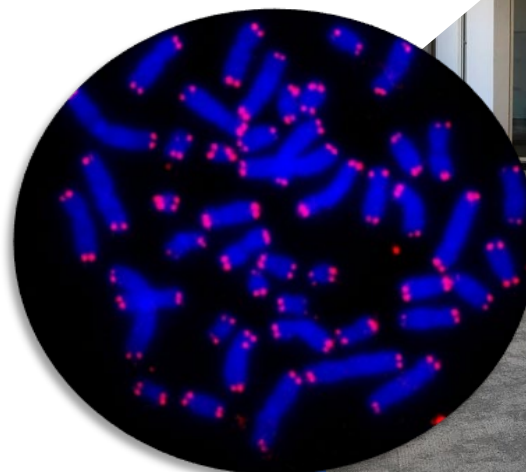
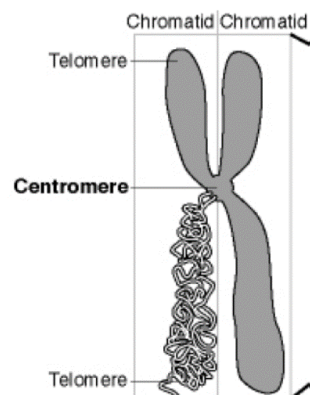
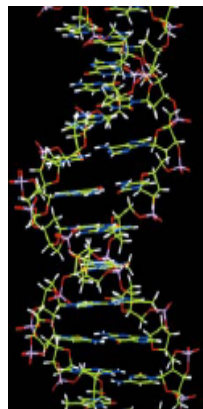


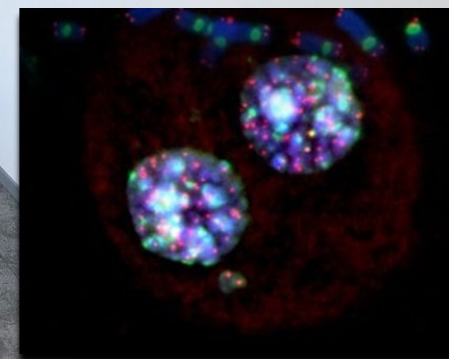


Société de services pour prévenir des risques du "cancer" (toxique pour l'ADN) et pour les perturbateurs endocriniens

Un CRO avec une expertise en génotoxicité



SEQENS'Lab

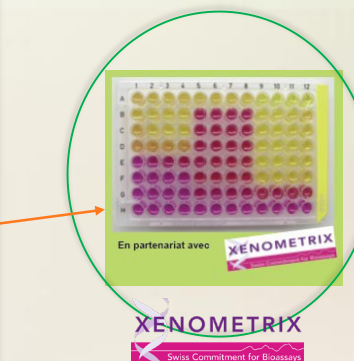
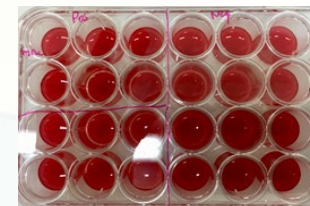
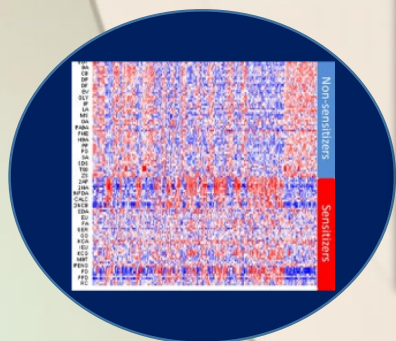
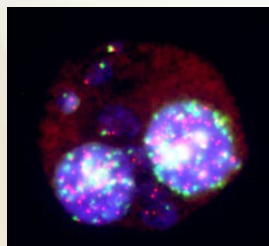
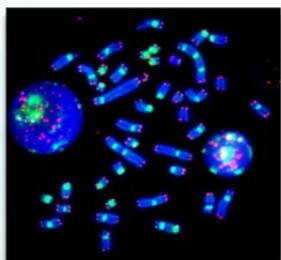


BPL conformité ANSM & COFRAC

SEQENS

Tests *in vitro* pour la caractérisation génotoxique

Test Names Guidelines	Description
Ames Test OECD 471	Detection des composés mutagènes
HLCA test (telo/centromère) OECD 473	Etude aberration Chromosomique
Micronucleus test (telo/centromere) OCDE 487	Detection des produits clastogènes/ aneugènes
<i>in vitro</i> Phototoxicity OECD 432	Sun effect on compound and on human skin
<i>in vitro</i> Cytotoxicity OECD 432	<i>In vitro</i> toxicity on cell lines
<i>in vitro</i> irritation/ corrosion OECD 431 /439	Irritation on reconstructed human epidermis
GARD (Genomic Allergen Rapid Detection) <i>in vitro</i> (LLNA alternative)	Hypersensitivity of pure test article or mixture in partnership with SENZAGEN
<i>in vitro</i> Endocrine disruptions	YES / YAS transfected yeasts in partnership with XenometriX
Expertise	Analyze the process of the test of the customer and propose tests or specific solutions

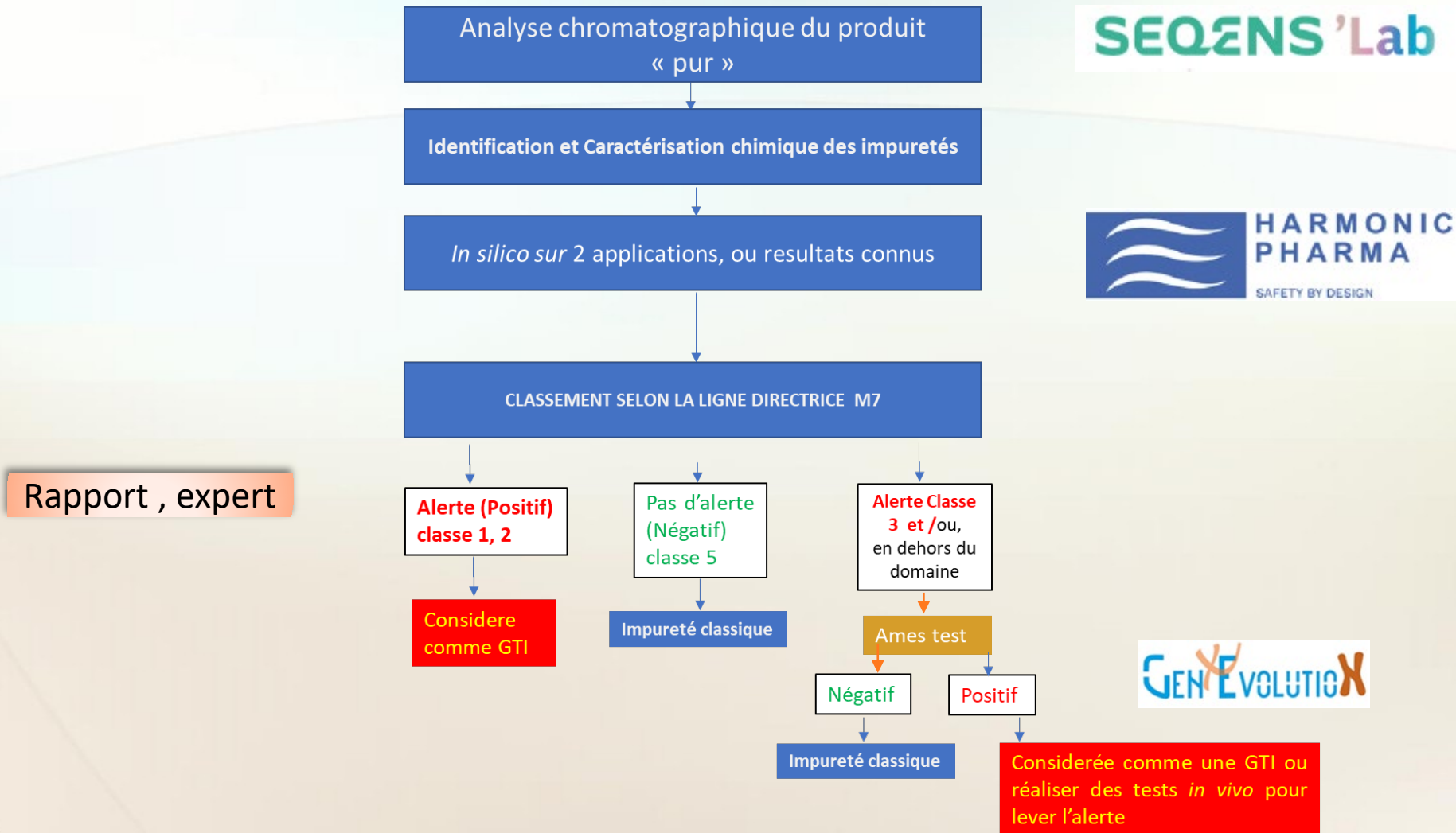


Liste non exhaustive où les tests de génotoxicité sont utilisés

- Echantillons environnementaux air, sol et eau
- Produits Chimiques Reach Annexe VII etc.
- Produits cosmétiques
- Préparation botanique
- Extraits plantes médicinales
- Equipements médicaux
- Alimentaire
 - Animaux
 - Humains
- Produits pharmaceutiques et impuretés pharmaceutiques (animal et humain)

Produits pharmaceutiques : les impuretés Génotoxiques

Rappel arbre décisionnel simplifié ligne directrice M7



Historique des différents types de test d'Ames OCDE 471 (St Louis)

Assay type	Top concentration	Compound require (mg)	Throughput (assay/week) ^a	Predictivity: GLP-Ames
Mini Ames (6-well plates)	1000 µg/well (~5 mg/plate)	25	7/week	~100%
Micro Ames (24-well plates)	250 µg/well (~5 mg/plate)	15	4/week	NA
Mini Ames mix strains (100 mm plates)	2000 µg/well	45	6/week	95%
BioLum Ames	~5 mg/plate	2.5–5	50/week	95%
Ames II TM	1000–5000 µg/mL	5–25	30/week	~92%
Ames MPF	5000 µg/mL	40	10/FTE	78%
5-Fluorouracil	5000 µg/mL	10	2/week	95%
SOS/umu	5000 µg/plate	5	4/week	83%
SOS Chromotest	1000 µg/mL	2	30/FTE	82%

