GENERAL CONSIDERATIONS

2.1 COMMENTS FROM JMPR ON A PILOT POCESS FOR JMPR TO RECOMMEND MAXIMUM RESIDUE LEVELS PRIOR TO NATIONAL GOVERNMENT REGISTRATION

Background

At the 40th Session of the Codex Committee on Pesticide Residues (CCPR), the Delegation of the United States (US) presented a document describing recommendations for the development of a process to accelerate the evaluation of new pesticides, which would allow JMPR to recommend maximum residue levels (MRLs) to CCPR before the new pesticide has been registered by national governments. This might facilitate the alignment of national MRLs with Codex.

CCPR agreed to establish an electronic working group led by the US delegation and co-chaired by Australia and Kenya; the objective of this working group was to prepare a discussion paper describing in more detail a proposal for a pilot process and report back to CCPR at its Forty-first Session (April 2009). CCPR noted that this pilot process would have significant implications. The Joint JMPR Secretariats requested comments from the present Meeting.

Comments from the JMPR on the pilot process

The Meeting indicated that it would embrace any development that would improve the efficiency with which public health is protected from exposures to pesticide residues.

The Meeting considered that there were several potential advantages in the proposal to accelerate the evaluation of new pesticides by giving the JMPR evaluator access to the relevant joint (work-share) assessment documents and deliberations of participating national governments and the full data packages. In particular, many of the technical issues involved would be identified by the governments and authorities during the commenting process. However, the Meeting noted that there are some issues that required further consideration before implementation of any pilot project.

The Meeting emphasized for the pilot process that all relevant procedural issues need to be resolved and the data need to be available at least 6 months prior to the annual meeting of the JMPR in September.

Successful completion of an evaluation by JMPR requires registered label information, including good agricultural practice (GAP), for estimation of maximum residue levels. GAP for a pesticide means more than just the maximum proposed use pattern (rate of application, pre-harvest interval, efficacy). It also includes advice relevant to worker/operator and environmental exposure as well as management of pesticide resistance. JMPR is concerned that national government evaluation of these additional aspects may lead to changes in the GAP that is ultimately registered. Those governments involved in the pilot project should ensure that the proposed GAP is as final as possible before submission of the residue data to the JMPR.

For the JMPR evaluation to be completed before final registration of the new pesticide by national governments, interaction is required between the JMPR evaluator preparing the first draft of documents for the Meeting and reviewers from governments and authorities participating in the pilot project. The Meeting noted that increased correspondence would increase time involved but not necessarily change the meeting process. However, the process timeframes should align with JMPR timeframes including the time needed to prepare papers for the Meeting. Therefore the JMPR Secretariats will need to assign evaluators/reviewers and provide them with the necessary contacts and access to relevant information.

2.2 COMMENTS ON THE "GLOBAL ASSESSMENT" OF CHLORANTRANILIPROLE IN TERMS OF ITS USEFULNESS AS A WORK-SHARING TOOL FOR JMPR

The Meeting had previously used work-sharing reports on trifloxystrobin (JMPR, 2004) and quinoxyfen (JMPR, 2006) to develop monographs for these chemicals. The Meeting had concluded that evaluations conducted by national and regional authorities were useful in the preparation of JMPR evaluations. Appropriate use of material from these evaluations reduced the amount of time required by the JMPR temporary advisor to prepare toxicological and residue monographs.

A pilot assessment entitled "Chlorantraniliprole (DPX-E2Y45) global assessment[1]" was conducted in 2006–2008 by several regulatory authorities under the auspices of the Organization for Economic Cooperation and Development (OECD) with the aims of accelerating the timeline between review and approval and furthering regulatory harmonization. Ten countries were involved in the preparation of a global assessment of chlorantraniliprole. The global assessment was presented in the OECD format.[2]

In continuation of its support of work-sharing, the present Meeting used this global assessment to aid in the preparation of a JMPR toxicology monograph on chlorantraniliprole, which was reviewed by the present Meeting at the request of the Codex Committee on Pesticide Residues (CCPR). The JMPR Secretariat provided the JMPR temporary advisors responsible for the preparation of the first draft of the JMPR monograph with the relevant documents used for toxicological evaluations in the global assessment of chlorantraniliprole.

The final version of the residue component of the global assessment was not available at the time the JMPR residue evaluation was prepared.

The Meeting made a number of comments on the usefulness of the toxicological component of the global assessment to assist the work of the JMPR.

Format of the global assessment

The general format of the toxicology component of the global assessment was similar to that of a JMPR monograph.

The study evaluations within each section were summarized at the end of the section. A summary of mammalian toxicology and the selection of end-points was then presented, with a brief conclusion that summarized the toxicological profile of the substance. Again, this had some similarities to the style of the JMPR monograph.

Since the toxicology of the substance under evaluation was summarized at several places in the global assessment, this leads to considerable redundancy.

Study evaluations in the global assessment

The study evaluations in the global assessment were lengthy, describing in great detail the study design, methods and materials, results and conclusions. In addition, the study evaluations often contained a considerable number of tables presenting the values for the parameters investigated, irrespective of whether or not these parameters were affected by treatment with chlorantraniliprole. As the studies with chlorantraniliprole were modern and complied with current OECD guidelines and the degree of toxicity observed was very low, the extensive descriptions of the study methods in the evaluations of the global assessment were of limited value. Owing to such lengthy description of basic information, the key findings of the study were not always immediately clear, although detailed

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[1] Referred to as 'Joint Review of Chlorantraniliprole (DPX-E2Y45)' by OECD

[2] OECD monograph guidance
http://www.oecd.org/document/59/0,3343,en_2649_34383_1916347_1_1_1_1,00.html

descriptions of the study results may avoid the need to consult the original study reports[3]. The description of arguments used in the identification of no-observed-adverse-effect levels (NOAELs) was also helpful for the preparation of the JMPR monograph.

These study evaluations formed a useful basis for the JMPR monograph, although it was necessary to considerably reduce the lengthy descriptions in order to focus on the essential points of the studies.

In general, the Meeting agreed with the conclusions of the global assessment for chlorantraniliprole. However, it should be noted that this was a straightforward assessment of a compound that was without potential for severe toxicity.

Reporting table, including comments of the peer reviewers

An extensive reporting table was provided with the global assessment, which presented the comments and questions that had been raised by the regulatory authorities or the applicant, and the response of the Rapporteur Member State.

The reporting table clarified the points of discussion, presented the different arguments raised by the participants and, in general, made clear what final decision was reached and on what basis. This table was considered to be very useful for the preparation of the JMPR monograph, although it was noted that a considerable part of the table dealt with minor issues (e.g., editorial points), which made it more difficult to identify the critical points of discussion.

Conclusion

The global assessment of chlorantraniliprole (particularly the accompanying reporting table with the reviewer comments) was helpful for the preparation of the JMPR monograph on this pesticide.

In summary, some suggestions are listed below that might make the global assessment more useful for the JMPR:

- Decrease the level of methodological detail provided.
- Reduce the level of reporting of inconsequential findings.
- Continue to give details of comments and responses by participants.
- If possible, separate critical discussion points from minor issues in the reporting table.

2.4 A PROCESS TO ENSURE THE SCIENTIFIC ROBUSTNESS AND TRANSPARENCY OF RETROSPECTIVE ANALYSES OF TOXICITY DATA ON PESTICIDE CHEMICALS

The current paradigm of toxicity testing that is used to assess the potential risk of pesticide chemicals has been in place for many years. Such risk assessments have been conducted for hundreds of chemicals. Together they form a rich database on the toxicity of these chemicals. Compilation and analysis (known as "retrospective analyses") of this existing extensive toxicity database can play an important role, for example, in refining test methods and guiding changes in data requirements, in identifying and prioritizing key issues associated with current tests for toxicity, in enhancing

[3] The Meeting noted that in 2001 and 2002 the OECD had published two guidance documents in the OECD *Series on Testing and Assessment* that recommended ways of providing an adequate level of detail in toxicology reports without including unnecessary information or duplicating information that was common to different types of studies.

interpretation of data from current tests for toxicity, and in supporting predictions of toxicity (e.g., building and testing of SAR/QSAR models).

A number of different retrospective analyses by national and supranational bodies of various studies of toxicity in experimental animals have either been completed or are ongoing. These retrospective analyses address issues such as the duration of a study of toxicity in dogs that is appropriate for the determination of an acceptable daily intake (ADI), the amount of additional information relevant to hazard and risk assessment provided currently by the bioassay for cancer in mice, and the contribution of the F_2 generation in studies of reproductive toxicity in rats in order to consider a possible replacement of the multigeneration study of reproductive toxicity by the "extended F_1" study.

Given the interest in retrospective analyses, the OECD Working Group on Pesticides has established a task group to develop a document that describes, in general terms, a process for improving the transparency and harmonization of retrospective analyses. In considering which organizations need to be involved in this process and what their roles should be, that task group asked the WHO Core Assessment Group on Pesticide Residues of the JMPR to comment on how retrospective analyses could be used most effectively to improve the risk assessment of pesticides.

Comments from the JMPR

The present Meeting acknowledged the importance of retrospective analyses of toxicity databases for pesticides and recommended that the WHO Core Assessment Group on Pesticide Residues of the JMPR or a working group established by the WHO Joint Secretariat of the JMPR could serve a valuable role in the review of these analyses that are conducted by national/supranational bodies. The JMPR would provide an independent international opinion on the scientific robustness and transparency of these analyses, make suggestions on how they may be improved, and provide comment on the implications of the results. If multiple analyses by different countries have been or will be conducted, the JMPR could also make recommendations on how to harmonize the approach and interpretation of the results. Retrospective analyses may be submitted to the JMPR/WHO Joint Secretariat for consideration by national authorities or other organizations or by the OECD Working Group on Pesticides. Given that the JMPR convenes once each year, in order for the JMPR to provide meaningful input, the analyses would need to be made available to the WHO Core Assessment Group at least 6 months before the JMPR annual meeting normally held in September and such analyses would need to be well documented (i.e., not anonymized, if possible).

The Meeting also recommended that the JMPR take on a pilot process and thus asked the JMPR/WHO Joint Secretariat to liaise with the OECD Working Group on Pesticides to identify a suitable retrospective analysis.

2.4 COMMENTS ON OECD DRAFT GUIDANCE DOCUMENT FOR DERIVATION OF AN ACUTE REFERENCE DOSE

The present Meeting discussed the most recent draft version of the OECD *Guidance Document for Derivation of an Acute Reference Dose* (Version 6, 30 June 2008), the purpose of which is to provide harmonized guidance on how to use all available information to derive acute reference values (ARV)[4] and how to proceed should additional data be necessary. Although it was not possible to discuss the document in detail since it was not provided to the JMPR before the present meeting, the Meeting was able to offer some general comments, summarized below.

[4] In the OECD draft guidance, the term "acute reference value (ARV)" is applied, which is related not only to the amount of a substance that can be ingested from food or drinking-water, but also that can be tolerated by dermal and inhalation exposures.

The OECD guidance document is generally based on the JMPR *Guidance on the Establishment of Acute Reference Doses,*[5] which is intended to be used for the assessment of dietary exposure to pesticide residues. In contrast to the guidance provided by JMPR, the most recent OECD guidance document also applies to dermal and inhalational exposure, which complicates the guidance offered, e.g., the principles for not setting an ARV based on a NOAEL of > 500 mg/kg bw are very specific for oral ingestion of pesticide residues.

The Meeting recommended that the OECD guidance document should address only oral exposure. The issues associated with setting ARVs for inhalation and dermal exposure, including route-to-route extrapolation methods, should be moved to a separate guidance document or to an annex attached to the current document.

The present Meeting noted that the provision of more guidance on issues relating to assessment of acute risk would improve both the WHO and the OECD guidance on setting of acute reference doses (ARfDs). Several of these issues were recently discussed and published by the JMPR (e.g., section 2.6 of the present report; sections 2.1 and 2.4 of the JMPR report 2007; section 2.4 of the JMPR report 2006).

2.5 CUMULATIVE RISK ASSESSMENT FOR PESTICIDE RESIDUES IN FOOD: ACTIVITIES OF THE EUROPEAN FOOD SAFETY AUTHORITY

The Meeting was informed that the Scientific Panel on Plant Protection Products and their Residues (PPR Panel) of the European Food Safety Authority had issued an opinion "to evaluate the suitability of existing methodologies and, if appropriate, the identification of new approaches to assess cumulative and synergistic risks from pesticides to human health with a view to set MRLs for those pesticides in the frame of Regulation (EC) 396/2005".[6] It was also informed of an ongoing application of the tiered approach provided in the opinion to risk assessment of cumulative dietary exposure of triazole fungicides. The Meeting was aware of other similar evaluations conducted by other bodies and considered the relevance of cumulative risk assessment for pesticide residues in food. The Meeting would continue to monitor ongoing activities in this field and eventually advise on the need for cumulative risk assessment for certain groups of compounds.

2.6 SAFETY FACTORS FOR ACUTE C_{MAX}-DEPENDENT EFFECTS: SPECIFIC CONSIDERATIONS WITH RESPECT TO CARBAMATES SUCH AS CARBOFURAN

General considerations

In deriving health-based guidance values for exposure-based risk assessment, i.e., ADI and ARfD, the JMPR uses the paradigm developed by the International Programme on Chemical Safety (IPCS) and widely adopted by risk-assessment bodies throughout the world. For toxicological effects that would be anticipated to have a biological threshold and for which there is an experimentally observable threshold, the ADI or ARfD, as appropriate, is derived from the NOAEL, or other suitable point of departure, by application of an appropriate safety factor.[7] The safety factor allows for inter-species

[5] In: Pesticide Residues in Food—2004. Report of the JMPR 2004, FAO Plant Production and Protection Paper, 178, FAO, Rome, pp 3–9.

