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ABBREVIATIONS USED IN THE MONOGRAPHS

3-APA 3-aminopropionamide

8-OH-dG 8-hydroxy-2'-deoxyguanosine

AA acrylamide

ABS acrylonitrile-butadiene-styrene

ADI acceptable daily intake
AED atomic emission detection

Ah aryl hydrocarbon

AhR aryl hydrocarbon receptor
ALARA as low as reasonably achievable

ALT alanine transferase
AR androgen receptor
ARA arachidonic acid
ARfD acute reference dose

ATDS Australian Total Diet Survey

AUC area under the curve
BCG Bacillus Calmette-Guérin
BDE brominated diphenyl ether

BMD benchmark dose

BMDL lower confidence limit on the benchmark dose

BMR benchmark response

Br-GC-MS bromination—gas chromatography—mass spectrometry

BROD benzyloxyresorufin O-deethylase

bw body weight

CAS Chemical Abstracts Service

CCFAC Codex Committee on Food Additives and Contaminants

cGMP cyclic guanosine monophosphate

CI confidence interval

CIAA Confederation of Food and Drink Industries of the European

Union

COX prostaglandin H synthase
CRM certified reference material
CV coefficient of variation
CYP cytochrome P450

Cys cysteine

dA deoxyadenosine dC deoxycytidine

DDT dichlorodiphenyltrichloroethane

dG deoxyguanosine
DHT dihydrotestosterone
DNA deoxyribonucleic acid

EA early antigen

ECD median effective concentration electron capture detection

ECNI electron capture negative ionization

ED₅₀ median effective dose electron impact

ELISA enzyme-linked immunosorbent assay
EPA Environmental Protection Agency (USA)

ER estrogen receptor

EROD 7-ethoxyresorufin O-deethylase

ESI electrospray ionization

EU European Union

FAO Food and Agriculture Organization of the United Nations

FCA Freund's complete adjuvant
FD fluorescence detection
FID flame ionization detection

FOB functional observational (test) battery

FSH follicle stimulating hormone

FT3 free triiodothyronine FT4 free thyroxine GA glycidamide

GC gas chromatography

GD gestation day

GEMS/Food Global Environment Monitoring System Food Contamination

Monitoring and Assessment Programme

GM-CSF granulocyte-macrophage colony stimulating factor

GSD geometric standard deviation
GST glutathione-S-transferase
GSTM1 glutathione-S-transferase M1
GSTT1 glutathione-S-transferase T1
hAR human androgen receptor

HPLC high-performance liquid chromatography
HRGC high-resolution gas chromatography
HRMS high-resolution mass spectrometry

IARC International Agency for Research on Cancer

IC₅₀ median inhibitory concentration IEF induction equivalency factor

lg immunoglobulin

IGF insulin-like growth factor

i.m. intramuscular i.p. intraperitoneal

IPCS International Programme on Chemical Safety

IRIS Integrated Risk Information System

IU international units

IUPAC International Union for Pure and Applied Chemistry
JECFA Joint FAO/WHO Committee on Food Additives
JMPR Joint FAO/WHO Meeting on Pesticide Residues

K_i inhibition constant

K_m Michaelis-Menten constant

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K_{ow} octanol-water partition coefficient

LC liquid chromatography

LD lactational day
LD₅₀ median lethal dose
LDH lactate dehydrogenase
LH luteinizing hormone

LOAEL lowest-observed-adverse-effect level

LOD limit of detection

LOEL lowest-observed-effect level

LOQ limit of quantification LOR limit of reporting

LRMS low-resolution mass spectrometry

LTP long-term potentiation

MAE microwave-assisted extraction
MAP mitogen-activated protein

MEK mitogen-activated protein kinase

MeO methoxy

ML maximum level
MOE margin of exposure
MPO medial preoptic area

mRNA messenger ribonucleic acid
MROD 7-methoxyresorufin *O*-deethylase

MS mass spectrometry m/z mass to charge ratio

N1-GA-dA N1-(2-carboxy-2-hydroxyethyl)-2'-deoxyadenosine

N3-GA-Ade N3-(2-carbamovl-2-hydroxyethyl)adenine

 N^6 -GA-dA N^6 -(2-carboxy-2-hydroxyethyl)-2'-deoxyadenosine

N7-GA-Gua N7-(2-carbamoyl-2-hydroxyethyl)guanine

NA not available; not analysed

NADH nicotinamide adenine dinucleotide, reduced form

NADPH nicotinamide adenine dinucleotide phosphate, reduced form

NAT *N*-acetyltransferase
NCV nerve conduction velocity

ND not detected

NHL non-Hodgkin lymphoma

NIH National Institutes of Health (USA)