Plus récemment le test « umu » refait surface

Table 1 Comparison of *umu* test results and chemicals tested for rodent carcinogenicity [22]

Carcinogenicity	<i>umu</i> test			
	+	—	±	Total
+	119	72	2	193
—	11	39	0	50
±	0	5	0	5
Total	130	116	2	248
Sensitivity	65 %	(119/193)		
Specificity	78 %	(39/50)		
Accuracy	65 %	(158/243)		

Table 2 Standard methods for the determination of the genotoxicity of water and wastewater using *umu* test

Year	Description	Country
1993	An official method of the water supply test method	Japan
1995	A standard method of the genotoxicity of water and wastewater (DIN 38415T3) [24]	Germany
1997	An official method of the wastewater test method	Japan
2000	A genotoxicity test of water and wastewater in International standardization Organization (ISO) Standards (ISO/CD 13829) [25]	ISO
2008	A standard method of the genotoxicity of water and wastewater (MS ISO13829)	Malaysia

Oda *Genes and Environment* (2016) 38:24
DOI 10.1186/s41021-016-0054-8

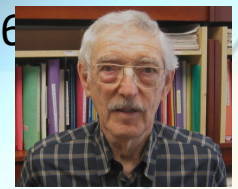
Ger

REVIEW

Development and progress for three decades in *umu* test systems

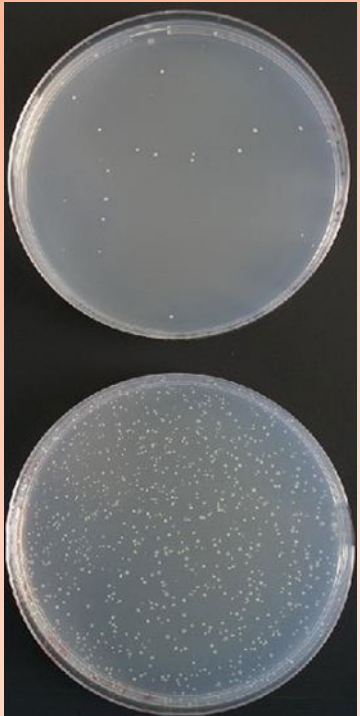
Yoshimitsu Oda

Juillet 2021



STANDARD AMES TEST : METHOD (OECD 471)

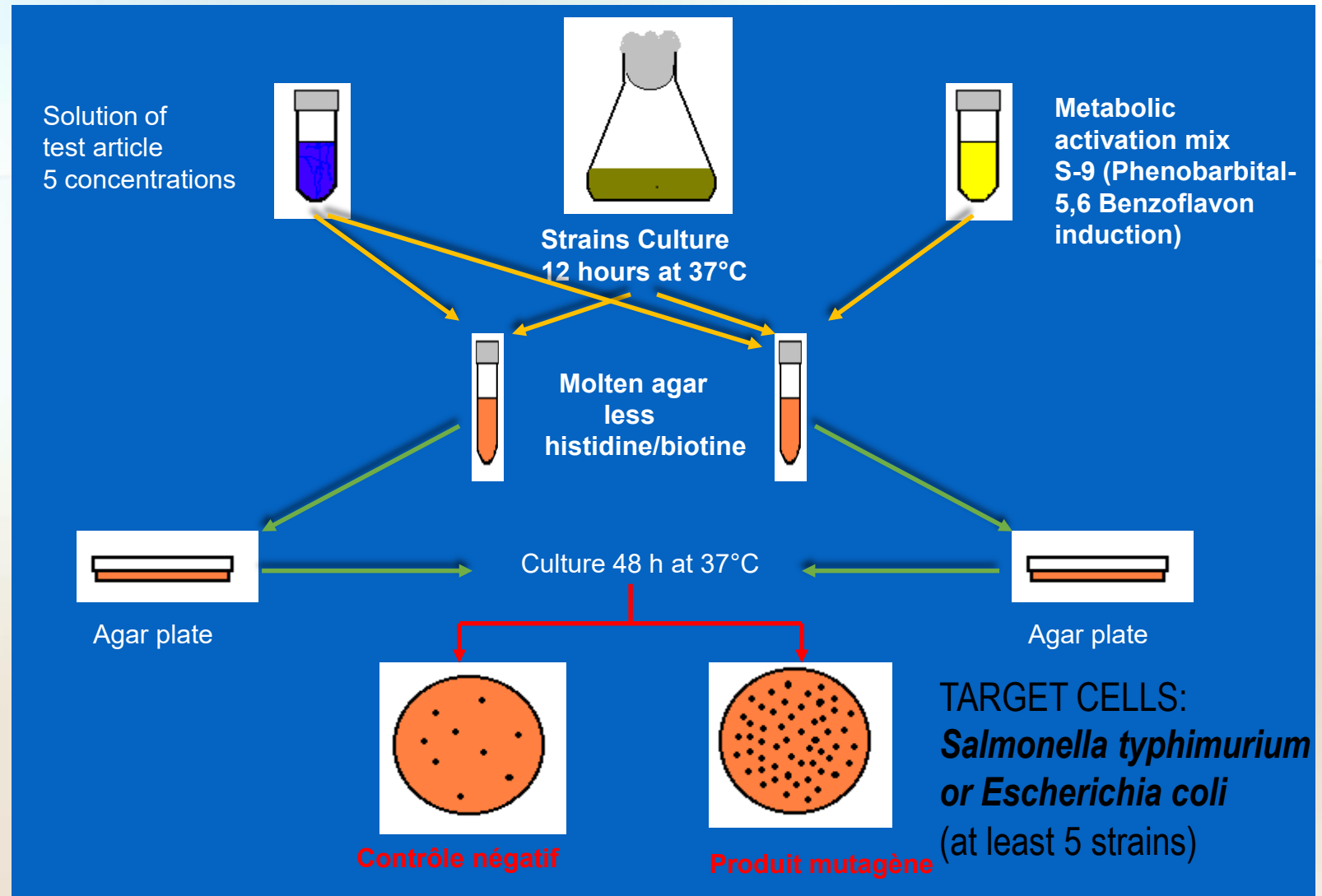
HISTIDINE (HIS-) AUXOTROPHIC
[mutants selected by Ames, without
histidine the strains did not growth]



MUTAGENS AGENT
+/- METABOLISM

REVERSE
MUTATION

HISTIDINE (HIS+) PROTOTROPHIC , [mutation =>
back to wild type]

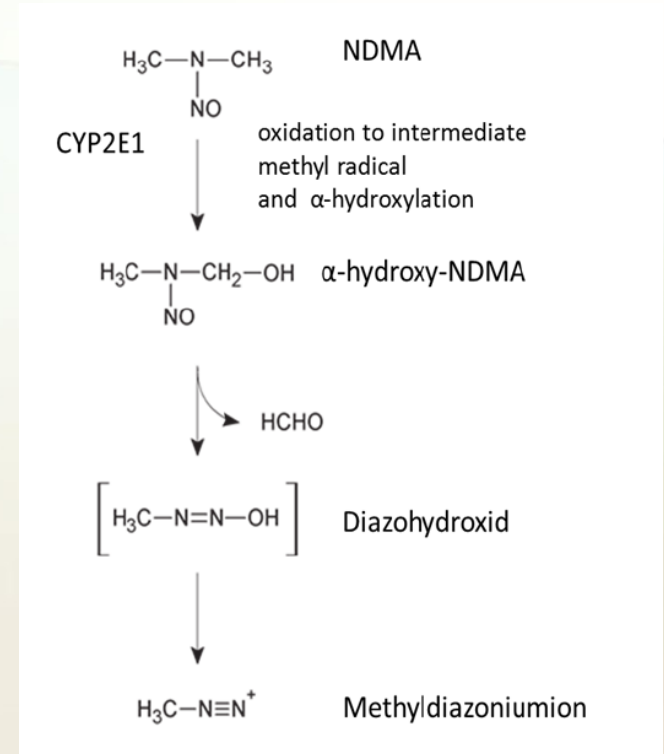


Les NITROSAMINES dans le médicament

MECANISME GENOTOXICITE DES NITROSAMINES

- « Les nitrosamines sont métabolisées principalement par les **CYP2A6 et CYP2E1** en mutagènes réactifs à l'ADN par méthylation (alkylation) à la position O6 de la guanine, à la position O4 de la thymidine et à d'autres lésions moins mutagène. Lorsqu'elle n'est pas corrigée, l'O6-méthylguanine peut être reconnue à tort comme étant de l'adénine, causant **des mutations de substitution GC>AT** pendant la réplication, cette mauvaise reconnaissance peut entraîner **des mutations TA>CG**. »
- « Les agents cancérigènes mutagènes agissent souvent au moyen de mécanismes multiples. La NDMA et la NDEA sont également clastogènes et hépatotoxiques et peuvent causer des dommages secondaires par la production de formaldéhyde et d'espèces réactives d'oxygène (Organisation mondiale de la Santé, 2002). Cependant, l'adduction **O6-alkyl-guanine est le mécanisme le plus répandu et le plus puissant lié au cancer**. »
- George E. Johnson et al, « Permitted daily exposure limits for noteworthy N-nitrosamines » Environ Mol Mutagen 2021 Jun 5. doi: 10.1002/em.22446.