[6] http://www.efsa.eu.int/EFSA/efsa_locale-1178620753812_1178712607885.htm

[7] Safety factors are also known as "assessment factors", "adjustment factors" (AFs) or "uncertainty factors" (UFs). In the IPCS document on chemical-specific adjustment factors (CSAFs), the term "uncertainty factor" applies to default factors, while "adjustment factor" applies to data-derived factors. In this IPCS terminology, the overall safety factor is known as the "combined uncertainty factor" (CUF).

and human inter-individual differences in sensitivity attributable to both toxicokinetics and toxicodynamics. When using data obtained from experimental animals, the default safety factor is 100. This comprises a factor of 10 to allow for inter-species differences and a factor of 10 for intra-species (human inter-individual) differences. The overall safety factor is the product of these two factors, i.e., 10 × 10.

While this approach allows for the use of data either from experimental animals (safety factor of 100) or from humans (safety factor of 10), it does not allow quantitative incorporation of specific information on toxicokinetic or toxicodynamic differences for a chemical, either between or within species, in the risk assessment. To overcome this limitation, IPCS recommended that the two 10-fold factors each be further subdivided into toxicokinetic and toxicodynamic sub-factors. The sub-factors agreed were 4-fold and 2.5-fold for inter-species toxicokinetic and toxicodynamic differences, respectively, and 3.16 ($10^{1/2}$) each for human inter-individual toxicokinetic and toxicodynamic differences. The resulting sub-factors were termed "default sub-factors" (uncertainty factors or UFs).[8] Where available, information on one or more specific sources of variability and uncertainty could be used to enable derivation of one or more chemical-specific adjustment factors, CSAFs, replacing the defaults.

Table 1 Values for IPCS default sub-factors for uncertainty[8]

Source of uncertainty	Default sub-factor		
	Toxicokinetic	Toxicodynamic	Combined
Interspecies variation	4.0	2.5	10
Human inter-individual variation	3.16	3.16	10

IPCS, International Programme on Chemical Safety

The overall or combined uncertainty factor (CUF; equivalent to the safety factor as used by JMPR) is obtained from the product of the CSAFs, using defaults for those sub-factors for which chemical specific information is not available. Hence:

Combined UF (safety factor) = (AK_{AF} or AK_{UF}) × (AD_{AF} or AD_{UF}) × (HK_{AF} or HK_{UF}) × (HD_{AF} or HD_{UF})

where AK represents inter-species toxicokinetic variability

AD represents inter-species toxicodynamic variability

HK represents human interindividual toxicokinetic variability

HD represents human interindividual toxicodynamic variability

AF represents a chemical-specific adjustment factor

UF represents a default uncertainty subfactor

CSAFs enable information on inter-species or human interindividual differences in the toxicokinetics or toxicodynamics of a specific chemical to be incorporated into the risk assessment. Although such information is often not available, information on pathways of elimination or mode of action may be available. As information is available on the extent to which some of these pathways or processes vary between or within species, an approach has been proposed to enable this information to be used to inform the choice of safety factors.[9] This approach is therefore somewhere between the

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[8] WHO. Chemical-specific adjustment factors for interspecies differences and human variability: guidance document for use of data in dose/concentration–response assessment. Geneva, World Health Organization, 2005 (http://whqlibdoc.who.int/publications/2005/9241546786_eng.pdf)

[9] Renwick AG, Lazarus NR. Human variability and noncancer risk assessment – an analysis of the default uncertainty factor. *Regul. Toxicol. Pharmacol.*, 1998;27:3–20.

normal default situation (100-fold safety factor) and the derivation of CSAFs on the basis of chemical-specific information. Such factors have been termed “categorical factors”.[10]

The default uncertainty factors for inter-species and human inter-individual toxicokinetic differences were derived on the basis of protection from long-term exposure to chemicals.[11] As such, these factors reflect differences in clearance processes, i.e., are-under-the-curve of concentration–time (AUC)-dependent effects. As the effects of acute exposure are often dependent on C_{max}, it is pertinent to ask whether this parameter varies to the same extent as AUC or clearance (*CL*) between or within species.

Kinetically, $C_{\max} = \dfrac{k_a \times D \times F\left(e^{-kt_{\max}} - e^{-k_a t_{\max}}\right)}{V \times (k_a - k)}$

where

k_a = absorption rate constant

k = elimination rate constant

V = apparent volume of distribution

t_{max} = time of maximum plasma concentration (C_{max})

F = systemic bioavailability

D = administered dose

Hence, C_{max} does not depend directly upon either *CL* or AUC. Although k depends upon both *CL* and V, in general k_a exceeds k. Hence, the main determinants of C_{max} are k_a and V, i.e., the rate of absorption and the volume of distribution.[12] These are determined largely by physicochemical properties and basic body composition. Basic body composition, e.g., the thickness and composition of the plasma membrane, major determinants of passive diffusion, do not vary widely between or within species. Analysis of a database on pharmaceuticals used in humans confirmed that C_{max} varied less between species than did *CL* or AUC.[11] Hence, it was concluded on the basis of these considerations that a reduction in the inter-species toxicokinetic factor (AK_{AF}) from the default of 4 to 2 was justified (Renwick, 2000) for rapidly eliminated compounds, the effects of which were dependent on C_{max}. The JMPR reached a similar conclusion at its meeting in 2000.

C_{max} is influenced by the presence of food in the gastrointestinal tract, for example, because o f effects on gastric emptying.[13] However, as it is assumed that a large portion of a particular relevant f ood commodity would be present when undertaking an acute risk assessment of residues of a pesticid e, this factor would make a less important contribution to inter-individual variability in Cmax.

Hence, some reduction in the adjustment factor for human toxicokinetic differences (HK_{AF}), from its default value of 3.16, would seem to be justified. The JMPR in 2000 had previously suggested that a 50% reduction would be appropriate. Hence, for compounds whose effects are dependent on C_{max}, and which are rapidly eliminated, the combined adjustment factor would be:

$$\text{CUF} = AK_{AF} \times AD_{UF} \times HK_{AF} \times HD_{UF}$$

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[10] Walton K, Dorne JL & Renwick AG. Categorical default factors for interspecies differences in the major routes of xenobiotic elimination. Hum. *Ecol. Risk Assess.*, 2001;7:181–201.

[11] WHO. Principles for the toxicological assessment of pesticide residues in food. Environmental Health Criteria 104. (http://www.inchem.org/documents/ehc/ehc/ehc104.htm)

[12] Renwick AG. The use of safety or uncertainty factors in the setting of acute reference doses. *Food Addit. Contam.*, 2000;17:627–635.

[13] Krishna R, Jensen BK. Pharmacokinetics: effects of food and fasting. In: Swarbrick J, editor. *Encyclopaedia of Pharmaceutical Technology*, Third Edition, Informa Healthcare, London; 2004: pp 2816–2828.

$= 2$ (categorical) × 2.5 (default) × 1.58 (categorical) × 3.16 (default)

$= 25$

The example of carbamates

The toxicological effects of carbamates such as carbofuran are C_{max} dependent. As carbamates are rapidly absorbed and eliminated, the above considerations would apply, and the combined uncertainty factor would be 25, rather than the default of 100.

The toxicity of carbamates such as carbofuran is caused by inhibition of neuronal acetylcholinesterase activity. The clinical signs indicate that neurons in the central nervous system are the primary target, and are responsible for the critical effects upon which the risk assessment is based. This is true for acute (single dose) and for long-term exposure. The NOAELs for the toxicological effect of carbofuran are the same, regardless of the duration of exposure. This is a consequence of the toxicokinetics of carbofuran, which is rapidly absorbed and eliminated, and the toxicodynamics of the effect, in which acetylcholinesterase is rapidly reactivated because of spontaneous hydrolysis. There is therefore no opportunity for progressive effects to develop, due to either bioaccumulation or to cumulative inhibition from one exposure to another.

Neuronal acetylcholinesterase, which is identical to the acetylcholinesterase protein expressed in erythrocytes, is well conserved between species. Studies in vitro have shown that erythrocyte acetylcholinesterase from a number of species, including humans, shows similar sensitivity to inhibition by carbamates.[14] This has been confirmed in vivo, for example with carbofuran (see report of the present Meeting). The NOAELs for inhibition of acetylcholinesterase activity by this compound and for effects dependent upon such inhibition in rats, dogs and humans were very similar (see report of the present Meeting). The default uncertainty subfactor for interspecies toxicodynamic differences (AD_{UF}) of 2.5 assumes that humans are more sensitive than the test species. As there is good evidence that this is not the case for carbofuran, some modification of AD_{AF} would be justified.

The default uncertainty subfactor for human inter-individual differences in toxicodynamics (HD_{UF}) is 3.16. In the case of carbamates such as carbofuran, such differences will depend on the level of expression of acetylcholinesterase and the rate of enzyme reactivation, which is a passive process. Rat pups were more sensitive to inhibition of acetylcholinesterase activity by carbofuran than were adults. Hence, in basing the risk assessment on this end-point, one component of potential variability within the population has already been taken into account and the remaining inter-individual differences are likely to be less than the default, as they are due to passive processes.

On the basis of the above considerations, the Meeting concluded that the default uncertainty sub-factors for toxicodynamic differences between and within species for carbofuran were conservative and that some modification of these sub-factors to account for the reduced variability expected for such compounds would be justified, on the basis of both chemical-specific and generic information. This, together with the arguments for categorical toxicokinetic factors for compounds where toxicity is dependent on C_{max}, provides strong support for the use of a combined uncertainty factor (safety factor) of no more than 25 for carbofuran.

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[14] Rao PS, Roberts GS, Pope CN & Ferguson PW. Comparative inhibition of rodent and human erythrocyte acetylcholinesterase by carbofuran and carbaryl. *Pestic. Biochem. Physiol.*, 1994;48:79–84.

2.7 TRANSPARENCY IN THE MAXIMUM RESIDUE LEVEL ESTIMATION PROCESS OF THE JMPR

The JMPR adopted the statistically based methodology used in the NAFTA[15] countries at its 2005 Meeting as an aid in the estimation of maximum residue levels (2005 Report). Prior to that, estimations of the maximum residue level (mrl) were based solely on the collective scientific judgment of the JMPR after careful consideration of the results of the relevant supervised trials. Values were rounded according to a step system (1, 2, 3, 5, 7, 10…). With the inclusion of the NAFTA spreadsheet in the estimation process, the step system of rounding was abandoned and values were rounded up to *one* significant figure (with the addition of 15). The Meeting has reported each year on its experiences with the NAFTA calculation routine.

The Meeting has been using the NAFTA spreadsheet as a tool and not as the primary determinant of estimations. This means that the evaluator considers the data set, the crop, the properties of the particular pesticide, and supporting data, and then proposes an estimate. This estimate is checked against the NAFTA spreadsheet. The evaluator's preliminary estimates are debated by the entire FAO expert group and may be changed on reconsideration of the data and knowledge of the particular pesticide and its uses and properties and the situations with each crop data set, as well as review of the NAFTA spreadsheet results. The estimation is not a simple matter of entering the residue trial numbers into a spreadsheet and recording the output.

The NAFTA spreadsheet is not a statistical model for the accurate estimation of maximum residue levels. Rather it is a decision-tree logic that utilizes statistical calculations to arrive at a reasonable maximum residue level that should be acceptable to different parties considering the same data set. It is designed to give a consistent decision, independent of the prejudice of the reviewer(s). The spreadsheet looks only at numbers and not at the basis of those numbers. The JMPR looks both at the numbers and the basis of those numbers (See General Consideration 2.8).

It is imperative that the JMPR consider all relevant aspects in arriving at its maximum residue level estimates. Otherwise, a value intended as an international trade standard may be set too low thereby creating trade difficulties for a commodity that was treated in accordance with a national GAP. On the other hand, the JMPR attempts to not overestimate the maximum residue level and thereby allow commodities in trade from applications in excess of the GAP. Many such aspects that cannot be factored in by a spreadsheet.

The 40th Session of the CCPR requested that the JMPR Secretaries consider providing brief explanations on the derivation of each maximum residue level estimate and publishing a calculation summary table.

The Meeting acknowledged that following the derivation of a maximum residue level from the data set recorded in the JMPR Report may not be a facile process.

A simple example will illustrate the process, but no number of examples can address all the situations encountered by the Meeting in reaching decisions on maximum residue levels. Residue data for the foliar application of spirotetramat to hops was considered by the Meeting. The data set consists of 4 independent data points: 2.8, 4.5, 5.8, 5.8 mg/kg. The data set is very small (n = 4) and is only acceptable because the crop is minor or specialty. There is little confidence that the four values include the maximum residue that might be encountered from treatment according to GAP. Moreover, the FAO realized from experience that residues on dried hops can be extremely variable. Therefore, the Meeting concluded to estimate 15 mg/kg, the choices being 6, 7, 8, 9, 10, 15, 20 mg/kg, and checked this against the statistical analysis which selected 8.85 mg/kg based on log normality at the 99th percentile. The opinion of the FAO experts was that a lesser value (such as 9 mg/kg) might lead to violations for crops treated in accordance with GAP.

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[15] North American Free Trade Agreement

The Meeting proposed to provide to the CCPR, on a trial basis, a concise form summarizing the derivation of maximum residue levels from the 2008 Meeting. The form will provide summary numerical information and will briefly state the basis for estimates as necessary. The “comments” indicate when the NAFTA spreadsheet recommendation is discounted, e.g., when there is an insufficient number of data values. The completed form for each pesticide considered is attached to this general consideration.