NK natural killer

NMA N-methylolacrylamide
NMDA N-methyl-D-aspartate
nNOS neural nitric oxide synthase
NOAEL no-observed-adverse-effect level

NOEL no-observed-effect level

NPD nitrogen-phosphorus detection

NQ not quantified

NTP National Toxicology Program (USA)

OECD Organisation for Economic Co-operation and Development

OH hydroxy OR odds ratio

PAH polycyclic aromatic hydrocarbon

PBB polybrominated biphenyl

PBDD polybrominated dibenzo-*p*-dioxin
PBDE polybrominated diphenyl ether
PBDF polybrominated dibenzofuran

PBPK physiologically based pharmacokinetic

PCB polychlorinated biphenyl

PCDD polychlorinated dibenzo-p-dioxin
PCDE polychlorinated diphenyl ether
PCDF polychlorinated dibenzofuran
PCE polychromatic erythrocyte
PCNA proliferating cell nuclear antigen

PFC plaque-forming cell
PKC protein kinase C
PLA₂ phospolipase A₂

PMTDI provisional maximum tolerable daily intake

PND postnatal day ppm part per million ppt part per trillion

PR progesterone receptor

PROD 7-pentoxyresorufin O-depentylase PTWI provisional tolerable weekly intake

PTWI_d daily equivalent of the provisional tolerable weekly intake

QA quality assurance QC quality control

QSAR quantitative structure–activity relationship

RIVM National Institute of Public Health and the Environment

(Netherlands)

RIVO Netherlands Institute of Fisheries Research

RNA ribonucleic acid RR relative risk

SAR Special Administrative Region

s.c. subcutaneous

SCOOP Scientific Cooperation on Food

SD standard deviation

SFE supercritical fluid extraction
SIM selected ion monitoring
SMR standardized mortality ratio
SPE solid-phase extraction
SRM selective-reaction monitoring

T3 triiodothyronine

T4 thyroxine

TBG thyroxine binding globulin

TCDD 2,3,7,8-tetrachlorodibenzo-*p*-dioxin

TD₅₀ chronic dose that results in one half of animals developing

tumours

TDS Total Diet Study

TEF toxic equivalency factor

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TGF transforming growth factor
TLC thin-layer chromatography
TPA tetradecanoyl-phorbol acetate
TSH thyroid stimulating hormone

TT3 total triiodothyronine

TT4 total thyroxine

TTC threshold of toxicological concern

TTR transthyretin

UDPGT uridine diphosphate glucuronosyltransferase

USA United States of America

US EPA United States Environmental Protection Agency

UV ultraviolet Val valine

V_d volume of distribution

V_{max} maximum rate of metabolism VMH ventromedial hypothalamic nucleus

v/v volume by volume

WHO World Health Organization

w/w weight by weight

JOINT FAO/WHO EXPERT COMMITTEE ON FOOD ADDITIVES Rome. 8–17 February 2005

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THE FORMULATION OF ADVICE ON COMPOUNDS THAT ARE BOTH GENOTOXIC AND CARCINOGENIC¹

The Committee has established procedures for determining health-based quidance values, such as the acceptable daily intake (ADI) or provisional tolerable weekly intake (PTWI), for chemicals that produce adverse effects that are thought to show a threshold in their dose-response relationships. Compounds that are both genotoxic and carcinogenic may show non-linear dose-response relationships, but the no-observed-effect level (NOEL) in a study of carcinogenicity represents the limit of detection in that bioassay, rather than an estimate of a possible threshold. Therefore, the Committee does not establish health-based quidance values for compounds that are genotoxic and carcinogenic using the NOEL and safety (uncertainty) factors. In the absence of evidence on the influence of non-linearity on the incidence of cancer at low levels of exposure, the advice given previously by the Committee for compounds that are both genotoxic and carcinogenic has been that intakes should be reduced to as low as reasonably achievable (ALARA). Such advice is of limited value, because it does not take into account either human exposure or carcinogenic potency and has not allowed risk managers to prioritize different contaminants or to target risk management actions. In addition, ever-increasing analytical sensitivity means that the number of chemicals with both genotoxic and carcinogenic potential detected in food will increase.