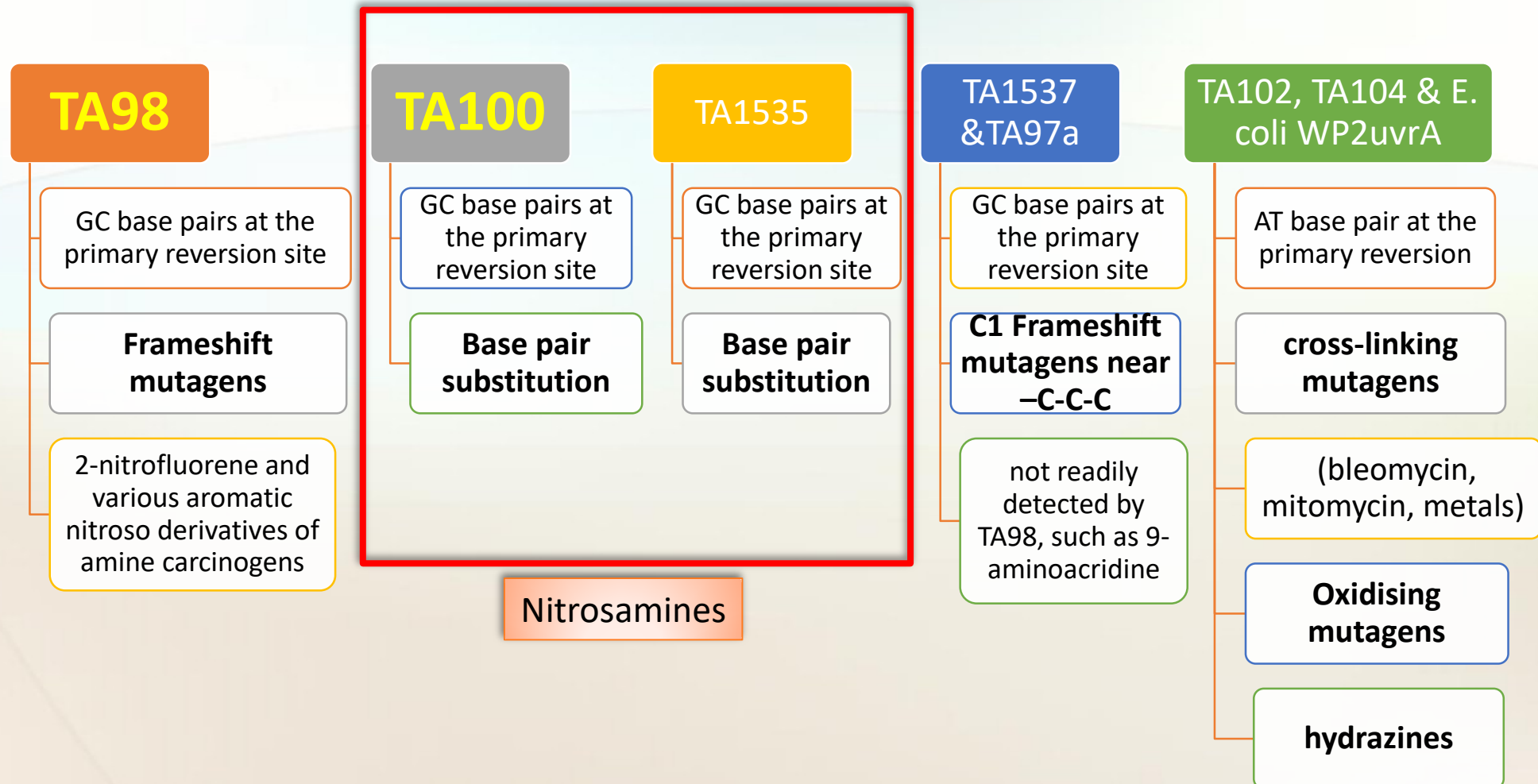
METABOLISATION: MOLECULES REACTIVES



Assessment report EMA/217823/2019

Metabolic activation of NDMA formation of the DNA-reactive methyl diazonium ion from NDMA (adapted from Sulc et al., 2010)

Test d'Ames: Les principales souches utilisées



Généalogie des souches TA100, TA1535 sont issues de la même souche TA1530

Nitrosamines

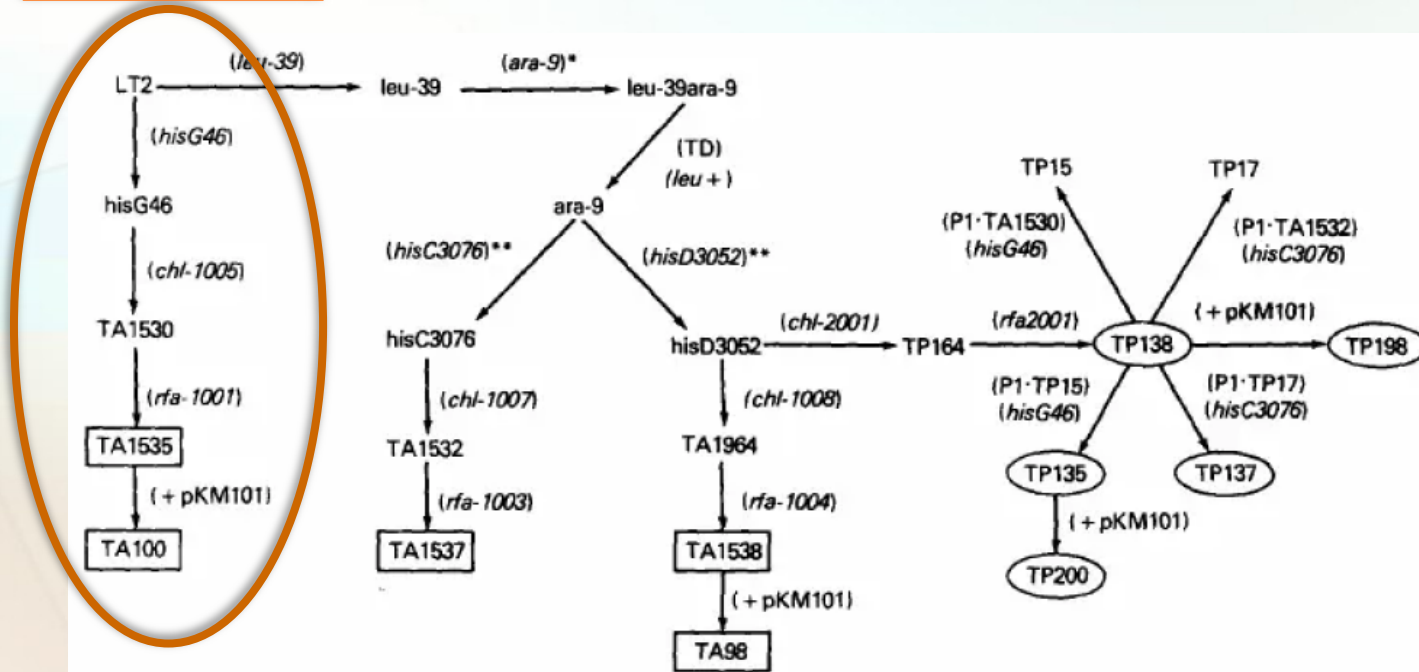


Fig. 1. Genealogy of Ames and isogenic tester strains. Ames tester strains in boxes; isogenic tester strains in ovals. Complete genotypes of all strains shown in Table 1. The allele or plasmid added at each step is shown in parentheses. * Indicates mutagenesis with ultraviolet light; ** indicates treatment with frameshift mutagen ICR364-OH. (TD) indicates that the *leu*⁺ allele was introduced by transduction (phage unspecified); (P1) indicates that allele was introduced by transduction with bacteriophage PlcmCl-100. The donor strain for the PlcmCl-100 transductions is shown after the "P1-". The allele transferred in each transduction is also indicated. All alleles not obtained by an indicated mutagenesis or transduction were derived by spontaneous mutation. (+pKM101) indicates that plasmid pKM101 was introduced by conjugation. Figure modeled after that published by Busch et al. (1986).

Mutation Research, 224 (1989) 453-464
Elsevier

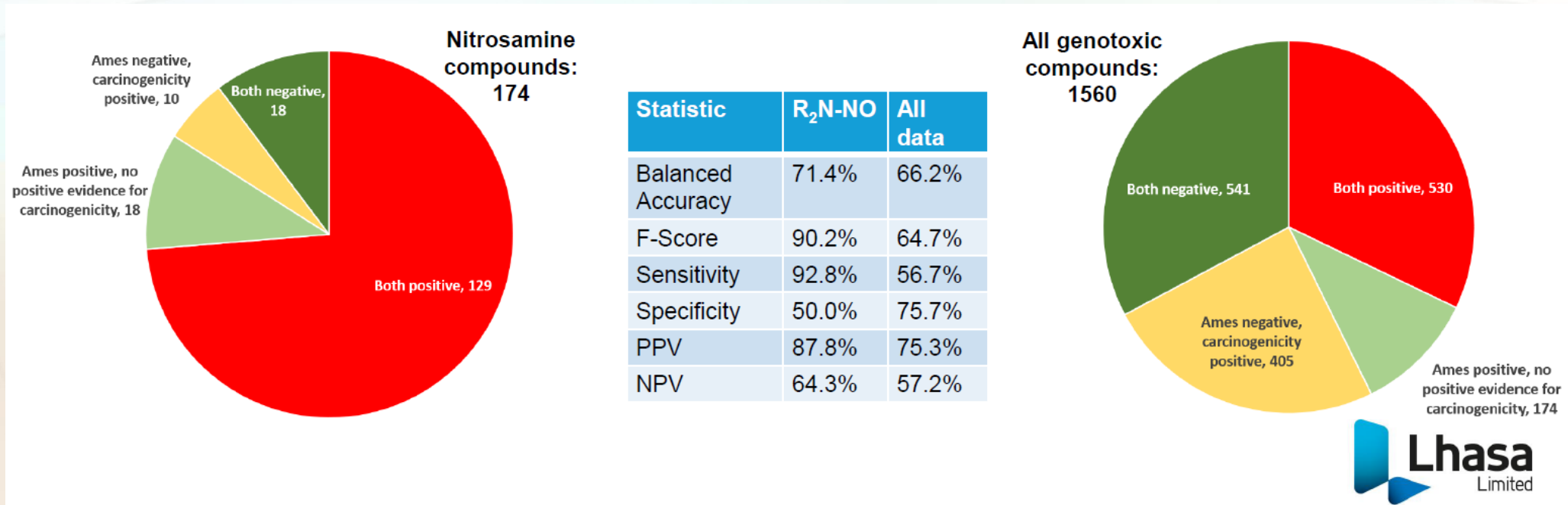
MUTGEN 01487

Isolation and characterization of an isogenic set of *Salmonella typhimurium* strains analogous to the "Ames" tester strains

David J. Popkin, Valerie M. Davis and Michael J. Prival
Genetic Toxicology Branch, Food and Drug Administration, Washington, DC 20204 (U.S.A.)