The JMPR requests that the members of CCPR review the forms, evaluate the usefulness of the information, and decide if they wish JMPR to include the information routinely in an annex to the JMPR Report.

Listed below are summaries of the derivation of MRL estimates.

Commodity	No. of Trials	Min. Value (mg/kg)	Max Value (mg/kg)	Mean (mg/kg)	STMR (mg/kg)	No. ≤ LOQ	Statistical Calculation		JMPR	
							Distribution Type	Estimate (mg/kg)	MRL (mg/kg)	Comment/ Explanation
AZOXYSTROBIN (229)										
Citrus fruit	8	2.6	8.8	5.1	4.9	0	Lognormal 95/99 rule, 99th	12.3	15	There are too few data points for the NAFTA calculator
Stone fruit	14	0.28	1.4	0.73	0.74	0	Lognormal 95/99 rule, 99th	1.79	2	Agreed
Berries and other small fruits, except cranberry, grapes, and strawberry	10	0.52	3.6	1.4	1.0	0	Lognormal 95/99 rule, 99th	4.48	5	There are too few data points for the NAFTA calculator
Cranberry	4	0.15	0.31	0.23	0.23	0	Lognormal 95/99 rule, 99th	0.46	0.5	There are too few data points for the NAFTA calculator
Grapes	15	0.11	0.80	0.48	0.53	0	Lognormal 95/99 rule, 99th	1.63	2	Agreed
Strawberry	7	0.26	4.5	1.8	1.3	0	Lognormal UCLMedian 95th	9.43	10	There are too few data points for the NAFTA calculator
Bananas and plantains	6	0.58	1.1	0.84	0.84	0	Lognormal 95/99 rule, 99th	1.40	2	There are too few data points for the NAFTA calculator
Mango	3	0.08	0.44	0.27	0.28	0	Lognormal 95/99 rule, 99th (Mean+3SD)	1.67 (0.81)	0.7	There are too few data points for the NAFTA calculator
Papaya	7	< 0.05	0.15	0.09	0.09	2	Lognormal 95/99 rule, 99th	0.23	0.3	There are too few data points for the NAFTA calculator
Bulb vegetables	7	0.67	6.3	2.6	2.2	0	Lognormal 95/99 rule, 99th (Mean+3SD)	11.1 (8.19)	10	There are too few data points for the NAFTA calculator
Brassica vegetables	8	0.25	2.3	1.3	1.2	0	Lognormal 95/99 rule, 99th (Mean+3SD)	6.86 (3.55)	5	There are too few data points for the NAFTA calculator
Fruiting vegetables, Cucurbits	14	0.03	0.75	0.23	0.17	0	Lognormal UCLMedian 95th	0.96	1	Agreed

Commodity	No. of Trials	Min. Value (mg/kg)	Max Value (mg/kg)	Mean (mg/kg)	STMR (mg/kg)	No. ≤ LOQ	Statistical Calculation		JMPR	Comment/ Explanation
							Distribution Type	Estimate (mg/kg)	MRL (mg/kg)	
Fruiting vegetables, other than Cucurbits, except fungi and sweet corn	11	0.08	1.4	0.48	0.35	0	Lognormal UCLMedian 95th	2.17	3	There are too few data points for the NAFTA calculator
Lettuce	20	< 0.01	1.6	0.46	0.28	5	Not lognormal Mean+3SD	1.97	3	Not lognormal distribution
Legume vegetables	6	0.11	1.5	0.94	1.0	0	Lognormal 95/99 rule, 99th (Mean+3SD)	7.34 (2.64)	3	There are too few data points for the NAFTA calculator
Soya beans, dry	19	< 0.01	0.33	0.09	0.06	1	Lognormal 95/99 rule, 99th (UCLMedian95th)	0.64 (0.33)	0.5	Lognormality plot indicated saturation, resulting in overestimated 95/99th percentile
Root and tuber vegetables	15	0.03	0.45	0.23	0.23	0	Not lognormal Mean+3SD	0.57	1	Not lognormal distribution
Artichoke, globe	3	1.6	2.4	1.9	1.8	0	Lognormal 95/99 rule, 99th	3.09	5	There are too few data points for the NAFTA calculator
Asparagus	6	< 0.01	< 0.02		0.01	6			0.01*	Data < LOQ
Celery	7	0.23	3.2	1.2	0.43	0	Lognormal UCLMedian 95th	3.12	5	There are too few data points for the NAFTA calculator
Witloof chicory (sprouts)	5	0.03	0.11	0.06	0.05	0	Lognormal 95/99 rule, 99th	0.24	0.3	There are too few data points for the NAFTA calculator
Barley and oat	38	0.01	0.28	0.08	0.08	0	Not lognormal Mean+3SD	0.28	0.5	Not lognormal distribution, HR value equal the estimate
Wheat, rye and triticale	31	< 0.01	0.14	0.02	0.01	13	Not lognormal Mean+3SD	0.09	0.2	Not lognormal distribution, HR value higher than the estimate
Maize	20	< 0.01	0.02	0.01	0.01	17			0.02	Most data < LOQ
Rice	16	0.07	3.3	1.1	0.68	0	Lognormal 95/99 rule, 99th (UCL Median 95th)	8.91 (3.85)	5	Lognormality plot indicated saturation, resulting in overestimated 95/99th percentile
Tree nuts, except pistachios	9	< 0.01	0.01	0.01	0.01	8			0.01	Most data < LOQ
Pistachios	3	0.25	0.48	0.39	0.44	0	Lognormal 95/99 rule, 99th	0.86	1	There are too few data points for the NAFTA calculator
Cotton seed	12	< 0.01	0.54	0.06	0.01	5	Not lognormal Mean+3SD	0.51	0.7	There are too few data points for the NAFTA calculator

Commodity	No. of Trials	Min. Value (mg/kg)	Max Value (mg/kg)	Mean (mg/kg)	STMR (mg/kg)	No. ≤ LOQ	Statistical Calculation		JMPR	Comment/ Explanation
							Distribution Type	Estimate (mg/kg)	MRL (mg/kg)	
Peanuts	11	< 0.01	0.13	0.03	0.01	5	Not lognormal Mean+3SD	0.14	0.2	There are too few data points for the NAFTA calculator
Sunflower seed	6	0.01	0.24	0.07	0.04	0	Lognormal UCLMedian 95th	0.31	0.5	There are too few data points for the NAFTA calculator
Herbs, fresh	7	17	48	26	23	0	Lognormal 95/99 rule, 99th	52.3	70	There are too few data points for the NAFTA calculator
Peanut fodder (dw)	11	1.8	15	6.8	5.1	0	Lognormal 95/99 rule, 99th	25.0	30	There are too few data points for the NAFTA calculator
Soya bean fodder (dw)	19	8.0	62	36	36	0	Not lognormal Mean+3SD	77.3	100	Not lognormal distribution
Straw and fodder (dry) of cereal grains, except maize (dw)	87	0.25	11	2.3	1.7	0	Lognormal 95/99 rule, 95th (95/99 rule, 99th)	8.57 (11.75)	15	HR higher that the estimate
Maize fodder (dw)	20	1.1	25	7.0	5.0	0	Lognormal 95/99 rule, 99th	32.3	40	Agreed
Dried herbs, except dry hops	4	135	235	169	152	0	Lognormal 95/99 rule, 99th (Mean+3SD)	297 (307)	300	There are too few data points for the NAFTA calculator
Hops, dry	4	5.7	12	9.9	11	0	Not lognormal Mean+3SD	18.5	30	There are too few data points for the NAFTA calculator
Almond hulls (dw)	5	0.77	3.3	2.0	2.1	0	Lognormal 95/99 rule, 99th	6.47	7	There are too few data points for the NAFTA calculator
BOSCALID (219)										
Banana	22	0.05	0.42	0.1	0.08	6	Log-normal 95/99	0.6	0.6	MLE method was used to replace the non-detects. AA 8.1×0.08=0.645
Kiwi	4	0.8	2.38	1.42	1.24	0	-		5	The Meeting took into account that post harvest treatment normally produce more uniform residue distribution than foliar application, AA 5.1×1.24=6.2
BUPROFEZIN (173)										
Citrus	16	0.11	0.46	0.26	0.23	none	95/99 rule	0.61	1	Good agreement
Mango	5	< 0.01	0.045	0.021	0.01	2	UCLmedian 95th	0.09	0.1	Too many data points below LOQ There are too few data points for calculator
Cucumber	8	< 0.01	0.1	0.043	0.035	1	95/99 rule	0.17	0.2	Too few data points for calculator

Commodity	No. of Trials	Min. Value (mg/kg)	Max Value (mg/kg)	Mean (mg/kg)	STMR (mg/kg)	No. ≤ LOQ	Statistical Calculation		JMPR	Comment/ Explanation
							Distribution Type	Estimate (mg/kg)	MRL (mg/kg)	
Tomato	8	0.05	0.52	0.27	0.24	none	95/99 rule	1.40	1	Too few data points for calculator
CHLORANTRANILIPROLE (230)										
Pome fruit	25	0.01	0.23	0.07	0.07	0	95^{th} lognormal	0.32	0.4	Agreed with expert opinion and modelling
Cherry (stone fruit)	8	0.06	0.57	0.25	0.2	0	99^{th} lognormal	1.13	1	Agreed with expert opinion and modelling
Grape	17	0.02	0.52	0.2	0.12	0	99^{th} lognormal	1.39	1	NAFTA calculator did not agree with experience, rounded down
Melons (cucurbits)	7	0.01	0.1	0.06	0.07	0	99^{th} lognormal	0.33	0.3	Agreed with expert opinion
Chilli pepper (fruiting vegetables other than cucurbits)	9	0.02	0.41	0.12	0.07	0	UCLmed 95^{th}	0.43	0.6	Agreed with expert opinion
Spinach (leafy vegetables)	7	3.4	8.9	6.86	7.3	0	99^{th} lognormal	14.16	20	Experience and modelling suggested higher residues, rounded to 20
Celery	7	0.99	3.6	2.34	2.1	0	99^{th} lognormal	6.46	7	Agreed with expert opinion
Cotton seed	13	0.01	0.25	0.07	0.05	1	UCLmed 95^{th}	0.29	0.3	Agreed with expert opinion
Cereal hay	11	0.01	0.15	0.06	0.05	1	UCLmed 95^{th}	0.28	0.3	Agreed with expert opinion
CYPERMETHRIN (118) (including alpha- and zeta-Cypermethrin)										
Alfalfa fodder	6	8.2	18	11.6	10.3	0	99	22.4	30	The MRL was estimated before the NAFTA SC was used. '*n*' is too small for the NAFTA calculator.
Bean straw	7	0.32	1.1	0.60	0.51	0	99	1.61	2	The MRL was estimated before the NAFTA estimate was calculated. '*n*' is too small for the NAFTA calculator.
Cabbage	53	0.003	0.65	0.047	0.02	30	X(mean)+3 SD	0.32	1	The MRL was estimated before the NAFTA estimate was calculated. There are too many '< LOQ' values for the NAFTA calculator.

Commodity	No. of Trials	Min. Value (mg/kg)	Max Value (mg/kg)	Mean (mg/kg)	STMR (mg/kg)	No. ≤ LOQ	Statistical Calculation		JMPR	Comment/ Explanation
							Distribution Type	Estimate (mg/kg)	MRL (mg/kg)	
Carambola	5	0.02	0.09	0.036	0.02	3	X+3SD	0.13	0.2	The MRL was estimated before the NAFTA estimate was calculated. '*n*' is too small for the NAFTA calculator. There are too many '< LOQ' values for the NAFTA calculator.
Cereal grains	26	0.01	0.22	0.052	0.036	4	95UCL	0.26	0.3	The MRL was estimated before the NAFTA estimate was calculated. The data originate from barley trials in 4 countries. There is no evidence for random or stratified random selection to represent areas of commercial production (an implicit assumption required by the NAFTA calculation).
Chilli peppers	6	0.24	0.69	0.47	0.495	0	99	1.2	2	The MRL was estimated before the NAFTA estimate was calculated. '*n*' is too small for the NAFTA calculator.
Cucurbits	8	0.01	0.048	0.019	0.01	5	X+3SD	0.06	0.07	The MRL was estimated before the NAFTA estimate was calculated. '*n*' is too small for the NAFTA calculator. There are too many '< LOQ' values for the NAFTA calculator.
Durian	6	0.04	0.47	0.21	0.135	0	99	1.32	1	The MRL was estimated before the NAFTA estimate was calculated. '*n*' is too small for the NAFTA calculator.

Commodity	No. of Trials	Min. Value (mg/kg)	Max Value (mg/kg)	Mean (mg/kg)	STMR (mg/kg)	No. ≤ LOQ	Statistical Calculation		JMPR	Comment/ Explanation
							Distribution Type	Estimate (mg/kg)	MRL (mg/kg)	
Grapes	18	0.01	0.09	0.028	0.01	10	X+3SD	0.11	0.2	The MRL was estimated before the NAFTA estimate was calculated. There are too many '< LOQ' values for the NAFTA calculator.
Leafy vegetables	12	0.01	0.52	0.11	0.066	1	UCLmed	0.48	0.7	The MRL was estimated before the NAFTA estimate was calculated. The data originate from lettuce trials in 4 countries. There is no evidence for random or stratified random selection to represent areas of commercial production (an implicit assumption required by the NAFTA calculation).
Leeks	8	0.01	0.03	0.015	0.01	4	X+3SD	0.04	0.05	The MRL was estimated before the NAFTA SC was used. '*n*' is too small for the NAFTA calculator. There are too many '< LOQ' values for the NAFTA calculator.
Legume vegetables	12	0.01	0.45	0.19	0.22	3	X+3SD	0.69	0.7	The MRL was estimated before the NAFTA SC was used. The data originate from bean trials in one country. There is no evidence for random or stratified random selection to represent areas of commercial production (an implicit assumption required by the NAFTA calculation).

