Table 6. Summary of *in vitro* and *in vivo* genotoxicity data for acetaldehyde, butanol, hexanal, acetoin and 4-methyl-2-pentanone.

Substance	Test system	Test objects	Concentration	Result	Reference
Acetaldehyde	Ames test	*Salmonella typhimurium* (TA100, TA102, TA104)	Not reported	Negative[b]	Dillon et al. (1992)
	Forward mutation assay	L5178y mouse lymphoma TK±	0.004–0.008 mol l^{-1}	Positive[a]	Wangenheim and Bolcsfoldi (1988)
	Sister chromatid exchange	Adult human lymphocytes	0.1–2.4 mM	Positive	He and Lambert (1985)
	Sister chromatid exchange	Adult human peripheral lymphocytes	100–400 μM	Positive	Helander and Lindahl-Kiessling (1991)
	Chromosomal aberration test	Chinese hamster embryonic diploid cells	0.002%	Positive	Furnus et al. (1990)
Acetoin	Reverse mutation	*Salmonella typhimurium* (TA100)	≦ 4500 μg/plate	Negative[c]/ positive[a]	Garst et al. (1983)
	Reverse mutation	*Salmonella typhimurium* (TA100)	420 μg/plate	Negative[a]	Kim et al. (1987)
Hexanal	Forward mutation assay	V79 Chinese hamster lung cells	3–30 mmol l^{-1}	Positive[a]	Brambilla et al. (1989)
	Unscheduled DNA synthesis assay	Adult human and rat hepatocytes	3–100 mmol l^{-1}	Negative[a]	Martelli et al. (1994)
	Ames test	*Salmonella typhimurium* (TA102, TA104)	Up to 1 mg/plate	Negative[a]	Marnett et al. (1985)
	Ames test (spot test)	*Salmonella typhimurium* (TA98, TA100, TA1535, TA1537)	3 μmol/plate	Negative[b]	Florin et al. (1980)
	Forward mutation assay	V79 Chinese hamster lung cells	3–30 mmol l^{-1}	Positive[a]	Brambilla et al. (1989)
Butanol	Ames test	*Salmonella typhimurium* (TA102)	Up to 5000 μg/plate	Negative[b]	Müller et al. (1993)
	Forward mutation assay	Chinese hamster ovary cells	0.2–1.6 μl ml^{-1}	Positive	WHO (1998)
	Sister chromatid exchange	Chinese hamster ovary cells	0.1–2.4 mM	Negative	Obe and Ristow (1977)
	Ames test	*Salmonella typhimurium* (TA98, TA100, TA1535, TA1537, WP2*uvrA*, TA102)	5000 μg/plate	Negative[b]	FSCJ (2005b)
	Sister chromatid exchange	Chinese hamster ovary cells	0.7 mg ml^{-1}	Negative[b]	FSCJ (2005b)
	Micronucleus formation	Male ICR mouse bone marrow	2000 mg kg^{-1} body weight	Negative	FSCJ (2005b)
4-Methyl-2-pentanone	Reverse mutation	*Salmonella typhimurium* (TA98, TA100, TA1535, TA1537, TA1538)	0.03–3.00 mg/plate	Negative[a]	O'Donoghue et al. (1988)
	Reverse mutation	*Salmonella typhimurium* (TA97, TA98, TA100, TA1535)	≦ 6667 μg/plate	Negative[a]	Zeiger et al. (1992)
	Reverse mutation	*Escherichia coli* (WP2*uvrA*)	8000 μg/plate	Negative[a]	Brooks et al. (1988)
	Gene conversion	*Saccharomyces cerevisiae*	5 mg ml^{-1}	Negative[b]	Brooks et al. (1988)
	Forward mutation	L5178Y/tk± mouse lymphoma cells	0.26–3.40 mg ml^{-1}	Negative[a]	O'Donoghue et al. (1988)
	Unscheduled DNA synthesis	Rat hepatocytes	8–80 μg ml^{-1}	Negative[a]	O'Donoghue et al. (1988)
	Chromosomal aberration	Rat hepatocytes	1000 μg ml^{-1}	Negative[a]	Brooks et al. (1988)
	Micronucleus formation	Male and female ICR mouse bone marrow	2500 mg kg^{-1} body weight	Negative	Kapp et al. (1993)

Notes: [a]Without metabolic activation.
[b]With and without metabolic activation.
[c]With metabolic activation.

risk for development of alcohol-related cancers, in particular of the oesophagus and the upper aero-digestive tract (Eriksson 2015). It has been reported that there is a relationship between the genetic polymorphism of alcohol dehydrogenase (ALDH) and alcohol metabolism. It is known that ALDH II-type deficiency is more common among Orientals (Yoshida et al. 1984). Although ALDH II-type deficiency is likely to increase the blood aldehyde levels in more susceptible humans than in less susceptible ones (Enomoto et al. 1991), other metabolic pathways are considered to function in a complementary manner (Kunitoh et al. 1996; Riveros-Rosas et al. 1997).