(Received 21 November 1988)
(Revision received 15 May 1989)
(Accepted 6 June 1989)

Environ $\frac{3}{4}$ des nitrosamines sont + dans le test d'Ames



Cependant.....

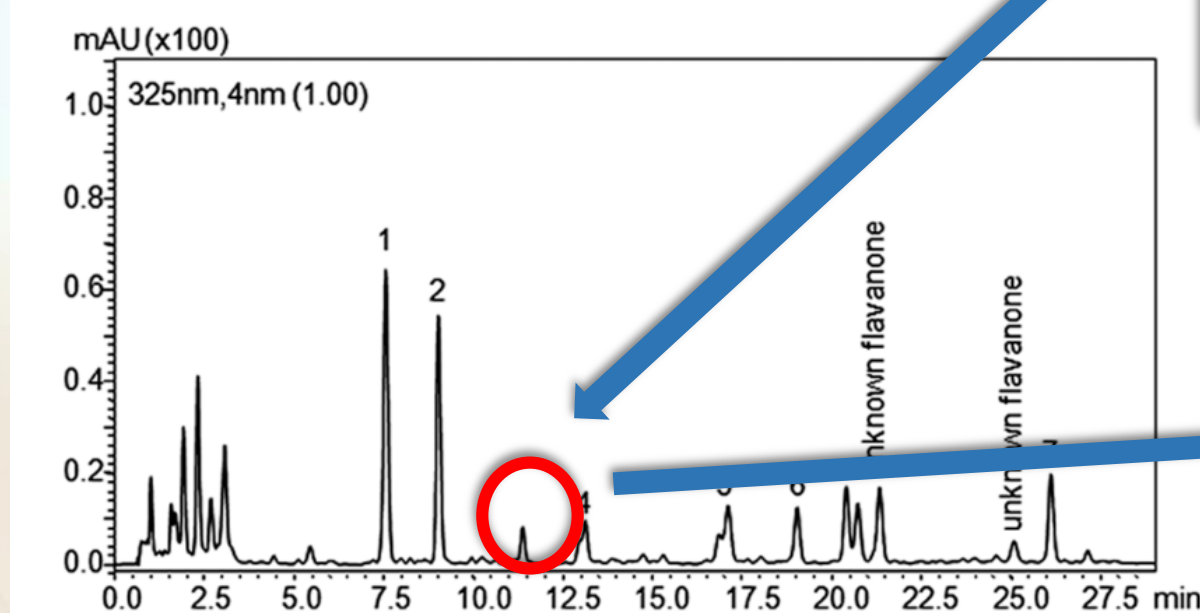
- Génotoxicité
 - Il n'y a pas de test unique qui détecte tous les produits génotoxiques
 - Mutation, clastogène, aneugène : *in vitro* et *in vivo*.
 - *In vitro* plus rapide et moins coûteux que les tests *in vivo* (ex test de cancérogenèse 2 ans et plusieurs millions d'euros).
 - Test suivants les lignes directrices OCDE complétées par les lignes directrices ICH-M7 TTC 1,5 µg/jour inférieur à la durée de vie (pharma) , EFSA (alimentaire) . SCCS (cosmétiques), ECHA (REACH annexe VII (1 à 10 tonnes)).
 - EFSA et OMS: Le seuil de préoccupation toxicologique (TTC) pour les produits chimiques génotoxiques est 0.0025 µg/kg pc/jour sauf pour les produits hautement cancérogènes comme les nitrosamines.
 - **Produit pur versus mélange complexe ?**

Impureté inattendue dans un
produit pur,
mélange d'impuretés,

Impureté inattendue

Supposons un pic de dégradation, impureté

- ⇒ Identification
- ⇒ Caractérisation *in silico* (QSAR...)
- ⇒ Synthèse mg to g
- ⇒ Test ...



Solution:

- Collecter le pic et le tester directement comme un échantillon
- Mais quantité limité de produit (< mg, = µg)

Les hautes performances de l'Analyse chromatographique 1/3

FOOD ADDITIVES & CONTAMINANTS: PART A
https://doi.org/10.1080/19440049.2019.1664772

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Value and limitation of *in vitro* bioassays to support the application of the threshold of toxicological concern to prioritise unidentified chemicals in food contact materials

Benoit Schilter^a, Karin Burnett^b, Chantra Eskes^c, Lucie Geurts^d, Mélanie Jacquet^e, Christian Kirchnawy^f, Peter Oldring^g, Gabriele Pieper^h, Elisabeth Pinterⁱ, Manfred Tacker^j, Heinz Traussnig^j, Peter Van Herwijnen^k and Alan Boobis^l

La forêt de pics est un mélange de plusieurs dizaines milliers de molécules/impuretés inconnues, dont la réactivité, la stabilité et l'innocuité sont inconnues: **comment les caractériser ?**

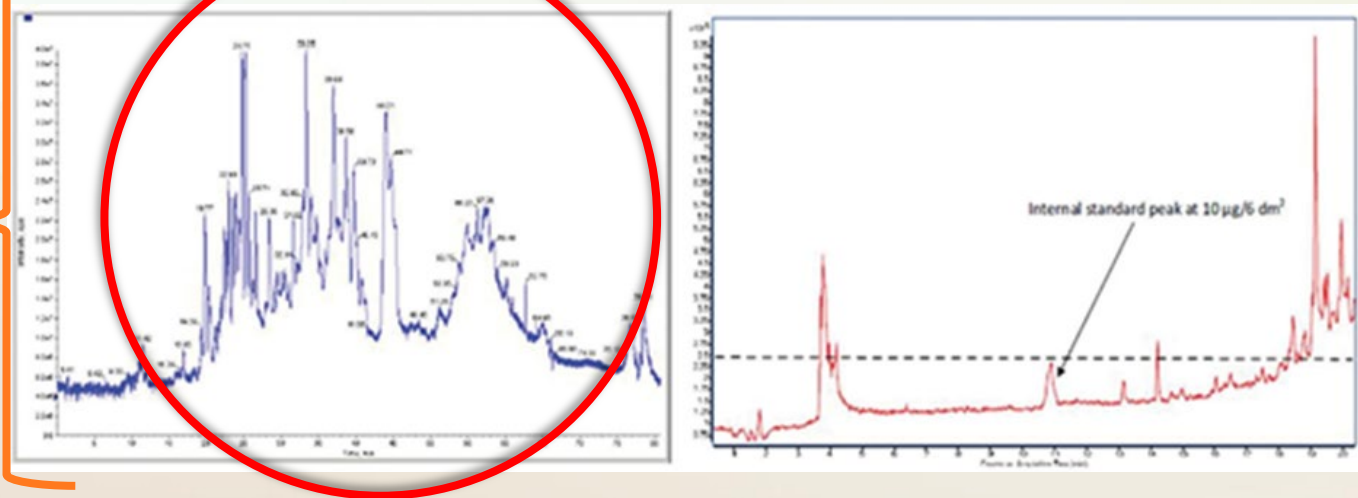


Figure 1. Illustrative examples of forests of peaks. Total ion chromatograms of extracts from FCMs are presented, along with a line (dashed) representing a 10 µg/6 dm² standard (right-hand panel). Such profiles are typical from many different FCM extracts or migrates.

Definitions 2/3

Box 1. Terminology associated with the concept of limit of detection (LOD) as used in the present manuscript.

- LOD** **Limit of detection (LOD).** In analytical chemistry, LOD is defined as the lowest concentration of an analyte in a sample that the analytical process can reliably detect, meaning that the signal of the analyte is statistically different from that of a blank.
- LOCD** **Limit of chemical detection (LOCD).** Used to describe the LOD for analytical chemistry methods.
- LOBD** **Limit of biological detection (LOBD).** Used to describe the LOD for bioassay-based methods.
- LEC** **Lowest Effective Concentration (LEC).** Defined as the lowest concentration that gave a measurable positive response in the bioassay. For a pure chemical, the LEC is obtained by establishing a concentration-response curve.
- cLOBD** **Calculated limit of biological detection (cLOBD).** LOBD in packaging migrate based on the LEC and accounting for the sample preparation procedure (including migration study protocol, migrate concentration, transfer into bioassay compatible solvent and then application in the bioassay). Concentration and dilution factors specific for each relevant sample preparation step are integrated into a factor which is applied to the LEC.
- tLOBD** **Target limit of biological detection (tLOBD).** LOBD required to comply with a predefined level of health (carcinogenic) risk. In practice, in the present paper, the total daily dose calculated to produce an excess carcinogenic risk of 1 in 10^5 (derived from a tumorigenic dose causing a 50% response in an animal cancer bioassay, TD50) as applied to 1 kg of packaged food for a 60 kg adult.

Test biologique versus analyse 3/3

Table 2. Calculated limits of biological detection (cLOBDs) for selected genotoxic chemicals in Ames plate incorporation test as compared to required target LOBDs (tLOBD) based on carcinogenic potency (TD50). For comparison, data derived from mammalian MLA hrp test are also provided.