The Committee at its present meeting considered a number of compounds for which genotoxicity and carcinogenicity are important issues. The Committee was aware of a number of recent developments relevant to the risk assessment of such compounds, including:

- a WHO workshop that developed a strategy for dose-response assessment and the formulation of advice (1);
- discussions within the European Food Safety Authority about a margin of exposure (MOE) that would indicate the level of priority for risk management action (2); and
- Australian recommendations for genotoxic and carcinogenic soil contaminants regarding a guideline dose that would be protective of human health based on a modified benchmark dose and the application of uncertainty factors to allow for interspecies differences, intraspecies variability, quality of the database and the seriousness of the carcinogenic response (3).

¹ Taken from section 2.1 of the Sixty-fourth report of the Joint FAO/WHO Expert Committee on Food Additives (see Annex 1, reference 174).

The Committee discussed approaches to the formulation of advice on contaminants that are both genotoxic¹ and carcinogenic, which would inform risk managers about the possible magnitude of health concerns at different levels of intake in humans.

Hazard identification would normally be based on data from studies on genotoxicity and from cancer bioassays. Some chemicals increase the incidence of cancer in experimental animals by non-genotoxic mechanisms, and establishing a health-based guidance value, such as a PTWI, would be appropriate. The present guidance relates to chemicals that are both genotoxic and carcinogenic.

Hazard characterization (dose-response assessment) would be based on the available dose-response data for cancer, which would mostly be derived from studies in rodents given daily doses many orders of magnitude greater than the estimated intakes in humans. Dose-response data from studies of epidemiology may also be used for hazard characterization and would avoid interspecies comparisons and extrapolation over many orders of magnitude. The recent WHO workshop recommended the use of the benchmark dose lower confidence limit (BMDL) as a starting point for hazard characterization based on data from a bioassay for cancer in animals when the data are suitable for dose-response modelling. The BMDL is the lower one-sided confidence limit of the benchmark dose (BMD) for a predetermined level of response, called the benchmark response (BMR), such as a 5% or 10% incidence. The BMD in most cases shows less variation than the BMDL for different mathematical models and may be more suitable for ranking different compounds in terms of their potency, while the BMDL may be more appropriate for risk characterization purposes because it reflects the quality of the data. The derivation and interpretation of a BMDL require considerable statistical and biological expertise.

A number of aspects of the database need to be considered in dose-response modelling, including data selection, model selection, statistical linkage, parameter estimation, implementation and evaluation (1). The dose metric used for modelling could be a biomarker, providing that it was critically related to the process by which cancer arises and had been validated in relation to the external dose or intake. For carcinogenesis, selection of the dose–response data for modelling will need to consider both site-specific incidences of tumours, especially for the site showing the greatest sensitivity, and combined data (e.g. numbers of tumour-bearing animals) for compounds that do not show clear organ specificity. Analyses based on the numbers of tumour-bearing animals may also be

¹ The present guidance does not address the situation where a compound shows genotoxicity, or has structural alerts for genotoxicity, but where a bioassay for cancer has not been performed. The Committee is aware of developments, such as the threshold of toxicological concern (TTC) for compounds with structural alerts for genotoxicity, that may allow the formulation of limited advice to risk managers, and would welcome a critical evaluation of such approaches.

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appropriate under other circumstances, for example in the assessment of complex mixtures of compounds that are both genotoxic and carcinogenic. Dose–response characterization should aim to define the BMDL for the carcinogenic response(s) of relevance to human health, at the lowest level of response (the BMR) that reliably defines the lower end of the observed experimental dose–response relationship. A BMR of a 10% incidence is likely to be the most appropriate for modelling of data from bioassays for cancer, because the values for different mathematical models show wider divergence at incidences below 10%. The consistent use of the same benchmark response, i.e. 10%, will facilitate comparisons of the risks associated with different compounds that are both genotoxic and carcinogenic. Non-cancer effects produced by compounds that are both genotoxic and carcinogenic may be analysed using the same approach, and comparison of the derived BMDL values and their associated slopes can help to identify the adverse effect that is critical to risk assessment of the compound.