Commodity	No. of Trials	Min. Value (mg/kg)	Max Value (mg/kg)	Mean (mg/kg)	STMR (mg/kg)	No. ≤ LOQ	Statistical Calculation		JMPR	Comment/ Explanation
							Distribution Type	Estimate (mg/kg)	MRL (mg/kg)	
Litchi	6	0.25	0.79	0.50	0.495	0	99	1.16	2	The MRL was estimated before the NAFTA estimate was calculated. '*n*' is too small for the NAFTA calculator.
Longan	6	0.25	0.47	0.33	0.3	0	99	0.54	2	The MRL was estimated before the NAFTA estimate was calculated. '*n*' is too small for the NAFTA calculator.
Mango	6	0.09	0.35	0.20	0.19	0	99	0.61	0.7	The MRL was estimated before the NAFTA estimate was calculated. '*n*' is too small for the NAFTA calculator.
Oilseeds	20	0.01	0.06	0.035	0.05	19	X+3SD	0.1	0.1	The MRL was estimated before the NAFTA estimate was calculated. There are too many '< LOQ' values for the NAFTA calculator.
Okra	6	0.01	0.2	0.095	0.08	0	UCLmed	0.92	0.5	The MRL was estimated before the NAFTA estimate was calculated. '*n*' is too small for the NAFTA calculator.
Papaya	6	0.08	0.23	0.14	0.135	0	99	0.31	0.5	The MRL was estimated before the NAFTA SC was used. '*n*' is too small for the NAFTA calculator.
Pea hay	10	0.24	1	0.44	0.37	0	99	1.09	2	The MRL was estimated before the NAFTA SC was used. The data originate from pea trials in 3 countries. There is no evidence for random or stratified random selection to represent areas of commercial production (an implicit assumption required by the NAFTA calculation).

Commodity	No. of Trials	Min. Value (mg/kg)	Max Value (mg/kg)	Mean (mg/kg)	STMR (mg/kg)	No. ≤ LOQ	Statistical Calculation		JMPR	Comment/ Explanation
							Distribution Type	Estimate (mg/kg)	MRL (mg/kg)	
Pea pods	6	0.02	0.13	0.052	0.04	0	99	0.22	0.2	The MRL was estimated before the NAFTA estimate was calculated. '*n*' is too small for the NAFTA calculator.
Peppers, sweet	6	0.02	0.07	0.043	0.05	5	99	0.13	0.1	The MRL was estimated before the NAFTA estimate was calculated. 'n' is too small for the NAFTA calculator. There are too many '< LOQ' values for the NAFTA calculator.
Pome fruit	34	0.05	0.56	0.21	0.205	0	95UCL	0.68	0.7	The MRL was estimated before the NAFTA estimate was calculated. The data originate from trials on apples and pears in the USA and it is understood that site selection was based on zones and percentage national production, i.e., stratified random selection. Sufficient data are available to minimize errors of extrapolation. The NAFTA estimate agrees with the JMPR estimate.
Rice	22	0.15	1.1	0.57	0.57	0	X+3SD	1.16	2	The MRL was estimated before the NAFTA estimate was calculated. The data originate from trials on rice in USA and it is understood that site selection was based on zones and percentage national production, i.e., stratified random selection. The NAFTA estimate agrees with the JMPR estimate.

Commodity	No. of Trials	Min. Value (mg/kg)	Max Value (mg/kg)	Mean (mg/kg)	STMR (mg/kg)	No. ≤ LOQ	Statistical Calculation		JMPR	Comment/ Explanation
							Distribution Type	Estimate (mg/kg)	MRL (mg/kg)	
Stone fruit	12	0.52	0.94	0.66	0.59	0	99	1.05	1	The MRL was estimated before the NAFTA estimate was calculated. ‘*n*’ is marginally too small for the NAFTA calculator and the lognormal probability plot is not ideal for extrapolation.
Straw and fodder of cereal grains	16	0.7	6.1	3.04	3.2	0	99	12.44	10	The MRL was estimated before the NAFTA estimate was calculated. The data originate from wheat trials in the USA, where it is understood that site selection was based on zones and percentage national production, i.e., stratified random site selection. The NAFTA estimate is higher than the JMPR estimate.
Strawberries	8	0.01	0.048	0.017	0.01	5	X+3SD	0.06	0.07	The MRL was estimated before the NAFTA estimate was calculated. '*n*' is too small for the NAFTA calculator.
Sugar cane	9	0.01	0.17	0.05	0.05	6	99	0.39	0.2	The MRL was estimated before the NAFTA estimate was calculated. '*n*' is too small for the NAFTA calculator.
Sugar cane	9	0.01	0.17	0.050	0.05	6	99	0.39	0.2	The MRL was estimated before the NAFTA estimate was calculated. '*n*' is too small for the NAFTA calculator. There are too many '< LOQ' values for the NAFTA calculator.

Commodity	No. of Trials	Min. Value (mg/kg)	Max Value (mg/kg)	Mean (mg/kg)	STMR (mg/kg)	No. ≤ LOQ	Statistical Calculation		JMPR	Comment/ Explanation
							Distribution Type	Estimate (mg/kg)	MRL (mg/kg)	
Sugar cane	9	0.05	0.17	0.068	0.05	6	X+3SD	0.19	0.2	The MRL was estimated before the NAFTA estimate was calculated. '*n*' is too small for the NAFTA calculator. There are too many '< LOQ' values for the NAFTA calculator.
Tomato	12	0.05	0.08	0.060	0.05	6	X+3SD	0.1	0.2	The MRL was estimated before the NAFTA estimate was calculated. There are too many '< LOQ' values for the NAFTA calculator.
CYHALOTHRIN (146) (includes lambda-Cyhalothrin)										
Citrus fruit	15	0.02	0.16	0.06	0.05	0	99^{th}	0.16	0.2	
Pome fruit	8	0.05	0.1	0.08	0.08	0	99^{th}	0.15	0.2	There are too few datapoints for NAFTA calculation
Cherries	10	0.05	0.18	0.12	0.13	0	99^{th}	0.28	0.3	There are too few datapoints for NAFTA calculation
Peaches and apricots	14	0.02	0.33	0.11	0.1	0	99^{th}	0.34	0.5	There are too few datapoints for NAFTA calculation
Plums	12	0.01	0.1	0.03	0.02	2	Mean+3xSD	0.15	0.2	There are too few datapoints to usethe NAFTA calculation
Berries and other small fruit	18	0.01	0.09	0.03	0.02	1	Mean+3xSD	0.13	0.2	
Olives	12	0.03	0.42	0.17	0.13	0	99^{th}	0.75	1	There are too few datapoints to usethe NAFTA calculation
Mango	5	0.01	0.07	0.03	0.03	0	99^{th}	0.15	0.2	There are too few datapoints to usethe NAFTA calculation
Bulb vegetables	8	0.02	0.11	0.06	0.05	0	99^{th}	0.15	0.2	There are too few datapoints to usethe NAFTA calculation
Flowerhead brassica	10	0.04	0.3	0.19	0.22	0	Mean+3xSD	0.5	0.5	There are too few datapoints to usethe NAFTA calculation

Commodity	No. of Trials	Min. Value (mg/kg)	Max Value (mg/kg)	Mean (mg/kg)	STMR (mg/kg)	No. ≤ LOQ	Statistical Calculation		JMPR	Comment/ Explanation
							Distribution Type	Estimate (mg/kg)	MRL (mg/kg)	
Head cabbages	6	0.01	0.17	0.08	0.08	0	99^{th}	0.74	0.5	There are too few datapoints to usethe NAFTA calculation
Fruiting vegetables, Cucurbits	22	0.01	0.02	0.01	0.01	16	Mean+3xSD	0.02	0.05	There are too many datapoints < LOQ for NAFTA calculation
Fruiting vegetables, other than Cucurbits except mushrooms	37	0.01	0.18	0.05	0.03	8	Mean+3xSD	0.19	0.3	Difference HR-MRL considered not sufficient
Legume vegetables	23	0.01	0.11	0.03	0.02	5	Mean+3xSD	0.11	0.2	
Pulses	33	0.01	0.05	0.01	0.01	32	not calculated	-	0.05	Too many datapoints < LOQ for NAFTA calculation
Root and tuber vegetables	15	0.01	0.01	0.01	0.01	15	not calculated	-	0.01*	There are too many datapoints < LOQ for NAFTA calculation
Asparagus	6	0.01	0.01	0.01	0.01	0	not calculated	-	0.02	Too few datapoints for NAFTA calculation
Barley grain	29	0.01	0.33	0.04	0.02	3	Mean+3xSD	0.22	0.5	MRL recommended above HR
Maize grain	29	0.01	0.01	0.01	0.01	18	not calculated	-	0.02	Too many datapoints < LOQ for NAFTA calculation
Oats, rye, triticale and wheat grain	33	0.01	0.03	0.01	0.01	25	not calculated	-	0.05	There are too many datapoints < LOQ for NAFTA calculation
Rice grain	16	0.06	0.79	0.34	0.295	0	99^{th}	1.33	1	
Sugar cane	9	0.01	0.03	0.02	0.02	2	Mean+3xSD	0.04	0.05	There are too few datapoints for NAFTA calculation
Oilseeds	16	0.01	0.15	0.02	0.01	10	Mean+3xSD	0.13	0.2	There are too many datapoint < LOQ for NAFTA calculation
Cereal straw and fodder, dry	16	0.17	1.6	0.7	0.54	0	99^{th}	2.73	2	
Almond hulls, dry	5	0.32	1.1	0.56	0.42	0	99^{th}	1.55	2	There are too few datapoints for NAFTA calculation
DIMETHOATE (027)										
Peppers, sweet	5	0.03	0.26	0.1	0.06	0	UCL med 95^{th}	0.52	0.5	There are too few data points for the NAFTA calculator
Lettuce. head	25	0.01	0.17	0.04	0.02	7	95^{th} lognormal	0.33	0.3	

Commodity	No. of Trials	Min. Value (mg/kg)	Max Value (mg/kg)	Mean (mg/kg)	STMR (mg/kg)	No. ≤ LOQ	Statistical Calculation		JMPR	Comment/ Explanation
							Distribution Type	Estimate (mg/kg)	MRL (mg/kg)	
IMIDACLOPRID (206)										
Almond hull	10	0.23	2.6	1.6	1.45	0	Mean+3SD, 99th Percentile	4.0	5	There are too few data points for the NAFTA calculator
Berries and other small fruits (except cranberries, grapes and strawberries)	7	0.38	2.8	1.20	0.89	0	95/99 Rule, 99th Percentile	6.0	5	There are too few data points for the NAFTA calculator
Coffee	5	0.19	0.48	0.34	0.35	0	95/99 Rule, 99th Percentile	0.80	1	There are too few data points for the NAFTA calculator
Peas (dry)	6	0.14	1.0	0.59	0.62	0	95/99 Rule, 99th Percentile	3.5	2	There are too few data points for the NAFTA calculator
Peas (pods and succulent, immature seeds)	4	0.20	3.8	1.30	0.60	0	UCLMedian 95%, 99th Percentile	7.0	5	There are too few data points for the NAFTA calculator
Peas, shelled (succulent seeds)	6	0.31	1.1	0.65	0.58	0	95/99 Rule, 99th Percentile	1.8	2	There are too few data points for the NAFTA calculator
Peanut	12	0.05	0.40	0.15	0.12	4	95/99 Rule, 99th Percentile	0.70	1	There are too few data points for the NAFTA calculator
Peanut fodder	12	0.95	24	10.8	8.7	0	UCLMedian 95%, 99th Percentile	55	30	There are too few data points for the NAFTA calculator
Pomegranate	3	0.42	0.55	0.47	0.43	0	95/99 Rule, 99th Percentile	0.70	1	There are too few data points for the NAFTA calculator
Radish leaves	5	0.53	2.7	1.28	0.70	0	95/99 Rule, 99th Percentile	6.0	5	There are too few data points for the NAFTA calculator
Strawberry	9	0.12	0.35	0.20	0.17	0	95/99 Rule, 99th Percentile	0.45	0.5	There are too few data points for the NAFTA calculator
Sunflower seed	7	0.05	0.05	0.05	0.05	7	95/99 Rule, 99th Percentile	0.05	0.05*	There are too few data points for the NAFTA calculator
Tree nuts	20	0.01	0.01	0.01	0.01	19	Mean+3SD, 99th Percentile	0.01	0.01*	19 values lower than LOQ
MALATHION (049)										
Wheat	3	13	15	14.3	15	0	Mean + 3SD	18	10	Actual level limited by amount applied in first post-harvest application. There are too few data points for NAFTA Calculation.