Chemicals	Ames test						Mammalian (MLA hrp)		
	LEC _{plate} ¹ (µg/plate)	LEC _i ² (mg/L)	cLOBD ³ (mg/L)	TD50 ⁴ (mg/kg/d)	tLOBD ⁵ (mg/L)	cLOBD/tLOBD ⁶	LEC ⁷ (mg/L)	cLOBD ⁸ (mg/L)	cLOBD/tLOBD ⁶
Aflatoxin B1	0.0038	0.0014	0.000035	0.0032	0.0000039	9.2	0.1	0.008	2083
1162-65-8									
Mitomycin C	na	0.0015	0.00004	0.00102	0.0000122	30.6	0.075	0.0075	6127
50-07-7									
IQ (2-amino-3-methylimidazo [4,5-f]quinoline)	0.005	0.0019	0.00005	0.812	0.00097	0.05	na	na	na
76180-96-6									
PhIP.HCl (2-amino-1-methyl-6-phenylimidazo [4,5-b]pyridine)	0.01	0.0037	0.00009	1.78	0.002	0.04	na	na	na
105650-23-5									
Methylnitrosoguanidine	0.034	0.013	0.00033	0.803	0.0009	0.3	0.025	0.0025	3
70-25-7									
2-Acetylaminofluorene	0.266	0.100	0.0025	1.22	0.0015	2	50	5	3415
53-96-3									
2-Nitrofluorene	0.57	0.21	0.005	0.285	0.00034	15	na	na	na
607-57-8									
Benzo(a)pyrene	0.57	0.21	0.005	0.956	0.0011	5	0.1	0.01	9
50-32-8									
Cyclophosphamide	2	0.7	0.02	2.21	0.003	7	1	01	38
6055-19-2									
Methyl methanesulfonate	19	7.4	0.175	31.8	0.039	5	5.5	0.55	14
66-27-3									
2,4 Diaminotoluene	20	7	0.2	2.47	0.003	62	na	na	na
95-80-7									
Dimethylnitrosamine	20	7	0.2	0.0959	0.0001	1609	50	5	43448
62-75-9									
7,12-Dimethylbenzanthracene	25	9	0.2	0.084	0.0001	2296	1	0.1	992
57-97-6									
N-Ethyl-nitrourea	33	12	0.3	0.948	0.001	269	0.4	0.04	35
759-73-9									
Formaldehyde	60	22	0.6	1.35	0.002	343	negative	na	na
50-00-0									

1: LEC_{plate}: Lowest Effective Concentrations (LEC) retrieved from (Duffy et al. 2006), expressed in mass/plate.

2: LEC_i = LEC_{plate} expressed in mass/L. For comparison with concentrations in migrates, LEC_{plate} in mass/plate were converted in mass/L by dividing by a factor of 2.7 (to account for the 2.7 ml of top agar plated) and then multiplied by 1000.

3: cLOBDs: calculated LOBDs. LOBDs calculated from the LEC_i, accounting for the various concentration/dilution steps in sample preparation, leading to a final concentration factor of 40. cLOBD = LEC_i/40.

4: TD50 = dose in animal carcinogenicity bioassay estimated to induce tumours in 50% of treated animals (from carcinogenic potency database (Gold)).

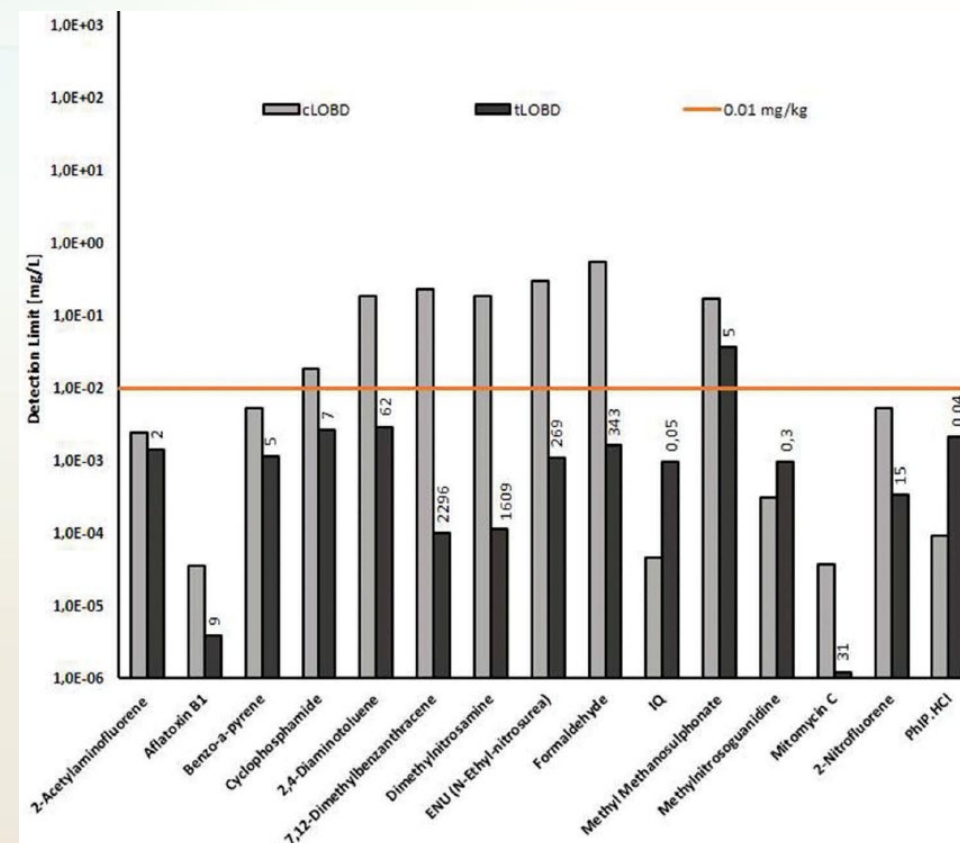
5: tLOBD: Target Limit of Detection based on an excess risk of 10⁻⁵. tLOBD = (TD₅₀ x 60)/50000.

6: ratio cLOBDs/tLOBD. A ratio <1 indicates that the theoretical LOBD derived from an available LEC (cLOBD) is sufficiently low to detect a level in the migrate corresponding to an excess risk < 10⁻⁵.

7: LEC obtained in mammalian cells (MLA hrp); Lowest Effective Concentrations (LEC), expressed in mass/L from (Green et al. 1976; Couch et al. 1978; Clive et al. 1979; Kaden et al. 1979; Phillips et al. 1980; Gupta and Singh 1982; O'Neill et al. 1982; Connor et al. 1983; Thompson et al. 1983; Zamora et al. 1983; Oberly et al. 1984, 1993; Wangenheim and Bolcsfoldi 1988; Eliopoulos et al. 1995; Speit and Hartmann 1995; Hakura et al. 2003; Valentin-Severin et al. 2003; Kawaguchi et al. 2010; Smith et al. 2013).

8: cLOBDs from mammalian-cell-based assays (MLA hrp). The cLOBDs were calculated from the LECs⁷ (in mg/L) divided by 10 (assuming a total theoretical concentration factor of 10).

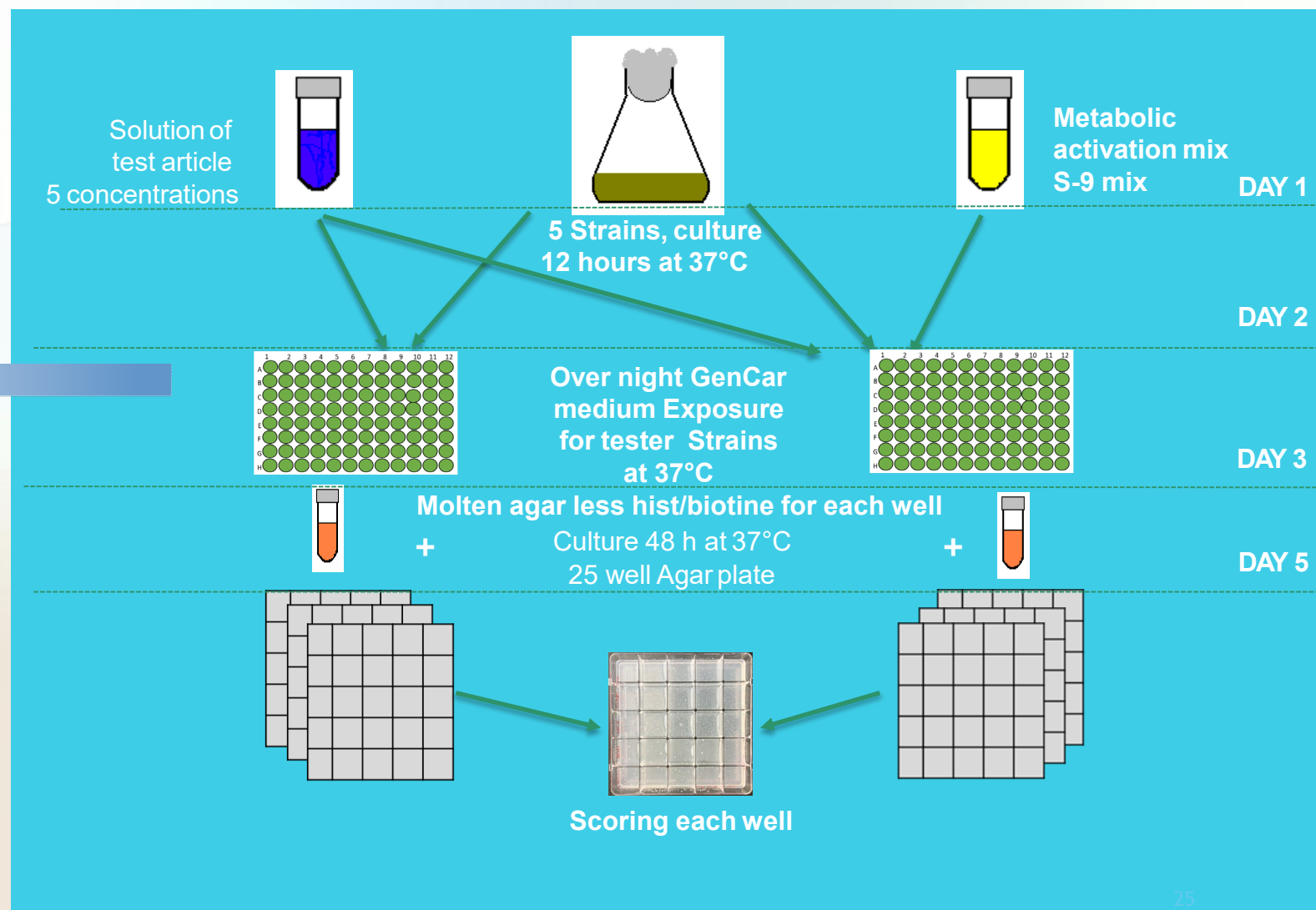
na: not available.