It is reported that approximately 1.3–3.9 μM of blood acetaldehyde levels can be detected in healthy persons (Lynch et al. 1983; Fukunaga et al. 1993). In Japan, the blood acetaldehyde level in man is not considered to exceed 14 μM even if the estimated daily intake of acetaldehyde (approximately 19 mg/person/day) is consumed at a time, and if 100% of it is absorbed and distributed in the body without being metabolised by the first-pass effect, as reported by FSCJ (2005a). However, the situation, in which the level of acetaldehyde, equivalent to that used as a flavouring ingredient, is consumed in daily dietary life, is far from being applicable to the above hypothesis. In fact, not all the orally ingested acetaldehyde is absorbed directly into the body, the majority of it is supposed to change into acetic acid via metabolism by ALDH and other enzymes in the gastrointestinal tract and liver (Tsutsumi et al. 1988; Yin et al. 1994; Kunitoh et al. 1996; Riveros-Rosas et al. 1997). JECFA has also concluded that acetaldehyde does not raise any safety concerns at the current levels of intake because ingested acetaldehyde will undergo complete metabolism to endogenous products.

Conclusions

In conclusion, the five acetals, acetaldehyde 2,3-butanediol acetal, acetoin dimethyl acetal, hexanal dibutyl acetal, hexanal glyceryl acetal and 4-methyl-2-pentanone propyleneglycol acetal, for flavouring foods pose no health risk to humans, and the intake of each substance as a food-flavouring ingredient is safe at the present levels of use.

Disclosure statement

Hiroyuki Okamura, Kenji Saito, Fumiko Sekiya, Shim-Mo Hayashi, Yoshiharu Mirokuji and Shinpei Maruyama are employed by flavour manufacturers whose product lines include flavouring substances. The views and opinions expressed in this article are those of the authors and not necessarily those of their respective employers. Hajime Abe, Yasuko Hasegawa-Baba, Atsushi Ono, Madoka Nakajima, Masakuni Degawa, Shogo Ozawa, Makoto Shibutani and Tamio Maitani declare that no conflicts of interest exist.

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Supplemental data

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Open TG-GATEs: a large-scale toxicogenomics database

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ABSTRACT

Toxicogenomics focuses on assessing the safety of compounds using gene expression profiles. Gene expression signatures from large toxicogenomics databases are expected to perform better than small databases in identifying biomarkers for the prediction and evaluation of drug safety based on a compound's toxicological mechanisms in animal target organs. Over the past 10 years, the Japanese Toxicogenomics Project consortium (TGP) has been developing a large-scale toxicogenomics database consisting of data from 170 compounds (mostly drugs) with the aim of improving and enhancing drug safety assessment. Most of the data generated by the project (e.g. gene expression, pathology, lot number) are freely available to the public via Open TG-GATEs (Toxicogenomics Project-Genomics Assisted Toxicity Evaluation System). Here, we provide a comprehensive overview of the database, including both gene expression data and metadata, with a description of experimental conditions and procedures used to generate the database. Open TG-GATEs is available from http://toxico.nibio.go.jp/english/index.html.

INTRODUCTION

Open Toxicogenomics Project-Genomics Assisted Toxicity Evaluation Systems (TG-GATEs) (Figure 1) is a toxicogenomics database that stores gene expression profiles and traditional toxicological data derived from *in vivo* (rat) and *in vitro* (primary rat hepatocytes, primary human hepatocytes) exposure to 170 compounds at multiple dosages and time points. The toxicology data is composed of biochemistry, hematology and histopathology findings with pathology imaging from the *in vivo* studies and cytotoxicity from the *in vitro* studies. The 170 compounds include representative known liver- and kidney-injuring pharmaceuticals, compounds and chemicals. These data have been generated and analyzed over the course of the 10-year Japanese Toxicogenomics Project (TGP), which was a joint government–private sector project organized by the National Institute of Biomedical Innovation (NIBIO), the National Institute of Health Sciences (NIHS) and 18 pharmaceutical companies (Figure 2).