The intake (exposure) assessment for a compound that is both genotoxic and carcinogenic is no different from that for other types of contaminants.

Risk characterization involves comparison of the estimated exposure with the identified BMDL. In principle, this can take different forms:

- Calculation of the margin of exposure (MOE, the ratio of the BMDL to the
 estimated intake in humans). The MOE can be used to prioritize different contaminants, providing that a consistent approach has been adopted. The
 acceptability of an MOE depends on its magnitude and is ultimately a risk
 management decision (1). To aid that decision, the risk assessor should
 provide information on the nature and magnitude of uncertainties in both the
 toxicological and exposure data. Although the risk assessor should not
 provide an assessment of the acceptability of the MOE, guidance should be
 given on its adequacy taking into account the inherent uncertainties and
 variability.
- Dose-response analysis outside the observed dose range. Quantitative dose-response analysis could be used to calculate the incidence of cancer that is theoretically associated with the estimated exposure for humans, or the exposure associated with a predetermined incidence (e.g. 1 in 1 million). In order to provide realistic estimates of the possible carcinogenic effect at the estimated exposure for humans, mathematical modelling would need to take into account the shape of the dose-response relationship for the high doses used in the bioassay for cancer and for the much lower intakes by humans. Such information cannot be derived from the available data on cancer incidence from studies in animals. In the future, it may be possible to incorporate data on dose-response or concentration-response relationships for the critical biological activities involved in the generation of cancer (e.g. metabolic bioactivation and detoxication processes, DNA binding, DNA repair, rates of cell proliferation and apoptosis) into a biologically based doseresponse model for cancer that would also incorporate data on species differences in these processes. However, such data are not currently

available. At present, any estimate of the possible incidence of cancer in experimental animals at intakes equal to those for humans has to be based on empirical mathematical equations that may not reflect the complexity of the underlying biology. A number of mathematical equations have been proposed for extrapolation to low doses. The resulting risk estimates are dependent on the mathematical model used; the divergence increases as the dose decreases, and the output by different equations can differ by orders of magnitude at very low incidences.

Linear extrapolation from a point of departure. Because the estimated risks at low doses are model-dependent, linear extrapolation from the BMDL, which is conservative and simple to apply, has been used as a matter of policy by some agencies in order to calculate levels of exposure associated with different theoretical incidences of cancer. The incidence used is regarded as an upper-bound estimate for lifetime risk of cancer, and the actual risk may lie anywhere between zero and the calculated upper-bound estimate. Calculation of the intake associated with an incidence of 1 in 1 million from the BMDL for a 10% incidence using linear extrapolation is simply equivalent to dividing the BMDL by 100 000, and this approach is therefore no more informative than calculation of an MOE.

Of the three options given above, the MOE and linear extrapolation from a point of departure are the most pragmatic and usable at the present time. Linear extrapolation from a point of departure offers no advantages over an MOE, and the results are open to misinterpretation because the numerical estimates may be regarded as quantification of the actual risk.

The Committee at its present meeting decided that advice on compounds that are both genotoxic and carcinogenic should be based on estimated MOEs. The strengths and weaknesses inherent in the data used to calculate the MOE should be given as part of the advice to risk managers, together with advice on its interpretation.

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ANNEX 5 APPROACH TO DOSE-RESPONSE MODELLING¹

At the present meeting, cancer dose–response data were analysed by dose–response modelling, in accordance with the International Programme on Chemical Safety (IPCS) document *Principles for modelling dose–response for the risk assessment of chemicals* (1). The statistical methods of dose–response modelling as applied at this meeting are briefly described below.