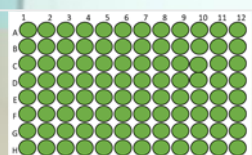
Constat....

- Dans l'état actuel des connaissances les essais biologiques *in vitro* peuvent fournir des informations supplémentaires importantes pour l'évaluation de l'innocuité des MCF. Toutefois , pour détecter de façon fiable les substances génotoxiques en deçà d'un seuil de 0,00015 $\mu\text{g/mL}$ (TTC),
- **il faut encore les améliorer.**
- *Néanmoins, les méthodes chimiques actuelles utilisées pour l'analyse des Emballages en contact avec les aliments migrent utilisent une limite de détection de 0,01 $\mu\text{g/mL}$ et sont donc également notables pour exclure la présence de toute substance génotoxique considérée par le TTC. Finalement la conduite des deux méthodes peut fournir des informations toxicologiques importantes sur une FCM pour rendre possible une évaluation de l'innocuité des substances inconnues.*

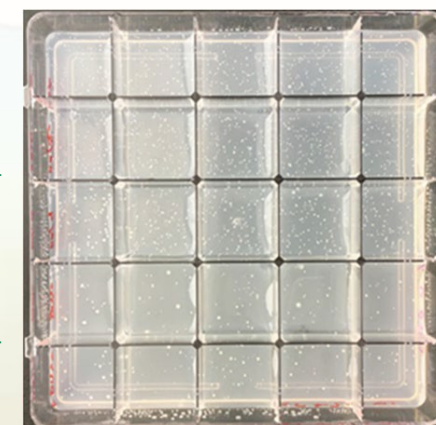
NANOAMES™ TEST : METHOD



Molecular
Biology



for PCR



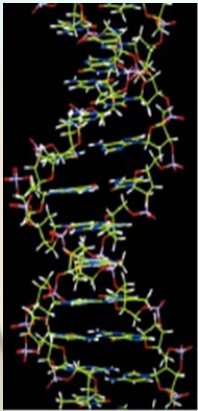


Test d'Ames ultra miniaturisé

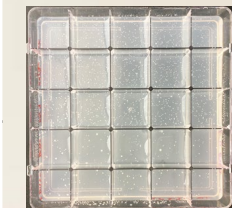
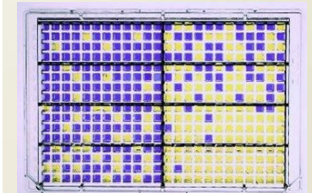
INNOVATION



Il existe différentes méthodes pour le test d'Ames.
Dans le cadre de la caractérisation d'impureté en très petite quantité, GenEvolutionN a ultra miniaturisé le test d'Ames « NanoAmesTM »



Test de mutagenèse	Méthodes	Test item Quantité	Commentaires
Ames test	Standard	250 mg/essai	5 souches
Effet nourricier Produit cytotox	« Treat and Wash » « Treat and plate »	250 mg/essai	5 souches
Screening/ impureté	MPF (fluctuation)	40 mg	5 souches
Screening/	Miniaturisé	35 mg	4 souches
Impureté non caractérisée	NanoAmes TM	70 µg/2 souches	5 souches



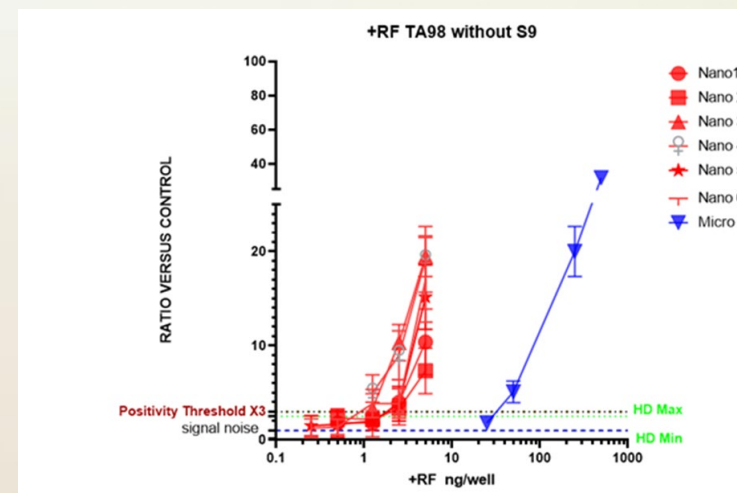
Test d'Ames Ultra-miniaturisé versus mini

- 14 produits de référence et deux produits négatifs ont été testés en utilisant la méthode ultra miniaturisée en pré-incubation sur les 6 souches TA98, TA100, TA97a, TA1535, TA102 et E.Coli, avec et sans activation métabolique.

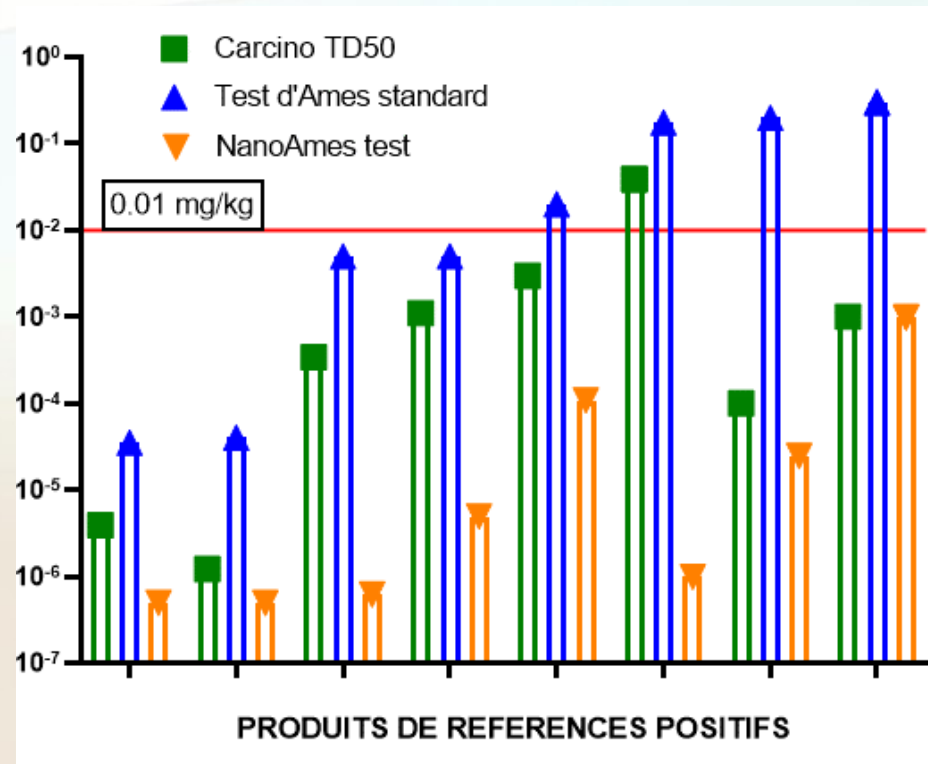
Bonne correspondance

	TA98		TA100		TA102		TA97a		TA1535		E.Coli ^W	
	Micro	Nano	Micro	Nano	Micro	Nano	Micro	Nano	Micro	Nano	Micro	Nano
+RF1 (-S9)												
+RF2 (-S9)												
+RF3 (-S9)												
+RF4 (-S9)												
+RF5 (-S9)												
+RF6 (-S9)												
+RF7 (+S9)												
+RF8 (+S9)												
+RF9 (+S9)												
+RF10 (-S9)												
+RF10(+S9)												
+RF11 (-S9)												
+RF11 (+S9)												
+RF12 (-S9)												
+RF12 (+S9)												
+RF13 (-S9)												
+RF13 (+S9)												
+RF14 (-S9)												
+RF14 (+S9)												
-RF15 (-S9)												
-RF15 (+S9)												
-RF16(-S9)												
-RF16(+S9)												

