPRA (p. 66). The 99% percentile from the EKE is 0.50 but the upper bound of the scaled beta distribution is only 0.51. This effectively ascribes to the experts a belief that there is a 1% chance that the parameter is greater than 0.5 but that if it is greater than 0.5 then it is 100% certain that it is between 0.5 and 0.51. Such a sharp boundary does not seem reasonable, unless there is a very strong rationale for why the value of the parameter indeed cannot be greater than 0.51. Similar problems show up in the scaled beta distributions used for N_{trade} in the *Citripestis* qPRA, p_{adult} in the *Elasmopalpus* qPRA, and the proportion infested with eggs, proportion infested with young larvae, and the proportion of organic waste going to private composting in the *Thaumatotibia* qPRA. Even when scaling does lead to such sharp boundaries, the scaling of beta distributions to a subset of the possible parameter range is likely to underestimate the uncertainty, in particular for proportions, probabilities and percentages. The parameters of an unscaled beta distribution can be approximately interpreted as the number of hits and misses that have been observed. If no pair of such parameters closely matches the uncertainty distribution from the EKE (i.e. the quantiles elicited) this therefore implies that there is no set of observations that would lead to the uncertainty elicited in the EKE. Therefore, a strong justification is required when the elicited quantiles for proportions, probabilities or percentages cannot be fit with a beta distribution. Such justifications could come from other forms of information or processes that only occur beyond specific cutoffs, e.g. rejection of the entire batch if more than a given proportion is defective, where all units in the batch are inspected.

G.2 Treating probabilities as proportions

All of the models in the qPRAs evaluated here include parameters that are described as probabilities[17]. In all of these models, these probabilities are multiplied with other model parameters to obtain the final estimated number of event (and uncertainties). In general, this approach is valid for proportions but not for probabilities. In this context the use of a proportion implies that a particular event will always happen for a given fraction of a population. For example, if the infestation of fruits is modeled using a proportion X (with associated uncertainty) then each batch of size N to which this proportion is applied will be assumed to contain exactly $X * N$ infested fruits. On the other hand, the infestation of fruits could also be modeled using a probability Y (again with associated uncertainty). If this probability Y is applied at the level of the batch, then the batch is either infested (with probability Y) or not infested (with probability $1\text{-}Y$). If the probability Y is applied at the level of the individual fruit, then for each fruit there is a probability ability Y that the fruit is infested. All of these implementations have the same *expectation* as long as $X = Y$, i.e. over a large number of batches the total number of infested fruit will be approximately the same in each implementation.

However, it is easy to construct examples where these approaches lead to quite different conclusions. For example, consider a 'batch' as rolling six dice, where rolling a six represents infestation, i.e. $X = Y = 1/6$. Use of a proportion then implies that each batch contains one infested fruit. Application of probability Y at the level of the batch yields one batch containing six infested fruits for each five batches containing no infested fruits (and no batches with any other number of infested fruits). And application of probability Y at the level of the individual fruit yields approximately 33% of batches containing no infested fruits, 40% of batches containing exactly one infested fruit, and 26% of batches containing two or more infested fruits. One key difference is that with the use of proportion, there is no possibility that a batch is *not* infested (unless $X = 0$).

In many cases, this treatment of the probabilities will have no effect on the resulting estimates, in particular where the number of (transfer) units and the uncertainty of the parameter estimates are large. However, when the number of units and/or the uncertainty of the parameter estimates are small[18], this treatment of probabilities *can* have a noticeable effect on the resulting uncertainty (see Table F10 and in particular Tables F11 and F12, as well as the preceding paragraph in appendix F.1 for an example regarding the *Elasmopalpus lignosellus* qPRA where the treatment of probabilities does make a difference). One major difference is that treating probabilities as probabilities (instead of proportions) allows assigning a non-zero probability to having zero founder populations (in a finite time period), whereas treatment of probabilities as proportions does not (unless the number of units or the proportions themselves become zero). However, this does not mean that treatment of probabilities as proportions leads to lower estimates. In practice, treatment of probabilities as proportions tends to decrease the width of the uncertainty interval at both ends. Ultimately, the difference comes down to the question what needs to be estimated: (i) the uncertainty about the average number of events (e.g. the number of founder populations) or (ii) the uncertainty about the number of events that may in fact occur. In the first case treatment of probabilities as proportions is appropriate. In the second case such treatment underestimates the variability and, therefore, the uncertainty of what may happen.

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[17] Note that these are different from the probabilities used for the probability distributions for the parameters.

[18] What is 'small' in this context is difficult to define exactly, since it also depends on how close the probability is to zero.