Commodity	No. of Trials	Min. Value (mg/kg)	Max Value (mg/kg)	Mean (mg/kg)	STMR (mg/kg)	No. ≤ LOQ	Statistical Calculation		JMPR	Comment/ Explanation
							Distribution Type	Estimate (mg/kg)	MRL (mg/kg)	
MANDIPROPAMID (231)										
Broccoli	6	0.29	0.70	0.46	0.435	0	95/99 Rule	1.0	2	There are too few datapoints to usethe NAFTA calculation
Cabbage, head	6	0.90	1.80	1.30	1.21	0	95/99 Rule	2.5	3	There are too few datapoints for NAFTA calculation
Celery	6	0.74	7.80	3.66	2.70	0	95/99 Rule and UCLMedian 95th	25	20	There are too few datapoints for NAFTA calculation
Cucumber	7	0.01	0.07	0.02	0.02	0	99/95 Rule	0.15	0.2	There are too few datapoints for NAFTA calculation
Grapes	13	0.20	0.85	0.47	0.43	0	95/99 Rule	1.5	2	Rounded up
Leafy vegetables	22	1.20	11.5	6.28	5.65	0	95/99 Rule	25	25	Agreed
Melons except watermelon	6	0.06	0.26	0.14	0.115	0	95/99 Rule	0.45	0.5	There are too few datapoints for NAFTA calculation
Onion, bulb	8	0.01	0.04	0.02	0.01	5	mean+3σ	0.05	0.1	There are too many values below LOQ
Peppers	9	0.04	0.38	0.17	0.12	0	95/99 Rule	0.80	1	There are too few datapoints for NAFTA calculation
Potatoes	17	0.01	0.01	0.01	0.01	17	Not calculated	-	0.01*	All values below LOQ
Spring onion	3	0.25	1.74	0.82	0.48	0	95/99 Rule	6.0	7	There are too few datapoints for NAFTA calculation
Summer squash	5	0.02	0.08	0.05	0.04	0	95/99 Rule	0.20	0.2	There are too few datapoints for NAFTA calculation
Tomato	11	0.02	0.20	0.07	0.06	0	95/99 Rule	0.30	0.3	Agreed
METHOMYL (094)										
Apples	15	0.03	0.17	0.1	0.09	0	95/99 Rule	0.26	0.3	
Grapes (wine)	11	0.01	0.2	0.09	0.09	0	Mean+3SD	0.24	0.3	There are too few data points for NAFTA calculation
Lettuce	16	0	0.07	0.02	0.01	8	95/99 Rule	0.09	0.2	50% < LOQ and HR almost twice the penultimate value
PROFENOFOS (171)										
Cotton seed	11	< 0.05	1.2	0.49	0.35	3	UCLMedian	2.5	3	There are too few data points for NAFTA calculation.
Mango	6	< 0.01	0.07	0.05	0.06	1	Mean+3SD	0.15	0.2	There are too few data points for NAFTA calculation.

Commodity	No. of Trials	Min. Value (mg/kg)	Max Value (mg/kg)	Mean (mg/kg)	STMR (mg/kg)	No. ≤ LOQ	Statistical Calculation		JMPR	Comment/ Explanation
							Distribution Type	Estimate (mg/kg)	MRL (mg/kg)	
Mangosteen	4	1.9	3.7	2.45	2.1	0	95/99 Rule	5.0	10	There are too few data points for NAFTA calculation.
Tomato	9	0.18	4.7	1.74	1.3	0	UCLMedian	9.0	10	There are too few data points for NAFTA calculation.
PROTHIOCONAZOLE (232)										
Barley, wheat straw	30	0.07	1.2	0.38	0.25	0	Log-normal	1.8	2	MRL estimated on dry weight basis, 7.4×Med would give 1.85
Peanut	12	0.02	0.02			12			0.02	Statistical methods are not applicable
Barley and wheat	32	0.01	0.02		0.01	28			0.05	28 values at or below 0.01. Statistical methods are not applicable
Rape seed	11	0.01	0.02	0.01	0.01	7			0.05	10 values at or below 0.01. Statistical methods are not applicable
SPINETORAM (233)										
Oranges	6	< 0.01	0.03		0.02	2	Mean+3SD	0.007	0.007	There are too few data points for NAFTA calculation.
Apple	10	< 0.01	0.03		0.01	4	Mean+3SD	0.05	0.05	There are too few data points for NAFTA calculation. There are too many values below LOQ.
Tomato	6	< 0.01	0.03		0.01	2	99/95 Rule	0.06	0.06	There are too few data points for NAFTA calculation.
Leaf lettuce	6	0.15	7.80	1.58	0.33	0	Mean+3SD	11	10	There are too few data points for NAFTA calculation.
Sugar beet	6	< 0.01	< 0.01		0.01	6			0.01(*)	There are too few data points for NAFTA calculation. There are too many values below LOQ.
Tree nuts	6	< 0.01	0.01		0.01	3^{Φ}			0.01	There are too few datapoints to usethe NAFTA calculation. There are too many values below LOQ. MRL based on pecan trial results, supported by trials on almonds. $^{\Phi}$In five trials, samples were

Commodity	No. of Trials	Min. Value (mg/kg)	Max Value (mg/kg)	Mean (mg/kg)	STMR (mg/kg)	No. ≤ LOQ	Statistical Calculation		JMPR	Comment/ Explanation
							Distribution Type	Estimate (mg/kg)	MRL (mg/kg)	
										harvested earlier than required PHI.
SPIROTETRAMAT (234)										
Citrus	23	0.10	0.32	0.17	0.18	3	Mean+3SD	0.37	0.5	
Pome fruit	18	0.04	0.49	0.15	0.13	0	LN99	0.65	0.7	Adequate *n* = 18.
Stone fruit	6	0.68	1.6	1.3	1.3	0	Mean+3SD	2.19	3	There are too few samples for NAFTA calculation. Supporting data from peaches and plums for cherry.
Grapes	15	0.06	1.0	0.37	0.32	0	LN99	1.50	2	Adequate *n* = 15.
Flowering Brassica	8	0.08	0.39	0.19	0.16	0	LN99	0.69	1	There are too few samples for NAFTA calculation. Diversity in flowering Brassica.
Cucurbit	21	0.02	0.13	0.04	0.02	12	Mean+3SD	0.15	0.2	Excessive LOQ for NAFTA calculation.
Fruiting vegetables	8	0.27	0.76	0.43	0.40	0	LN99	0.93	1	Small field trial data set but substantial supporting data from greenhouse trials. There are too few samples for NAFTA calculation.
Leafy vegetables	10	0.61	5.0	2.5	2.8	0	Mean+3SD	6.95	7	Based on mustard green, but substantial supporting data from lettuce, spinach. There are too few samples for NAFTA calculation.
Potato	20	0.02	0.37	0.13	0.09	0	LN99	0.66	0.8	Adequate *n* = 20.
Celery	8	0.26	2.4	0.81	0.42	0	Mean+3SD	3.33	4	There are too few samples for NAFTA calculation.
Tree nuts	11	0.02	0.25	0.08	0.05	0	LN99	0.29	0.5	There are too few samples for NAFTA calculation.
Hops (dry)	4	2.2	4.9	3.9	4.25	0	LN99	8.85	15	Very small data set. Known variability in hops residues.
Almond hulls	6	1.3	4.7	3.4	4.05	0	LN99	10.55	10	There are too few samples for NAFTA calculation.

Commodity	No. of Trials	Min. Value (mg/kg)	Max Value (mg/kg)	Mean (mg/kg)	STMR (mg/kg)	No. ≤ LOQ	Statistical Calculation		JMPR	
							Distribution Type	Estimate (mg/kg)	MRL (mg/kg)	Comment/ Explanation
TEBUCONAZOLE (189)										
Pome fruit	13	< 0.05	0.47	0.21	0.19	2	LN, 99^{th}	0.82	1	
Plums	22	< 0.02	0.12	0.06	0.06	5	LN, 99^{th}	0.2	0.2	
Elderberries	4	0.32	0.73		0.37	0	NA		2	There are too few datapoints to usethe NAFTA calculation
Mango	8	< 0.05	<0.1		0.02	6	LN, 99^{th}	0.24	0.1	Too few data points to use the SC 75% of the values < LOQ
Papaya	6	0.06	1.2	0.35	0.18	0	UPL Median 95^{th}	2.07	2	There are too few datapoints to usethe NAFTA calculation
Leek	12	0.03	0.44	0.21	0.20	0	μ ± 3SD	0.5	1	There are too few datapoints to usethe NAFTA calculation
Garlic	7	< 0.02	0.06	0.03	0.02	4	μ ± 3SD	0.07	0.1	There are too few datapoints to usethe NAFTA calculation
Onions	11	< 0.02	0.06	0.04	0.05	8	μ ± 3SD	0.09	0.1	Too few data points to use the SC 73% of the values < LOQ
Brassicas	19	< 0.05	0.56	0.17	0.07	8	μ ± 3SD	0.66	1	42% of the values < LOQ
Melons	20	< 0.01	0.10	0.05	0.05	2	μ ± 3SD	0.12	0.2	There are too few datapoints to usethe NAFTA calculation
Watermelon	5	< 0.01	0.04	0.02	0.02	2	LN, 99^{th}	0.08	0.1	There are too few datapoints to usethe NAFTA calculation
Sweet corn	4	< 0.01				4	NA		0.1	There are too few datapoints to usethe NAFTA calculation
Tomato	15	0.03	0.46	0.21	0.19	0	LN, 99^{th}	1.06	1	
Head lettuce	8	0.18	3.2	1.21	0.98	0	UPL Median 95^{th}	8.8	5	There are too few datapoints to usethe NAFTA calculation
Beans	8	0.12	1.2	0.51	0.49	0	LN, 99^{th}	2.05	2	There are too few datapoints to usethe NAFTA calculation
Soya beans	28	< 0.01	0.06	0.03	0.02	7	μ ± 3SD	0.09	0.1	-
Carrot	13	< 0.1	0.22	0.14	0.12	3	LN, 99^{th}	0.28	0.5	23% of the values < LOQ
Artichoke	6	< 0.05	0.32	0.18	0.15	1	LN, 99^{th}	0.73	0.5	Too few data points to use the SC 16% of the values < LOQ
Barley	37	< 0.05	1.1	0.19	0.06	17	μ ± 3SD	1.08	2	46% of the values < LOQ

Commodity	No. of Trials	Min. Value (mg/kg)	Max Value (mg/kg)	Mean (mg/kg)	STMR (mg/kg)	No. ≤ LOQ	Statistical Calculation		JMPR	Comment/ Explanation
							Distribution Type	Estimate (mg/kg)	MRL (mg/kg)	
Rice	8	0.11	0.97	0.36	0.28	0	LN, 99th	1.5	2	There are too few datapoints to usethe NAFTA calculation
Maize	4	< 0.1					NA		0.1	There are too few datapoints to usethe NAFTA calculation
Peanut	19	< 0.01	0.08	0.04	0.04	13	μ ± 3SD	0.1	0.1	-
Rape seed	26	< 0.05	0.28	0.09	0.09	3	LN, 95th	0.39	0.5	There are too few datapoints to usethe NAFTA calculation
Coffee	5	0.02	< 0.1			3	NA		0.1	There are too few datapoints to usethe NAFTA calculation. 60% of the values < LOQ
Hops	8	5.8	21	11	9.65	0	LN, 95th	31.5	30	There are too few datapoints to usethe NAFTA calculation
Barley straw	36	0.16	19.3	3.6	2.5	0	LN, 95th	22.6	30	

[a] **95LN** is the 95% upper confidence bound on the point estimate of the 95th percentile.

99LN is the 99% point estimate.

UCL Median 95 is the 95th percentile of the upper confidence limit of the median value (50th percentile), assuming a coefficient of variation of 1 and a lognormal distribution. In such cases the 95th percentile is 3.9 times the median. The value is 3.9 times the upper confidence limit on the median.

Mean + 3 SD is the mean plus three standard deviations. According to the Chebychev Rule, at least 89% of measurements are within three standard deviations of the mean, and this is regardless of the shape of the frequency distribution.

Dw - dry weight, LOQ, limit of quantification; NA - NAFTA, SC – Statisical calculator, SD - Standard deviation

2.8 NATURE OF RESIDUE DATA POPULATIONS AND METHODS FOR COMBINING RESIDUE TRIAL DATA SETS

The JMPR estimates maximum residue levels (indicated with mrl to distinguish from the Codex MRL) for use as Codex MRLs.[16] The recommended maximum residue levels (mrl) are based on supervised trials reflecting the highest of the nationally recommended dosage and shortest pre-harvest intervals. The number of such trials is usually limited. In order to improve the reliability of the estimated supervised trial median residues (STMRs), the JMPR regularly combined those data sets which reflected similar use patterns and they appeared to come from similar residue populations, and verified the assumption with the Mann-Whitney U-test.[17] The JMPR has recently been exploring the approach of combining data sets for estimation of mrls.

Statistical methods of mrl estimation generally aim to estimate a prescribed percentile value (e.g., 95th percentile) for the underlying population based on the available data. This involves making assumptions regarding the underlying distribution and estimating the range of residues beyond the observed values. In particular, care is required in selection of data which should be:

- from a single population or the equivalent of a single population;
- a random sample (or equivalent such as stratified random) from the population;
- available in sufficient number to provide some assurance about the data distribution and to minimize the errors of extrapolation required to estimate high percentiles.

The NAFTA Working Group published the final version of a method for the statistically based estimation of the MRLs.[18] The Working Group stated that “when the sample size is 15 or larger, the calculated MRLs consistently provide narrower ranges”, and “if the data set has less than 10 data points, the MRL calculations ... are not very precise”.

An independent review of the NAFTA calculator noted that for small sample sizes the methods employed lead to “both poor theoretical grounding and poor simulation performance” which is “not surprising given the problem of extreme percentile of an unknown distribution based on a small sample is an extremely difficult one”. It was suggested that “rather than trying to modify the appropriate tolerance limit calculation so that its performance in small samples is less variable (and thus less appropriate), it is more sensible to simply place a lower limit on the allowable size of

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[16] Codex Alimentarius Procedural Manual: Codex maximum limit for pesticide residues (MRLP) is the maximum concentration of a pesticide residue (expressed as mg/kg), recommended by the Codex Alimentarius Commission to be legally permitted in or on food commodities and animal feeds. MRLs are based on GAP data and foods derived from commodities that comply with the respective MRLs are intended to be toxicologically acceptable.