As specified by relevant regulations, toxicity assessments in the pre-clinical stage of drug development must be conducted using whole animals and cells. In animals, general toxicity in liver and kidney is evaluated with physiological, hematological and biochemical measurements and pathology assessment. In cells, the evaluation of cytotoxicity is conducted by measuring cell viability parameters and morphological changes, often with the use of microscopy. These approaches ensure detection of a certain level of toxicity that might be associated with a given test compound. However, gene expression data is expected to permit the detection of potential toxicities that may not be observable by conventional assessments, thereby facilitating more accurate and predictive decision-making based on toxicity mechanisms (1).

Over the past 10 years, TGP data had been generated at NIHS, NIBIO and several designated contract research organizations using defined standard operating procedures (SOPs). The resulting data were stored, managed and analyzed in a closed version of the database, TG-GATEs. Open TG-GATEs was developed as a publicly available version of the same database, in which the results of 20 118 GeneChip assays are stored along with associated toxicological data and 25 TB of digitized pathology images. Open TG-GATEs is one of the largest public toxicogenomics databases in the world. Using the TG-GATEs data, 36 biomarker sets for specific toxicity mechanisms have to date been defined dur-

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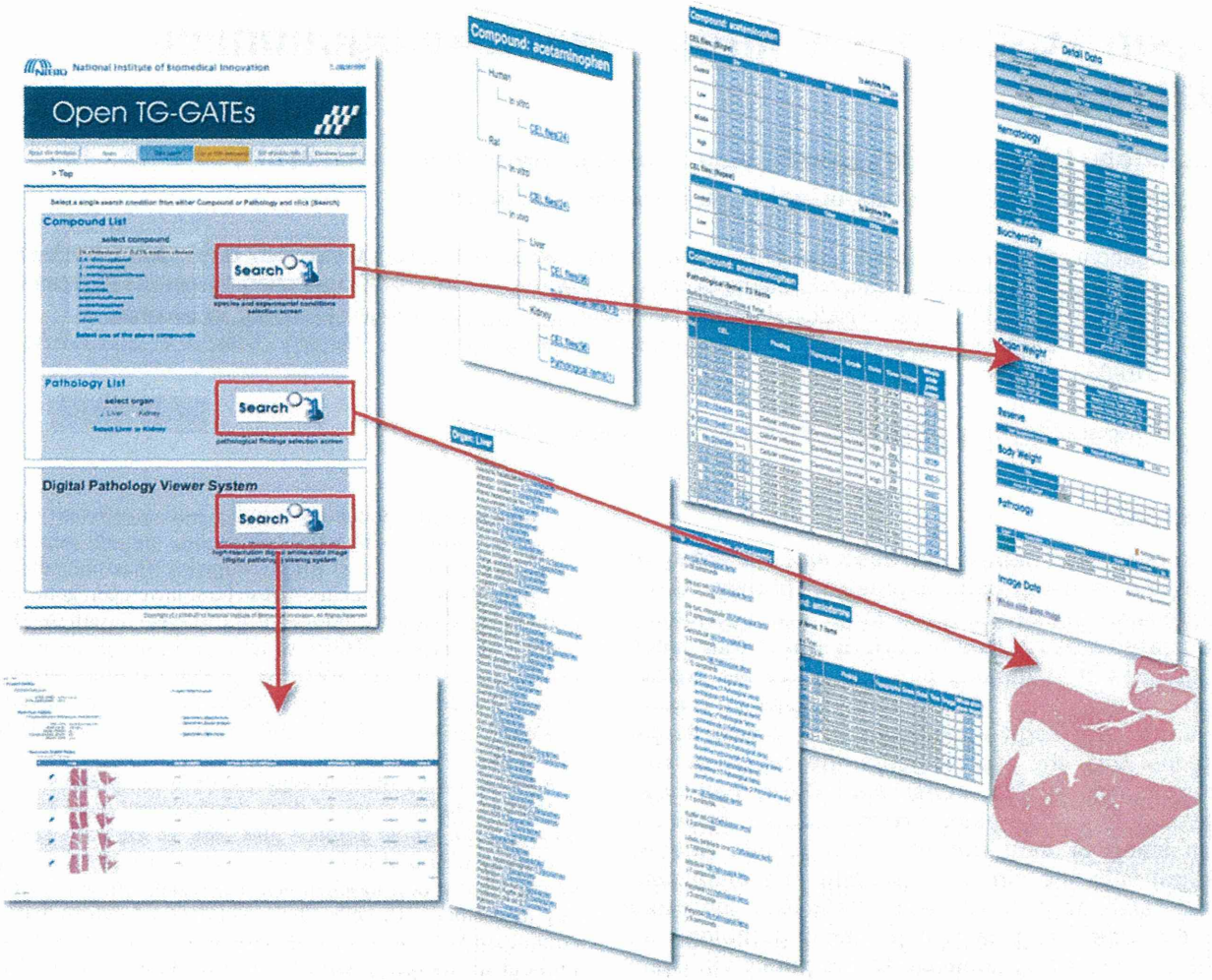