À des doses plus faibles



Conséquences: comparaison Ultra miniaturisation versus Ames standard



NanoAmes

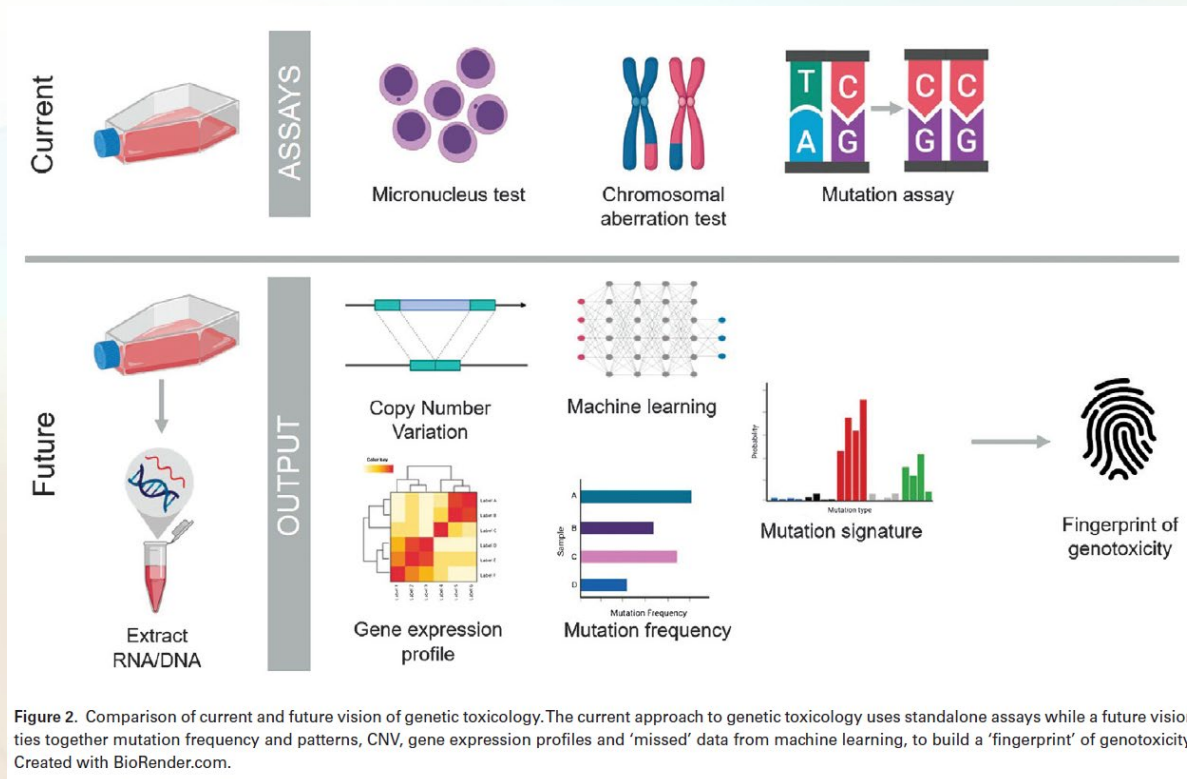
cLOBD/tLOBD
 0,126
 0,404
 0,0018
 0,0045
 0,036
 2,52644E-05
 0,246
 0,985

Ames standard

cLOBD/tLOBD" paper
 9,2
 30,6
 15
 5
 7
 5
 2296
 269

FOOD ADDITIVES & CONTAMINANTS: PART A
<https://doi.org/10.1080/19440049.2019.1664772>

Conclusion



The promise of toxicogenomics for genetic toxicology: past, present and future

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Received 21 August 2019; Editorial decision 31 January 2020; Accepted 10 February 2020.

Automatisation des techniques

ARN/ADN expression

In silico => AI = « machine learning »

Integrated solution

As part of the Seqens'Lab ecosystem, we provide you with a suitable solution to investigate the mutagenic potential of impurities and secure your development according to ICH M7 guidelines

Identification of impurities along the synthesis of APIs

SEQENS'Lab



<https://www.seqens.com>

***in silico* analysis from chemical structure of impurities**

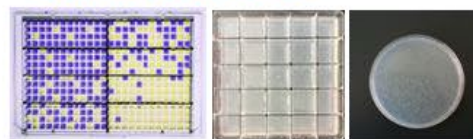


www.harmonicpharma.com

<https://gti.harmonicpharma.com/>

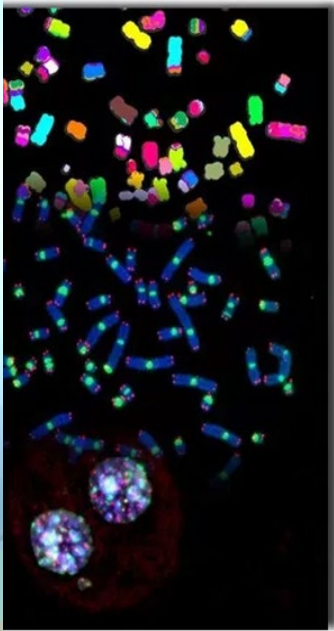
***In vitro* Ames test :
Ames/NanoAMES – non
GLP or GLP compliant**

GENEVOLUTION



www.genevolution.fr





- **Nestlé:** Maricel Marin-Kuan, Gabriele Scholz et Benoît Schilter
- **Servier:** Véronique Gervais
- **XenometriX :** Dimitrios Spiliotopoulos et Nicole Weilad-Jaegi
- **Biomnigene:** Alexandre Douablin
- **GenEvolutionN:** Olivier Cariou, Nina Coulange, Isabelle Mouche
Laure Malésic, Françoise Gigan et Michèle Loeffler



Références

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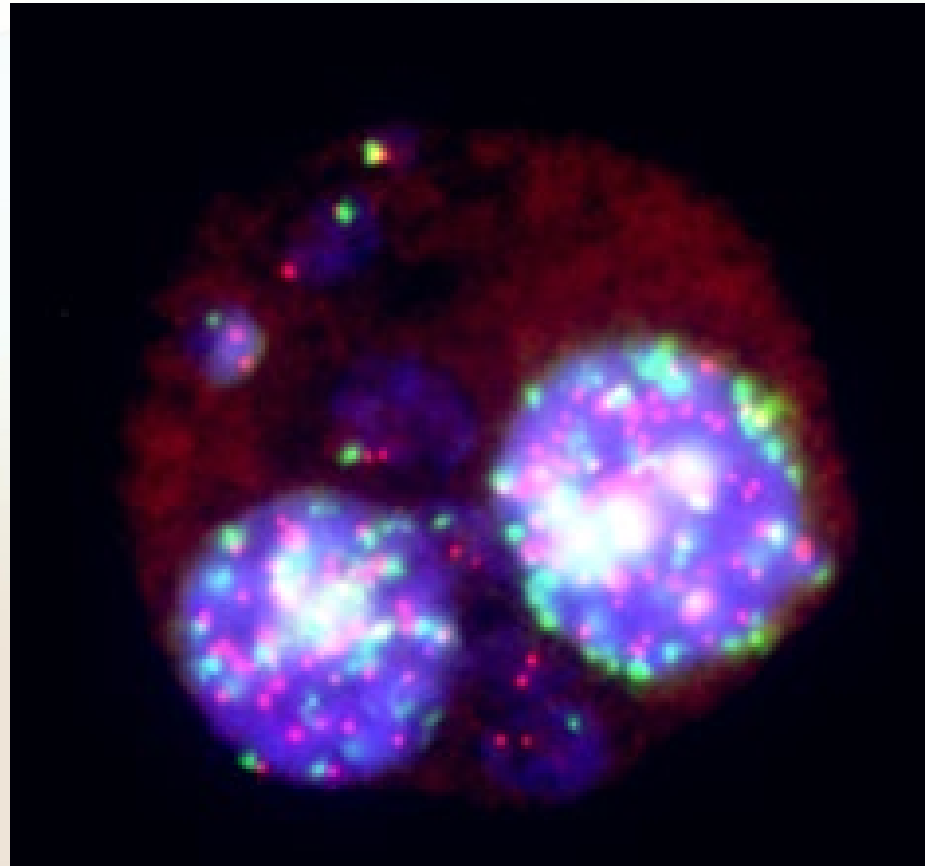


ANNEXE

Cytogenetic tests

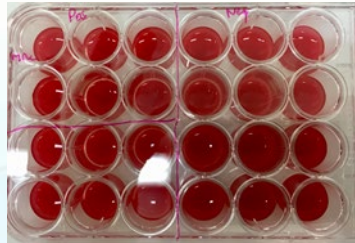
Micronucleus OECD 487

GLP



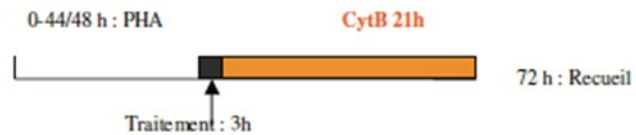
in vitro Micronucleus test (OECD 487)

3- hour short treatment with and without metabolic activation, then a long treatment 24-hour in the absence of metabolic activation. In case of cycle delay, a long alternative treatment could be performed :

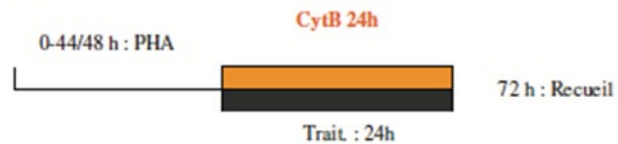


In presence of phytohemagglutinine ,
Blocked by cytochalasine B

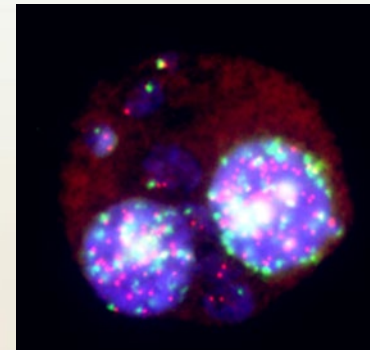
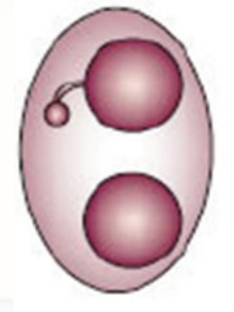
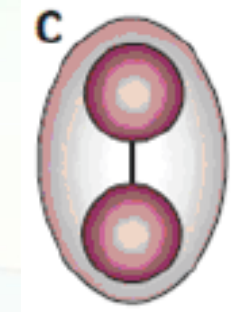
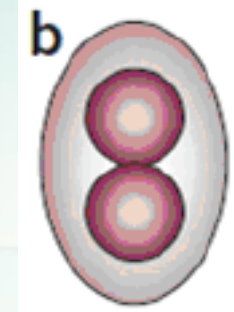
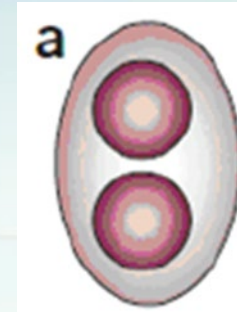
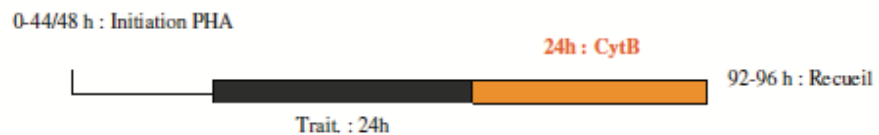
• traitement court (+/-S9) 3h + 21h