Codex MRLs, which are primarily intended to apply in international trade, are derived from estimations made by the JMPR following:

(a) toxicological assessment of the pesticide and its residue; and

(b) review of residue data from supervised trials and supervised uses including those reflecting national good agricultural practices. Data from supervised trials conducted at the highest nationally recommended, authorized or registered uses are included in the review. In order to accommodate variations in national pest control requirements, Codex MRLs take into account the higher levels shown to arise in such supervised trials, which are considered to represent effective pest control practices.

[17] In: Pesticide Residues in Food—2001. Report of the JMPR 2001, FAO Plant Production and Protection Paper, 167, p. 14

[18] http://www.pmra-arla.gc.ca/english/pdf/mrl/calc2-eng.xls

samples to be used in mrl setting." The review strongly recommended that no adopted methodology allow the setting of an MRL based on a sample of less than 15 observations.

The individual or combined residue data sets available for estimation of STMR or mrls typically vary from 3 to 50 or more (minimum of 1 to a maximum of 71). Figure 1 shows the frequency of the number of trials, from which the mrls were estimated by the JMPR from 2002 to 2007, excluding those trials with over 80% of non-detected residues.

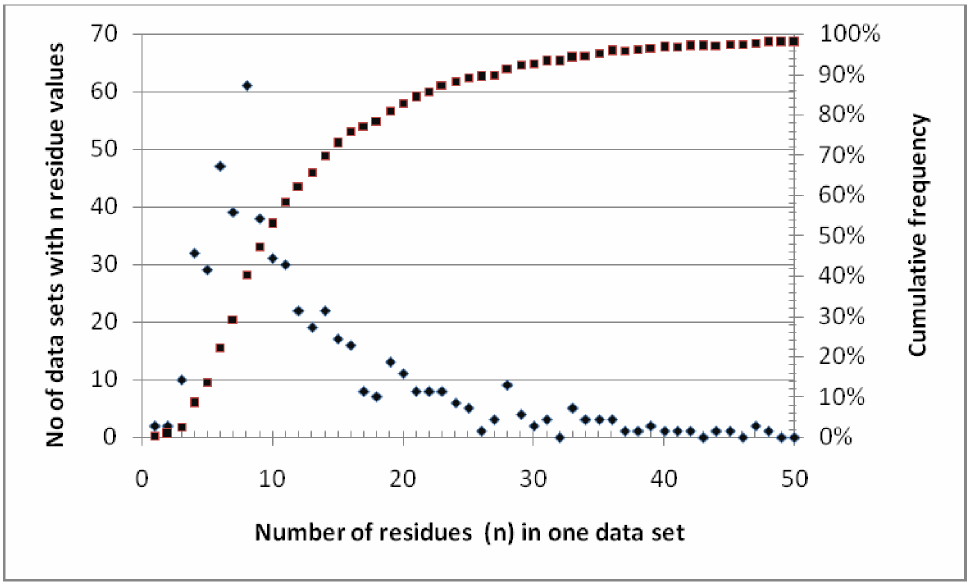

Figure 1 Frequency of occurrence of data sets consisting of *n* residue values used by JMPR between 2002 and 2007

The figure indicates that most frequently the STMR/mrl estimates were based on 8 (61), 6 (47) and 9 (38) supervised trials, and data sets consisting of 9 or less trials represented 47.2% of the 551 cases studied.

In the majority of cases (70%) less than 15 relevant residue trials were available to JMPR for estimating an mrl. The number of available trials reflects the requirements of national regulators. The use of combined sets of observations, from related, but not identical, field trials (i.e., deriving from similar GAPs) may allow more reliable use of statistical methods for estimating mrls, as they consist of larger number of observations than the individual ones. However, the validity of mrl estimates based on combined data sets is reliant on the comparability of the information from the individual trials. The various data sets derived from supervised trials carried out in various countries or on similar crops cannot be automatically pooled together. The distribution of residue data shall be carefully examined and only those which may be expected to form the same populations should be combined.

The proper evaluation of residue data requires the understanding of the nature of residue populations and the limitations of the estimations based on small samples.

1. Nature of residue data populations

1.1 Between fields variability of residues

Due to the large number of factors affecting the distribution and magnitude of the residues within a field trial, the variability of residues among field trials in composite samples of typical size of 12–25 units is large (typical co-efficient of variation (CV) values are in the range of 60 to 110%[19]).

Statistical analysis of supervised trial data sets with minimum 15 residue values, evaluated by the JMPR between 1997 and 2007, indicates that in many cases (70% of 144 data sets) log-normality of the data sets cannot be excluded. Although this should not be taken as evidence that the underlying populations conform to log-normal distributions, the following discussion will proceed on the assumption of log-normality for residue populations.

Figures 2 and 3 illustrate the hypothetical log normal distribution of residues simulating thousands of supervised trials where a crop has been harvested at different times after application at the same rate, say 1 kg ai/ha. Table 2 contains the parameters of the distributions used for constructing the figures.

Table 2 Parameters used to generate the lognormal curves of hypothetical residues.

PHI (days)	7	14	21	28	All data
Limited decline					
Mean ln(residue)[a]	-0.78	-0.88	-0.98	-1.08	
SD ln(residue)[a]	0.98	0.98	0.98	0.98	
Median[a]	0.46	0.42	0.38	0.34	0.39
95th percentile[a]	2.30	2.08	1.88	1.70	2.00
Moderate decline					
Mean ln(residue)	-0.78	-1.08	-1.38	-1.68	
SD ln(residue)	0.98	0.98	0.98	0.98	
Median	0.46	0.34	0.25	0.19	0.29
95th percentile	2.3	1.7	1.26	0.94	1.62

[a] Parameters of the hypothetical log-normal distribution

The graphs have been constructed to examine the case where the application rate is the same in two countries but the pre-harvest interval (PHI) is different, however the conclusions would equally apply to other situations (different application rate, same PHI; different application rate and different PHI).

The graphs can be thought of as the actual distribution of residues from which a small number of residue trial data are evaluated in MRL estimation. Although for each graph there is significant overlap in the distributions, each distribution has a different 95th percentile and could potentially lead to a different MRL recommendation for GAPs that have different PHI values.

In the first example (Figure 2) there is limited decline in residues with time, the median for residues at 7 days PHI is 0.46 mg/kg and at 28 days 0.34 mg/kg while the 95th percentiles are 2.3 and 1.7 mg/kg respectively. In the second example the decline in residues is moderate with median values of 0.46 mg/kg at 7 days and 0.19 mg/kg at 28 days while the 95th percentiles are 2.3 and 0.94 mg/kg respectively.

[19] Ambrus A., 2000. Measurement of uncertainty in pesticide residue analysis: implications in legal limits, Ital. J. Food Sci. N. 3 vol 12. 259-278.

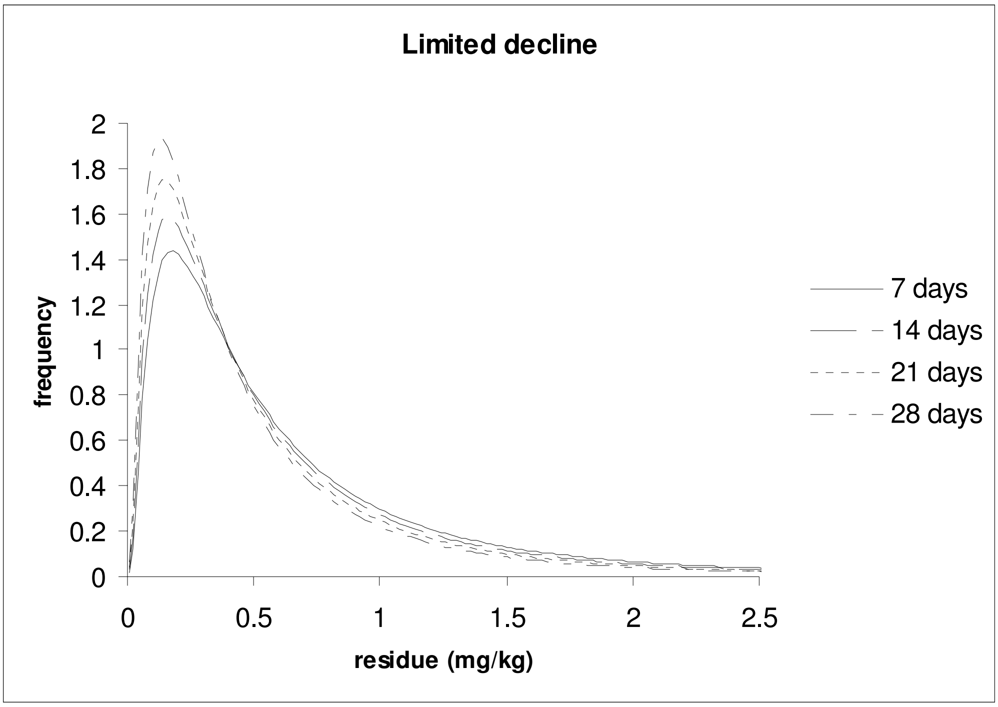

Figure 2 Distribution of residues at different PHIs following treatment with a pesticide with limited decline in time

Under practical conditions the true distribution of the residues is not known, we can only estimate them from a small number of samples.

We may assume that a set of trials conducted at maximum label conditions is equivalent to a random sample taken from a large residue population resulted from the pesticide application according to maximum GAP that occur in typical farming practice. The set of such trials is then considered as a stratified random sample representing the agriculture practice where the maximum amount of pesticides (dosage rate, number of applications) were used at shortest PHI permitted by the national GAP. Thus the residues indicate their upper concentration range that may be present in marketed commodities treated according to the particular GAP.

In reality, many crops are treated with longer PHIs and/or lower application rates resulting in residues lower than the MRLs, as indicated by the results of market place monitoring programmes, where only a very small proportion of the marketed commodities contains residues close or above the MRL.

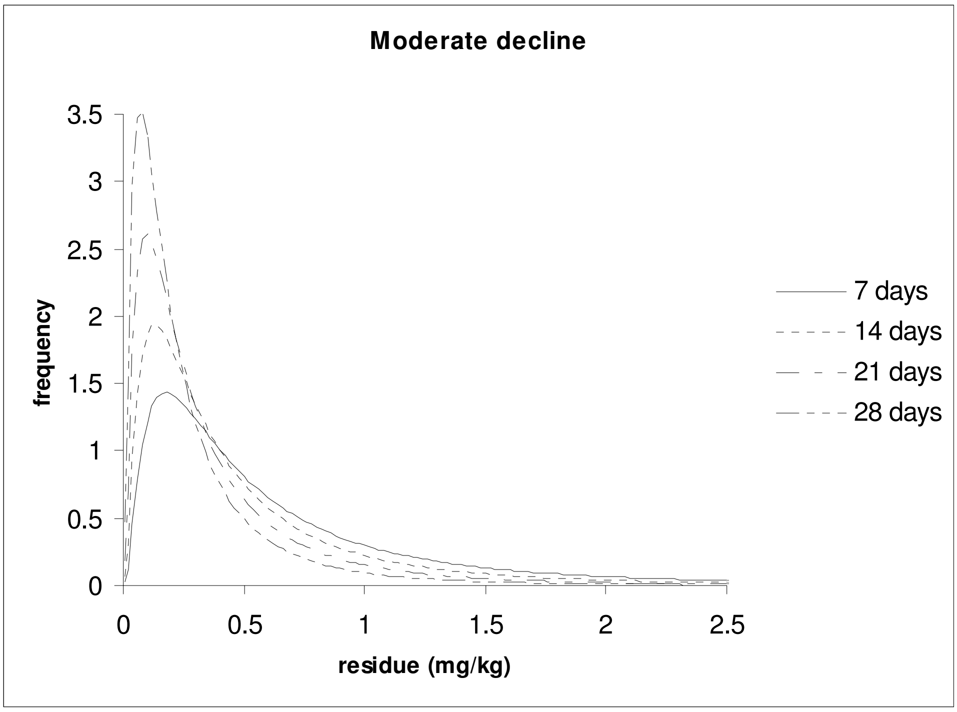

Figure 3 Distribution of residues at different PHIs following treatment with a pesticide with moderate decline in time

1.2 Variability of residues deriving from sampling

The inevitable variability of residues resulting from the wide dispersion of the residues within and among fields is illustrated with the results of random samples of size 4–50 drawn with replacement from a fixed parent population.

In the described process 1000 samples, consisting of either 50 or 30 residue values, were drawn with replacement from the parent population shown in the left column of Table 3. From the 1000 samples ordered according to their mean residue, the 975^{th} (R0.975) and 25^{th} (R0.025) samples were taken and their maximum, mean, median, minimum, CV and SD values were listed in the columns under R0.975 and R0.025. Similarly the parameters of samples ordered according to their median values are listed under columns P0.975 and P0.025.

Even when 1000 random samples, representing 50 and 30 residue trials (sample size), were drawn with replacement from a theoretical parent sample population with log-normal distribution and a CV value of 0.77, the characteristics of the populations showed substantial variation. The results are summarized in Table 3.