Figure 1. Open TG-GATEs offers hierarchical access from compound and pathology lists to hematology, biochemical parameters and digitized pathology images. Gene expression data are stored as CEL files, which require software capable of interacting with the Affymetrix data file format. Thus, users will have to convert the primary data into a general-purpose format using various algorithms such as MAS5.0, RMA, etc.

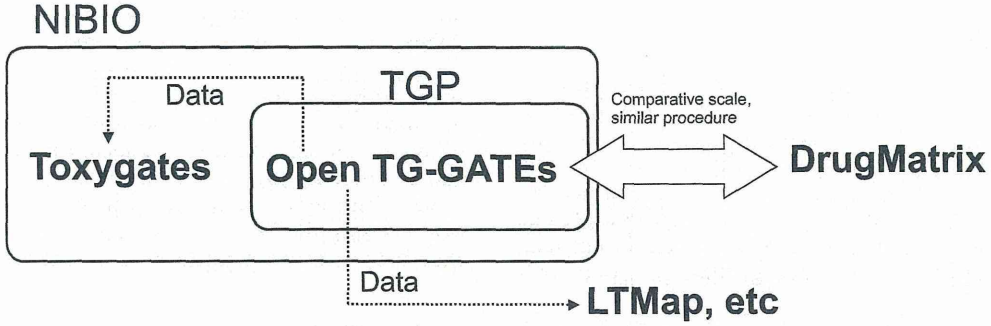

Figure 2. The relationship of the databases and organizations are shown. The dotted line shows the data distribution. NIBIO: National Institute of Biomedical Innovation, TGP: Toxicogenomics project in Japan.

ing project development, and several of these biomarker signatures have been published (2–6).

In the present paper, we describe the data structure and background from a toxicological point of view, along with characteristics of the data relating to experimental conditions. We believe that the data and information in Open TG-GATEs will allow users to gain a greater understanding of toxicity mechanisms and to develop biomarkers for safety assessments of pharmaceutical drug candidates.

MATERIALS AND METHODS

Data framework

The gene expression data for a test compound were derived from administration of individual compounds at up to four dose levels and eight time points (corresponding to four single-dose studies and four repeated-dose studies). Studies involving microarray hybridization analysis were performed using three biological replicates of liver and kidney in rat. Biochemistry and hematology data from individual animals were also obtained and stored. The pathology images were digitized and annotated prior to addition to the database. For human and rat primary hepatocytes, test compounds were tested at up to four dose levels and three time points using duplicate microarray hybridization analysis. For primary hepatocytes, cell viability data was also obtained.

Species and target organ selection

For many years, the rat has been the preferred animal system for pre-clinical toxicological assessment. As a result, more data concerning toxicological mechanisms and endpoints have been accumulated for rat than for any other animal. Therefore, the rat was selected because identification of gene expression changes would have the potential to explain the mechanistic basis of the knowledge accumulated in this animal. Liver is the major organ for metabolism, detoxification of pharmaceuticals and other compounds. Furthermore, clinically significant adverse effects often occur in liver as well as in kidney. *In vitro* experiments in human and rat primary hepatocytes were included for two reasons: first, to provide a bridge between the *in vivo* and *in vitro* data; and second, to permit extrapolation from rat data to human results.

Compound selection

The tested compounds, shown in Supplementary Table S1, were selected based on literature searches and consensus among pharmaceutical and government toxicologists participating in the TGP. The majority of the compounds were pharmaceuticals with reported liver or kidney toxicity. However, some of the compounds were not pharmaceuticals or known hepato- or nephro-toxins, and instead corresponded to chemicals that had well studied mechanisms of toxicity; these compounds were included as reference chemicals.

Dose setting

For the *in vivo* studies, the highest dose was selected to match the level demonstrated to induce the minimum toxic effect over the course of a 4-week toxicity study. In principle, the ratio of the concentrations for the low, middle and high dose levels was set as 1:3:10. For the *in vitro* studies, the highest concentration was defined as the dose level yielding an 80–90% relative survival ratio. However, for compounds that dissolved poorly in the vehicle, the highest concentration was defined by the maximum solubility of the compound. In principle, the ratio of the concentrations for the low, middle and high dose levels was 1:5:25.