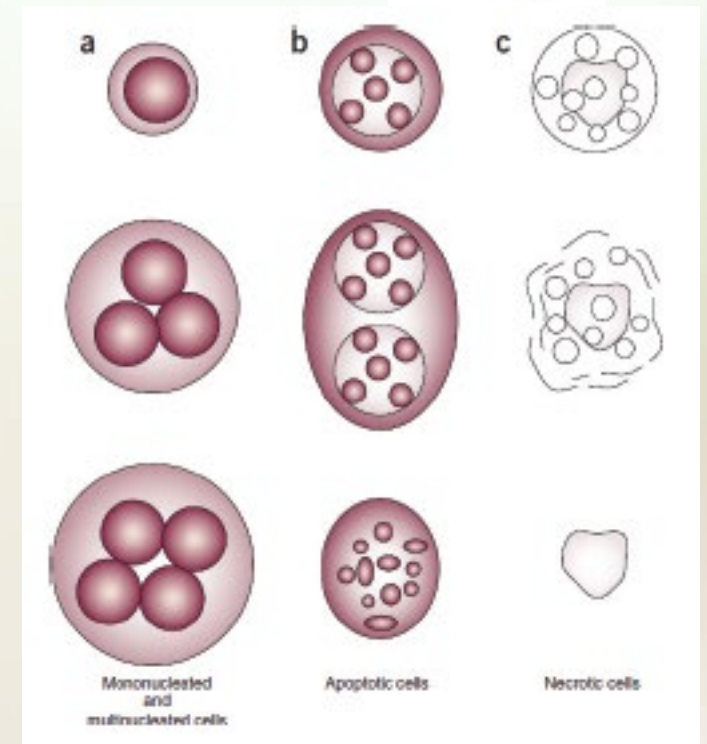
• traitement long (-S9) 24+0h



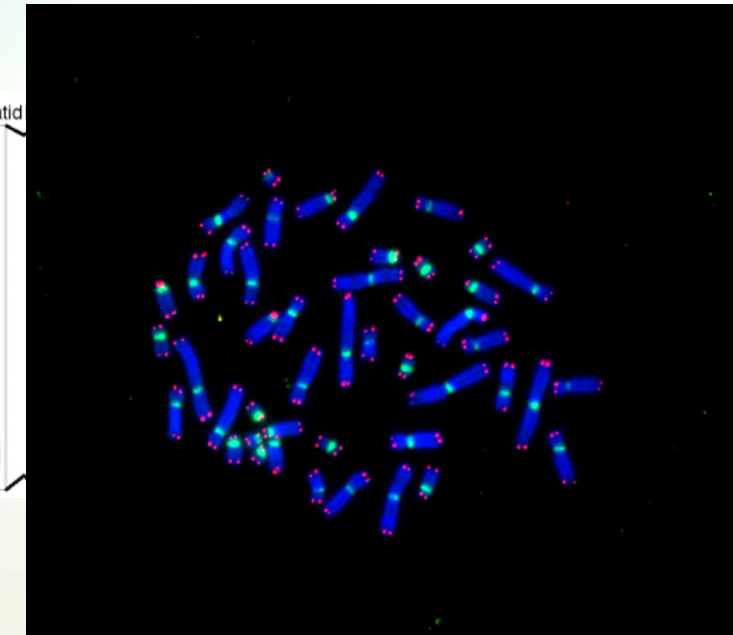
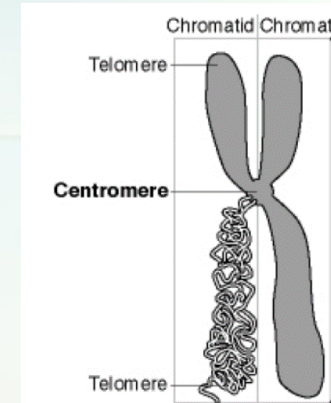
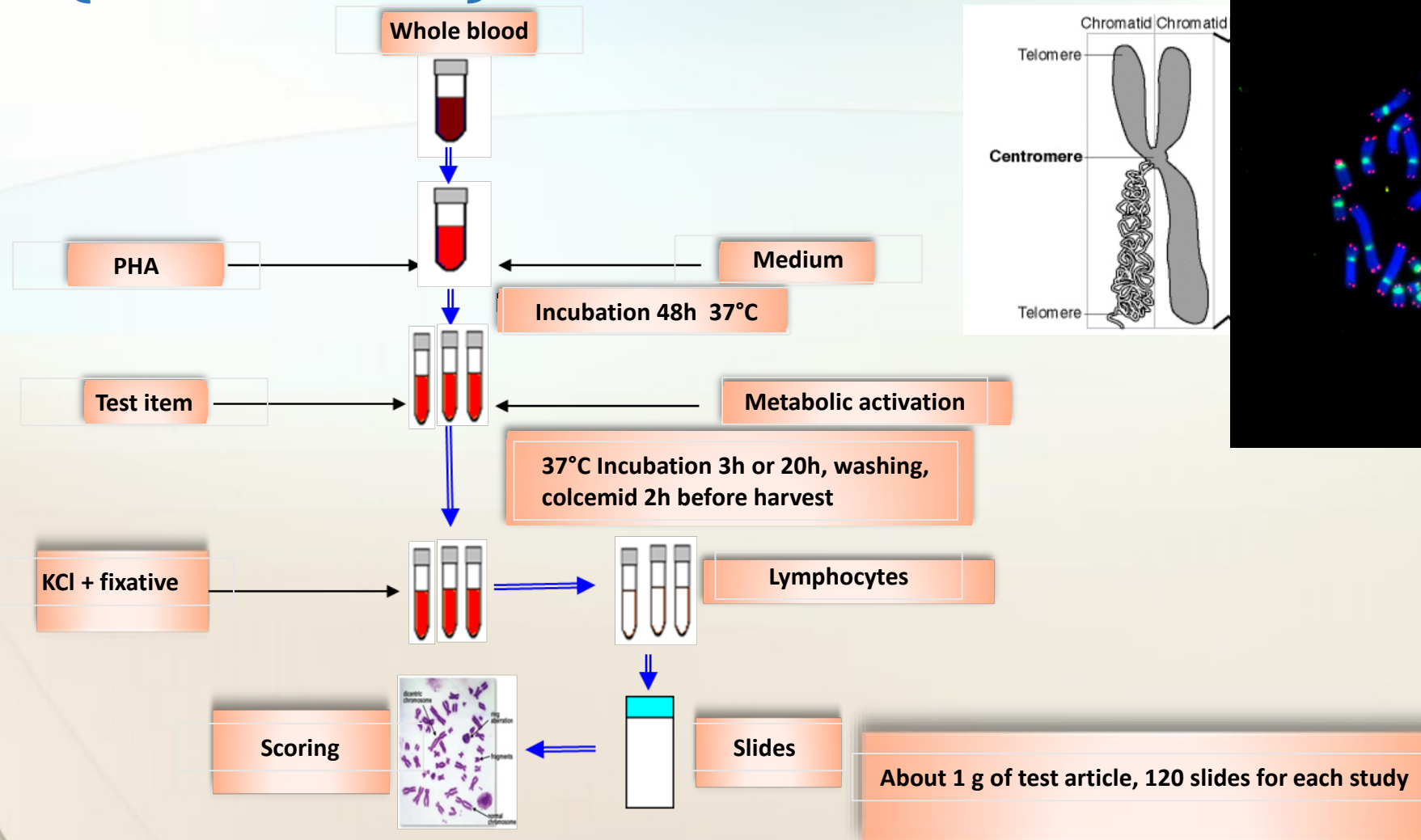
• traitement 24+24h :



Double staining :
show aneugen, or
Clastogen (m-Fish)



Chromosomal aberration test: Method (OECD 473)





Un CRO avec une expertise en genotoxicité

INNOVATION

GenEvolutionN
Holding SAS
(Février 2018)

Règlementaire BPL

GenEvolutionN
Prospective
Division
(Février 2017)

Activité de Recherche
Transfert de
technologie

JEI

GenEvolutionN
Testing Division
(Juin 2017)

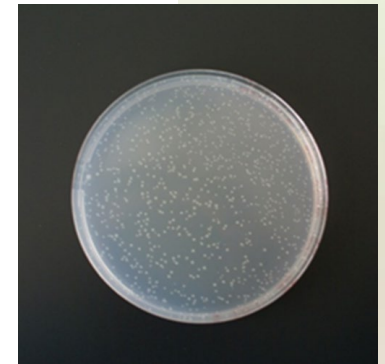
Tests Réglementaires

ANSM
GIPC COFRAC

OECD 471 guideline -bacteria

13. At least five strains of bacteria should be used. These should include four strains of *S. typhimurium* (TA1535; TA1537 or TA97a or TA97; TA98; and TA100) that have been shown to be reliable and reproducibly responsive between laboratories. These four *S. typhimurium* strains have GC base pairs at the primary reversion site and it is known that they may not detect certain oxidising mutagens, cross-linking agents and hydrazines. Such substances may be detected by *E.coli* WP2 strains or *S. typhimurium* TA102 (19) which have an AT base pair at the primary reversion site. Therefore the recommended combination of strains is:

1. *S. typhimurium* TA1535, and
2. *S. typhimurium* TA1537 or TA97 or TA97a, and
3. *S. typhimurium* TA98, and
4. *S. typhimurium* TA100, and
5. *E. coli* WP2 uvrA, or *E. coli* WP2 uvrA (pKM101), or *S. typhimurium* TA102.



In order to detect cross-linking mutagens it may be preferable to include TA102 or to add a DNA repair-proficient strain of *E.coli* [e.g. *E.coli* WP2 or *E.coli* WP2 (pKM101).]