Table 3 Characteristic parameters of samples drawn with replacement from a log-normally distributed parent populations with a CV of 0.77

	Parent population	Sample populations (1000 samples of *n* trials)							
	n = 10 000	*n* = 50		*n* = 50		*n* = 30		*n* = 30	
Sample		R0.975[20]	R0.025	P0.975[21]	P0.025	R0.975	R0.025	P0.975	P0.025
Max	25.21	13.54	16.14	11.14	16.14	19.39	9.60	14.08	8.05
Mean	3.52	4.32	2.82	3.84	2.87	4.59	2.63	3.22	2.90
Min	0.20	0.52	0.73	0.73	0.56	0.73	0.73	0.44	0.52
Median	2.78	3.55	2.39	3.47	2.19	2.96	2.37	2.46	2.07
CV	0.77	0.69	0.83	0.59	0.94	1.04	0.75	0.87	0.72
SD	2.717	2.973	2.350	2.253	2.705	4.782	1.959	2.802	2.077

Notes: Parent population consists of residues in samples taken from 10 000 trials

Columns marked with R0.975 and R0.025 show the maximum, mean, median and minimum co-efficient of variation and standard deviation for the dataset representing the 97.5th and 2.5th percentile of residues in 1000 samples, each with *n* = 30 or 50 residue values, ordered according to their average residues. The columns P0.975 and P0.025 show the same parameters of samples ordered according to their median

The range of R0.025 and R0.975 encompasses the values obtained from samples corresponding to the 2.5% and 97.5% of the sample populations (covering the 95% centre portion of the of the sample population)

When small number of trials (4–10 data points) is sampled from the same parent population, the variability in individual sample mean, median, maximum and minimum residues is larger and show inverse relationship with the square root of sample size.

The expectable variation is demonstrated with the 66 trial data obtained with tolylfluanid on tomato.[22] As the range of residues measured as parent tolylfluanid and the sum of the parent compound and its metabolite (DMST) was very similar, for this example the 33 residue values for tolyfluanid have been combined with the 33 values for the sum of tolyfluanid and DMST, in order to obtain a reasonably large realistic data set used as parent population for simulation of sampling. Table 4 shows the individual residue values for samples that represent the 2.5th and 97.5th percentile of 1000 data sets ordered first according to their median residues and then sets having the same median values were ordered by their maximum residue values.

[20] R0.975 refers to the individual dataset that is at rank represented by the 97.5th percentile when datasets are ordered by average.

[21] P0.975 refers to the individual dataset that is at rank represented by the 97.5th percentile when datasets are by ordered median

[22] In: Pesticide Residues in Food—2002. Report of the JMPR 2002, FAO Plant Production and Protection Paper, 172.

Table 4 Residues in data sets obtained with random sampling from a parent population of 66 residue values

N	Percentile	Individual residues in the relevant data set									
4	P.025	0.05	0.05	0.19	0.49						
	P.975	0.18	0.4	1.27	1.4						
5	P.025	0.05	0.07	0.14	0.14	0.48					
	P.975	0.07	0.27	0.67	0.77	1.27					
6	P.025	0.07	0.15	0.15	0.18	0.27	0.56				
	P.975	0.05	0.42	0.47	0.77	0.77	0.99				
8	P.025	0.04	0.08	0.1	0.15	0.22	0.24	0.6	0.72		
	P.975	0.18	0.4	0.54	0.59	0.59	0.67	1.5	1.5		
10	P.025	0.05	0.07	0.15	0.15	0.16	0.23	0.47	0.5	0.54	0.67
	P.975	0.14	0.29	0.34	0.35	0.54	0.59	0.6	0.7	1.4	2.2

Table 5 includes the characteristic parameters of the original residue population (66 data points) called parent population and the samples covering the 95% range of sample populations (between 2.5th and 97.5th percentiles).

Comparing the estimated maximum residue levels based on the NAFTA and the traditional JMPR procedures indicates the uncertainty of the estimation based on small number of residue data points (samples). For instance, there is 95% probability that we may get random samples from the same ‘true’ parent data population leading to an estimated mrl ranging from 1–6 mg/kg for sample size of 5 or from 1.5–3.5 for sample size of 10 with NAFTA method and 0.5–2 and 1–3 with the JMPR procedure for the same samples.

The large inevitable variation of residues in small samples underlines the importance of proper selection of valid residue data which form the data base for the estimation of the mrls, especially in those cases where statistically based estimation of mrls is aimed, for instance, by applying the NAFTA calculation method.

Table 5 Characteristic values of original supervised residue data set and those of 1000 samples of size *n* withdrawn from the original residue data

n	Percentile	Residues in samples [a]				Estimated MRLs		
		Max	Med	Mean	Min	NAFTA		JMPR
66		2.20	0.370	0.452	0.040	1.8	2	3
4	P.025	0.49	***0.120***	0.195	0.050	1.3	1.5	0.7
	P.975	1.40	**0.835**	**0.813**	0.180	6	6	2
5	P.025	0.48	0.140	***0.176***	0.050	1	1	0.5
	P.975	1.27	0.670	0.610	0.070	6	6	2
6	P.025	0.56	0.165	0.230	0.070	1	1	0.7
	P.975	0.99	0.620	0.578	0.050	1.6	2	2
8	P.025	0.72	0.185	0.269	0.040	1.3	1.5	1
	P.975	1.50	0.590	0.746	0.180	3.5	3.5	2
10	P.025	0.67	0.195	0.299	0.050	1.3	1.5	1
	P.975	2.200	0.565	0.715	0.140	3.5	3.5	3

Notes: [a] The values presented represent the 95% range of the 1000 small samples

The maximum observed median and mean values of all data are indicated with bold and the minimum values are with bold-italics numbers

2. Principles of selection of residue data for estimation of mrls

2.1 Estimation based on the residues derived from the maximum (one) GAP

In accordance with the Codex definitions and general practice of the JMPR, the mrls are primarily estimated based on the GAP that leads to the highest residue (**ONE GAP**, the critical or **maximum GAP**), i.e., the trials represent the maximum residue anticipated when a pesticide is applied according to the one GAP (label directions, usually maximum permitted application rate, shortest PHI). The Codex Alimentarius definition (JMPR practice) implies that only the results of “supervised trials conducted at the highest nationally recommended, authorized or registered use” are included in mrl estimation (i.e., one maximum GAP per country, one of these is used to select data for mrl estimation).

The focus on one GAP allows for alternative GAP to be assessed if there is an identified dietary intake problem.

As a general precondition, for reliable estimation of maximum residue levels an adequate number of independent trials are required which reflect the national maximum GAP and conducted according to well designed protocols that consider geographical distribution and the inclusion of a number of different growing and management practices, and growing seasons.

Maximum residue level estimates may be based on an accepted/recognized extrapolation of trial data to cover commodities within a group which had shown similar residue pattern. Application should be made using equipment and spray volumes likely to give rise to the highest residues. As weather (not climate) is usually the major factor in determining the resultant residues for such trials, only one field trial would normally be selected per trial site if multiple plots/trials are conducted in parallel.

The decline rate of a pesticide may be different at various geographical locations depending on, among others, the weather, cultivation mode and soil conditions. Under practical conditions the number of trials which can be performed for a given commodity is limited. On the other hand, a larger data set *representing statistically not different residue population* provides more accurate estimation of the selected percentile than a small data set derived from trials representing the critical GAP but only if the data are not biased by missing a segment of the underlying population such as might occur if data were from a single season and from the same region, and consequently did not reflect the actual range of growing conditions and management practices.

Consequently, where only limited number of trial data is available from the ‘ONE’ GAP assumed to lead to the highest magnitude of residues, one approach is to consider those GAPs which may possibly lead to similar magnitude of residues, and this assumption can be confirmed based on prior experience and with suitable statistical methods described in section 3.

2.2 Consideration of all trials conducted at various maximum GAPs

As an alternative to the selection of the ONE GAP described in section 2.1, the other possibility would be to include all trials in the residue data set used for estimation of mrls provided that residues are derived from trials conducted with maximum dosage rate at shortest PHI permitted by any relevant national maximum GAP.

Though, from global trade prospective such an approach may better reflect the residue population in traded commodities, this method leads to two conceptual problems as it would include residue data with significantly lower median (mean) values, which would result in lower estimated daily intake than that obtained from the residues reflecting the highest GAP, and lower MRLs if the latter one would be calculated with the NAFTA procedure.

The effect of combining all residues deriving from any maximum GAP is illustrated with an example:

Lets assume that the data set A, showing lognormal distribution (0.050, 0.060, 0.070, 0.100, 0.130, 0.140, 0.140, 0.140, 0.160, 0.170, 0.210, 0.210, 0.230, 0.270, 0.270, 0.280, 0.290, 0.330, 0.340, 0.340, 0.380, 0.380, 0.410, 0.440, 0.490, 0.500, 0.570, 0.570, 0.680, 0.680, 0.730, 0.800, 0.840, 0.860, 0.900, 0.900, 0.900, 0.910, 0.920, 1.060, 1.070, 1.170, 1.210, 1.360, 1.430, 1.480, 1.800, 1.890, 1.990, 3.550) would be combined with additional low residue values (15×0.05 and 16×0.10) representing a different maximum GAP. The estimated maximum residues based on 95UCL calculation would be 3.51 mg/kg and 2.24 (based on California mean+3×SD), respectively, leading to mrl estimates of 4 mg/kg and 2.5 mg/kg, regardless that the maximum valid residue value is 3.55 mg/kg. The median values would be 0.5 mg/kg and 0.17 mg/kg, respectively.

Combination of such data is clearly inappropriate as the deterministic approach used for estimation of daily intake aims to identify the highest residue level, which a certain portion of the world populations might be exposed to.

The above approach would also contradict with one of the purposes of Codex MRLs as MRLs for trade and it would also be unfair to growers of a country with critical GAP if the estimated mrl would be much lower than the residues expected after applying the pesticide at maximum GAP.

It should be noted that:

1. there is a subtle difference in the two selection procedures and the mrl recommendations will differ. In scenario 1 with data set A, the residues at the high end of the distribution dominate and this leads to an estimation of a larger mrl value. In scenario 2, adding trials with low residues, as occurs when datasets are combined, gives a smaller estimate for the 95th percentile even though the highest residue remains the same;
2. the mrl estimated with the NAFTA method may also be different where similar data sets are combined due to the different calculation methods used depending on the size of the sample and the distribution of residues.
3. In special cases where residues do not show evidence of decline and do not scale with application rate, such as triadimefon/triadimenol in grapes (JMPR 2007) it may be appropriate to consider wider range of GAPs.

3. Statistical methods for deciding on the similarity of data sets

As it was shown in section 1, the inevitable sampling variation may lead to an inaccurate estimation of the true residue population resulted from the use of a pesticide according to maximum GAP. The NAFTA statistical procedure for estimation of mrls claimed to provide reasonable estimates based on samples larger than 15, and the estimation becomes more precise if it is based on larger residue data sets.

Under practical conditions such number of trials reflecting the critical GAP is rarely available; one approach is to combine similar data sets. While similarity of data is extremely difficult to assess statistically and should primarily be based on other scientific criteria, tools are available that can be used to ascertain if data sets come from populations characterized by similar median/mean and variance.

In view of the skewed distribution of residues and the difficulties of describing the residue distribution with parametric methods, distribution free statistical methods should be applied for testing the similarity of sample populations.

The JMPR routinely applied the Mann-Whitney U test for comparing two data sets before they were combined. However, there are cases where more than two data sets should be compared. In such cases the U-test is not applicable, and the so called Kruskal-Wallis H-test may be used. It assumes that the samples are taken from continuous populations of similar shape, the errors in individual residue values are independent. Thus, if the null hypothesis is rejected we do not know whether the median values, the shape or the variance of the tested populations are different. It is applicable for ***k*** independent samples, provided that the data sets are not too small (≥ 4). For the purpose of the test, samples are independent if the supervised trials had been carried out at different sites.

The null hypothesis, H_0, is that the ***k*** independent sets of samples were taken from the same parent population. The calculation is illustrated in Table 5 with the example of deltamethrin residues in leafy vegetables (2002 JMPR) and performed as follows:

4. Mark, with different colours and or letters, the residue values belonging to the ***k*** data sets consisting of N_i residue values to enable the distinction of data sets from each other.
5. Combine the residues from the ***k*** data sets in one data set consisting of $N=\sum N_i$ residue data, and arrange the residues in ascending order.
6. Determine the rank number of individual residues (r_i) giving the same rank for the same residue values (ties) and calculate the sum of the ranks (R_i) for each data set.
7. Calculate the H statistics and the correction factor (C_f) for the ties.

$$H = \frac{12}{N(N+1)} \sum_{i=1}^{k} \left(\frac{R_i^2}{N_i} \right) - 3(N+1)$$

$$C_f = 1 - \frac{\sum_j T_j}{N^3 - N}$$

Where $T_j = t^3 - t$, and t is the number of ties. For instance the residue values of 0.03 occur twice, so t =2 and $T_j = 2^3 - 2 = 6$. The value of 0.1 occurs 5 times, so t = 5 and $T_j = 5^3 - 5 = 120$.

8. Calculate the corrected H_c value:

$$H_c = \frac{H}{C_f}$$

9. The H_c value follows χ^2 (chi square) distribution with ν = k-1 degrees of freedom. If $H_c \leq \chi 2_{0.05,\nu}$ the null hypothesis is retained, which indicates that the tested residue populations are not significantly different and can be combined for the estimation of mrls.