For each tumour end-point considered relevant, the quantal dose—response models given in Table 1 were fitted to the dose—incidence data:

Table 1. Dose-response models used

Model	Model equation	Constraints
One-stage	$R = a + (1-a)(1-\exp(-x/b))$	0 ≤ <i>a</i> ≤ 1,
Two-stage	$R = a + (1-a)(1-\exp(-(x/b)-c(x/b)^2))$	0 ≤ <i>a</i> ≤ 1
Log-logistic	$R = a + (1-a)/(1 + \exp(c \log 10(b/x)))$	$0 \le a \le 1, c \ge \ln(10)$
Log-probit	$R = a + (1-a) \Phi(c \log 10(x/b))$	0 ≤ <i>a</i> ≤ 1
Weibull	$R = a + (1-a)(1-\exp(-(x/b)^c))$	$0 \le a \le 1, c > 1$
Proast M2	$y = \exp(bx)$, th1	
Proast M3	$y = \exp(b \ x^d) \ , \ th1$	<i>d</i> ≥ 1
Proast M4	$y = c - (c-1)\exp(-bx)$, th1	

Φ denotes the (cumulative) standard normal distribution function.

The first five of these models directly relate the incidence (R, expressed as a fraction) to the dose (x). In these models, the parameter a (also expressed as a fraction) reflects the incidence in the controls, the parameter b denotes the slope and parameter c can be considered as a shape parameter. The last three models (Proast M2–M4) are a specific family of models that assume an underlying continuous response (indicated by y), which is translated into a binary response

¹ Taken from Annex 3 of the Sixty-fourth report of the Joint FAO/WHO Expert Committee on Food Additives (see Annex 1, reference 174).

(incidence) by incorporating a cut-off point (th1) in the normal distribution around y, below which an animal does not respond, and above which it does respond.

Some of the models are nested members of a larger family of models. Two models are nested when the one model can be seen as an extension of the other (simpler) model by incorporating one or more parameters. For instance, the two-stage model is an extension of the one-stage model by including parameter c. Also, the Proast models are a nested family of models (2). Nested models can be formally compared with each other as follows. Inclusion of an extra model parameter should result in a higher log-likelihood value, and if this increase is >1.92, inclusion of the parameter has resulted in a significantly better fit (log-likelihood ratio test). If the increase is <1.92, the fit is not significantly better, and the parameter is omitted.

When dose–response data are available from more than one study, or for both sexes, these models are fitted simultaneously to both such subgroups. This was done either by assuming all parameters in the model being the same for all subgroups or by assuming only the background response parameter (a) being different, or only the slope (b). When all parameters are assumed to be the same, a single curve results, otherwise different curves for the subgroups will result. A model in which a parameter is assumed to be different represents a model that is nested to the same model with the parameter assumed the same for the subgroups. Hence, the log-likelihood ratio test can be used for testing if an additional background or slope parameter results in a significantly better fit.

Selection of models

In general, those models that do not result in a significantly worse fit than the saturated model (one parameter per data point) are considered to be acceptable. For instance, when the saturated model has eight parameters (i.e. eight observed incidences available), a fitted dose—response model with three parameters should result in a log-likelihood that is no more than 5.54 lower than the log-likelihood associated with the saturated model. Table 2 summarizes the critical differences in log-likelihood values for various numbers of degrees of freedom (= difference in number of parameters between the models to be compared).

For those models that were considered acceptable according to the criteria mentioned, the benchmark dose (BMD) values as well as the benchmark dose lower confidence limit (BMDL) values were calculated. All BMD and BMDL values were calculated for a 10% extra risk, defined as:

$$extra \ risk = \frac{R(BMD) - R(0)}{1 - R(0)}$$

This represents the additional-response fraction divided by the tumour-free fraction in the controls.

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Table 2. Critical differences in log-likelihood values making an increase by a number of parameters (= number of degrees of freedom) to result in a significantly better fit

Number of degrees of freedom	Critical difference in log-likelihood (α = 0.05)
1	1.92
2	3.00
3	3.91
4	4.74
5	5.54
6	6.30
7	7.03
8	7.75

The BMD and BMDL values were estimated by the bootstrap method, usually performing 500 bootstrap runs. These values therefore contain some random error, but usually no more than about 10% for the BMDL.

The calculations were performed using the dose–response software package PROAST, version V07 (developed at the National Institute of Public Health and the Environment [RIVM], Bilthoven, The Netherlands), which is freely available.

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