The critical $\chi^2_{0.05}$ values are:

ν	2	3	4	5	6
$\chi^2_{0.05}$	5.9915	7.8147	9.4877	11.0705	12.5916

Table 6 Illustration of the calculations for Kruskal-Wallis test for comparison of multiple independent samples

	Independent residue data sets			All residues	Corrected ranks	Corrected rank numbers for sample sets			Ties	T_j
	Curly kale	Lettuce	Spinach			Curly kale	Lettuce	Spinach		
No of data	8	10	16	34	34	8	10	16		
Sum of ranks, R_i					595	160	215.5	219.5		
R_i^3/N_i						3200	4644.02	3011.27		
	0.07	0.07	0.03	0.03	1.5			1.5	2	6
	0.08	0.12	0.03	0.03	1.5			1.5		
	0.1	0.13	0.04	0.04	3			3		
	0.11	0.15	0.06	0.06	4			4		
	0.32	0.18	0.08	0.07	5.5	5.5			2	6
	0.32	0.18	0.09	0.07	5.5		5.5			
	0.34	0.25	0.09	0.08	7.5	7.5			2	6
	0.39	0.26	0.1	0.08	7.5			7.5		
		0.29	0.1	0.09	9.5			9.5	2	6
		0.41	0.1	0.09	9.5			9.5		
			0.1	0.1	13	13			5	120
			0.14	0.1	13			13		
			0.17	0.1	13			13		
			0.2	0.1	13			13		
			0.5	0.1	13			13		
			1	0.11	16	16				
				0.12	17		17			
				0.13	18		18			
				0.14	19			19		
				0.15	20		20			
				0.17	21			21		
				0.18	22.5		22.5		2	6
				0.18	22.5		22.5			
				0.2	24			24		
				0.25	25		25			
				0.26	26		26			
				0.29	27		27			
				0.32	28.5	28.5			2	6
				0.32	28.5	28.5				
				0.34	30	30				
				0.39	31	31				
				0.41	32		32			
				0.5	33			33		
				1.0	34			34	17	156

The performance of the Kruskal-Wallis test is facilitated by an Excel template, which performs the calculations for 7 data sets after inserting the residues composing of the data sets and arranging the ranks corrected for ties for each sample set.

The ranks are corrected for ties accurately if the sum of corrected ranks is equal to the total number of samples.

4. Recommendations

The Meeting confirms the applicability of its current practice and emphasizes the importance of the following principles:

1. Only the results of "supervised trials conducted at the highest nationally recommended, authorized or registered uses" should be considered in mrl estimation (i.e., maximum GAP per country)
2. Where prior experience indicate that the agricultural practice and climatic conditions lead to similar residues the critical GAP of one country can be applied for the evaluation of supervised trials carried out in another country.
3. Statistical calculations in support for mrl estimation should only be used where the data are suitable for those data to yield valid conclusions. Considerations should include:
    - o data from a single population or the equivalent of a single population;
    - o the data should be from a random sample or stratified random sample from the population; and
    - o sufficient data (≥ 15) should be available to minimize the errors of extrapolation to the required high percentile values;
    - o the number of residue values below the LOQ and the residue distribution around LOQ;
    - o no statistical test should be applied for excluding potential outliers; residue data should only be excluded if experimental evidence indicates that the data is invalid.
4. If a sufficient number of trials is available reflecting the maximum GAP of one country or geographical region, the mrl estimates should be based those residue data alone.
5. When considering combining different residue data, the distribution of residue data shall be carefully examined and only those datasets combined which may be expected to arise from the same parent populations based on comparable GAP. The expert judgement (see also point 6) could be assisted with appropriate statistical tests (e.g., Mann-Whitney U-test or Kruskal-Wallis H-test)
6. The focus on one GAP allows for alternative GAP to be assessed if there is an identified dietary intake problem. In such cases, where residue data permits, an alternative national GAP is considered and the supporting residue data sets are used for estimation of mrls which do not raise acute intake concern.
7. In cases, where only small number of residue data are available, mrl estimates should take into account:
    - o the highest values, median value and approximate 75^{th} percentile value in the available data set of supervised residue trials;
    - o residue levels resulting from application rates other than the label rate (for instance, using residues below LOQ in samples derived from double rate treatments to support no detectable residues following the application at maximum label rate, using highest residues from samples taken at longer intervals than PHI);
    - o experience of typical distributions of residue data from supervised trials;
    - o knowledge of residue behaviour from the metabolism studies (e.g., is it a surface residue, does it translocate from foliage to seeds, roots, etc.); and
    - o knowledge of residue trials on comparable crops.
8. The Meeting does not consider it appropriate to combine residue data sets deriving from different GAPs without sufficient justification. This method would include residue data with

different median (mean) values, which would result in lower estimated daily intake and also lower mrls if the latter would be calculated with the NAFTA statistical calculator.

9. There may be some situations which are not covered by the general principles outlined in this section. Such cases require a casa-by-case consideration and expert judgement based on all available information and prior experience.
10. Principles used for the evaluation of data sets for one pesticide-commodity combination may be applied for evaluation of residues within one commodity group (e.g., application of 'one GAP' principle for estimating mrl for a group based on the highest residues data set obtained in one commodity).

2.9 EVALUATION FOR FOLLOW-UP CROPS

The JMPR 2006 recommended the CCPR to request member countries to provide information on how residues in follow crops are regulated at the national level. This information will be taken into account in making recommendations based on the evaluation of residues in follow crops.

In member countries which provided information (Australia, the EU, Japan and the United States) residues in follow crops are regulated either by setting specific MRLs for "other plant commodities or crop groups" according to the residue definition for primary treated crops or by setting label restrictions on the type of succeeding crops and/or the plant back interval after harvest. The Meeting recognized that neither approach is applicable for the JMPR, since label restrictions are limited to national authorisations and MRLs for "other plant commodities" are currently not supported by the Codex classification system for foods and animal feeds.

For an estimation of possible residues in follow crops the Meeting must rely on the information provided. In 2006 the JMPR emphasized that in cases where residues in follow crops may occur at levels above the LOQ, in addition to the minimum data requirements as specified in the *FAO Manual*, the data submitters should automatically provide information on metabolism in root or tuber vegetables, environmental fate studies and the results of field studies on follow crops carried out at various times after the application of the pesticide.

Field studies on follow crops in particular provide important information for an estimation of possible residues levels under more realistic conditions. By comparing these residues with results obtained from supervised residue trails on primary treated crops (if available) a decision can be made if the recommended maximum residue levels are also sufficient for commodities from follow crops including theoretical additional treatments with the same active substance in subsequent years.

More realistic maximum residues expected in succeeding crop groups (e.g., root and tuber vegetables, leafy vegetables or cereals) can be estimated based on an extrapolation from the representative follow crops used in the field studies. For such an extrapolation the metabolism in rotational crops as well as the aerobic metabolism in soil must be investigated sufficiently. The estimation of residues level must be based on the maximum annual application rate according to the labels provided, the residue definition for enforcement purposes proposed for plant commodities and the residue data for representative crops obtained from follow field studies. In addition the interval between last treatment and the crop rotation must be taken into account when considering the degradation rate in soil under field conditions, in order to estimate a realistic concentration of the active ingredient in the soil at the planting/sowing of the following crops.

As an example, chlorantraniliprole (5.6) evaluated by JMPR 2008 various studies on follow crops were provided to the Meeting conducted according to the maximum seasonal application rate.

For the leafy vegetables group investigated in lettuce, spinach and Swiss chard residues found were in the range of < 0.01 to 0.01 mg/kg. In comparison to the group maximum residue level recommended for leafy vegetables of 20 mg/kg no significant contribution to total residues in these commodities by follow-crops is expected by the Meeting.

Root and tuber vegetables gave residues ranging from < 0.01 up to 0.01 mg/kg in turnip, beet and radish roots. Under consideration of the maximum residue level recommended for root and tuber vegetables of 0.01 mg/kg, the Meeting decided to combine residues from direct treatment and follow-crops to recommend a maximum residue level of 0.02 mg/kg and an STMR of 0.01 mg/kg for root and tuber vegetables.

Cereals are not registered for direct treatment using chlorantraniliprole according to the labels provided. In follow crop studies, residues in cereal grain, forage and straw/hay of up to < 0.01, 0.083 and 0.15 mg/kg were found, respectively. Based on this data the Meeting recommended maximum residue levels and STMR values of 0.02 and 0.01 mg/kg for cereal grain and 0.3 and 0.051 mg/kg (dry-weight based) for straw and fodder of cereal grain, respectively. For cereal straw and hay also a highest residue of 0.17 mg/kg (dry-weight based) was recommended. For cereal forage an STMR of 0.022 mg/kg and a highest residue of 0.083 mg/kg were used in the livestock animal's dietary burden.

For pulses only two data points from follow crop studies with detections below the LOQ of 0.01 mg/kg were available. The Meeting considered two trials on pulses to be inadequate for the purpose of estimating maximum residue levels.

No trials on residues in follow crops were available on brassica vegetables, stalk and stem vegetables, legume vegetables, bulb vegetables, oilseeds, grass/pasture and legume animal feeds. No recommendations were given for commodities of these crop groups.

In view of the purpose of these studies the Meeting pointed out that all information obtained is utilized in estimating the maximum residues in follow crop commodities after treatment of the primary crops according to the GAP. In most cases the data provided are not intended for an estimation of median residues in plant commodities used in the dietary risk assessment or livestock animal dietary burden resulting in an overestimation of the exposure.

The Meeting also noted that several special cases for residues in follow crops besides the normal agricultural farming exist. Examples may be the transfer of carbendazim from treated cereal straw used as substrate for fungi cultivation or clopyralid in manure and compost made from cattle excreta. In these special cases where an unexpected transfer into follow crops is observed, data submitters as well as member countries are encouraged to submit additional data suitable to assess residues in these commodities. Helpful data might be transfer studies for the individual scenario as well as monitoring data for commodities without authorizations for direct treatment.

2.10 SELECTION OF REPRESENTATIVE COMMODITIES WHEN ESTABLISHING COMMODITY GROUP MRLS

The Codex Classification of Foods and Animal Feeds is being revised by CCPR with one of the aims being to facilitate the establishment and interpretation of Codex MRLs.

In 2007, JMPR reported on 'Crop groups and commodity group MRLs'. The proposed draft revision of the Codex Classification of Foods and Animal Feeds was an agenda item of the 2008 session of the CCPR. The agenda item included a proposal for guidance on the selection of representative commodities.[23]

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[23] Codex Alimentarius Commission. *Report of the 40th Session of the Codex Committee on Pesticides Residues, 14–19 April 2008, Hangzhou, China*, (ALINORM 08/31/24). Draft document outlining the principles of and guidance on the selection of representative crops for the purpose of extrapolation of MRLs. The selection of representative commodities, principles and guidance. Addendum II to CX/PR 08/40/4.

The document (CX/PR 08/40/4) provided advice to JMPR about the use of representative crops and commodities for the purposes of residue extrapolation to commodity groups. Suggestions are based on practices from JMPR, USA, EU and Japan.

Ideally, groupings should be chosen so that members of the crop group, or sub-group, would be subject to the same GAP and the resultant commodities would form a group, or sub-group, with similar residue characteristics.

Representative crops and commodities should then be chosen according to their commercial importance and their residue characteristics.

The most important crop from a commercial perspective may not be the most important from a residue perspective. For example, Chilli peppers because of their size, normally have a higher residue than sweet peppers for the same GAP and are likely to drive a peppers MRL. However, a group MRL should not generally be established on the basis of data from a minor crop only.

The Meeting noted that the selection of representative crops and corresponding commodities for particular crop and commodity groups would be very valuable to proponents planning residue trials.

JMPR evaluates available data, whether on a 'representative' commodity or not. In estimating a group MRL, JMPR includes available data, if valid and sufficient, from all commodities whether potentially representative or not. Residue behaviour cannot always be predicted, and therefore the residue data driving the group MRL will not necessarily arise from suggested 'representative' commodities.

The Meeting looked forward to further progress with commodity grouping and representative commodities. Careful attention to grouping will assist the JMPR to propose group MRLs more often.

2.11 PROPORTIONALITY OF PESTICIDE RESIDUE CONCENTRATIONS AND APPLICATION RATES IN SUPERVISED TRIALS

JMPR often receives residue data from supervised trials on crops where the application rates in the trials do not match the GAP rate. Maximum residue level estimates are based on trials with application at the GAP rate. Applications at other rates are commonly used as additional evidence and context for the GAP trials. However, it would be advantageous to make more direct use of the data if possible.

The Meeting was aware of research work on 'proportionality', including the work reported at the IUPAC Congresses in 1998[24] and 2006.[25] Conclusions were drawn from JMPR residue data summaries. Also, side-by-side trials were initiated in USA. Until now, the data analysed have included only foliar uses of insecticides and fungicides.

Before the results of such work can be applied to residue evaluation, it is important to examine the conditions where proportionality is valid and where it is not. For example, proportionality may not apply to the use of herbicides or plant growth regulators on crops because the different application rates may have different effects on the crop.

Where proportionality is valid, the residues from trials other than the GAP rate could be adjusted to values equivalent to the GAP rate.

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[24] Banasiak U, Hohgardt K, Koinecke A, Plass R and Moll E. 1998. Extrapolation of residue data - based on the RUEDIS Information System. Abstract. IUPAC International Congress on Pesticide Chemistry, London, August 1998.

[25] Villanueva P and Hamilton DJ. 2006. Is the resulting residue proportional to pesticide application rate? Abstract. IUPAC International Congress on Pesticide Chemistry, Kobe, August 2006.

The Meeting invited research workers to publish their findings in the scientific literature and to describe the boundary conditions where ‘proportionality’ has been validated. This would provide a basis for JMPR and national authorities to make more use of non-GAP rate trials in residue evaluation.