Animal treatment

The experimental procedures for the animal studies have been described previously (7,8) and are summarized here in brief. Animal experiments were conducted by four different contract research organizations. The studies used male Crl:CD Sprague-Dawley (SD) rats purchased from Charles River Japan, Inc. (Hino or Atsugi, Japan) as 5-week-old animals. After a 7-day quarantine and acclimatization period, the animals were allocated into groups of 20 animals each using a computerized stratified random grouping method based on body weight. Each animal was allowed free access to water and pelleted food (radiation-sterilized CRF-1; Oriental Yeast Co., Tokyo, Japan). For single-dose experiments, groups of 20 animals were administered a compound and then fivw animals/time point were sacrificed at 3, 6, 9 or 24 h after administration. For repeated-dose experiments, groups of 20 animals received a single dose per day of a compound and five animals/time point were sacrificed at 4, 8, 15 or 29 days (i.e. 24 h after the respective final administration at 3, 7, 14 or 28 days) (Figure 3). Animals were not fasted before being sacrificed. To avoid effects of diurnal cycling, the animals were sacrificed and necropsies were performed between 9:00 a.m. and 11:00 a.m. for the repeated-dose studies. Blood samples for routine biochemical analyses were collected into heparinized tubes under ether anesthesia from the abdominal aorta at the time of sacrifice.

The experimental protocols were reviewed and approved by the Ethics Review Committee for Animal Experimentation of the NIHS and by the respective contract research organizations.

Sampling sites of liver and kidney for *in vivo* study

For liver, the sampling site was selected to avoid the hepatic portal vein and choosing a hepatic parenchymal area of the limbic lobe where tissue thickness was consistent. Three tissue fragments were obtained per animal. The center portion was sliced and used as a sample for analysis of pathology. If pathological lesions were identified upon visual inspection, the sampling procedure was repeated at a second location distal from the affected area. For kidney, samples were obtained from the left kidney. Fragments of 1-mm thickness, including a portion of the cortex and medullary regions, were sliced horizontally against the long axis of the kidney using four aligned razors. Three fragments were obtained from each rat. If pathological lesion were identified upon visual inspection, the sampling procedure was repeated using the right kidney.

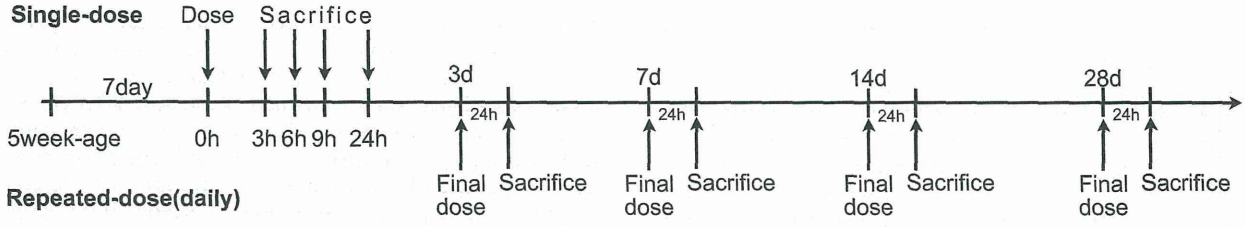

Figure 3. Time lines summarizing the procedures used for *in vivo* studies of single- and repeated-dose toxicity. For the repeated-dose studies, only the final dose is shown.

Hepatocyte treatment

Human cryopreserved hepatocytes were purchased from Tissue Transformation Technologies, Inc. (Edison, NJ, USA) and CellzDirect, Inc. (Pittsboro, NC, USA). Six lots of human hepatocytes were used during the course of the project. The lot information is shown in Supplementary Table S2. Rat primary-cultured hepatocytes were prepared as described previously (9), and were derived from 5-week-old male SD rats that had been subjected to a 5-day observation period after arrival. The lot information of the rat primary-cultured hepatocytes is provided in Supplementary Table S3. The detailed procedure for the measurement of cell viability parameters is described in the Supplementary information.

GeneChip analysis

The experimental procedure for the analysis of gene expression has been described previously (7,8), with the pertinent points briefly summarized here. In general, we selected rats of moderate body weight (the middle three of five animals). All CEL data in Open TG-GATEs passed quality control (QC). QC was performed at each step of the sample preparation and at the image-scanning step of GeneChip analysis. A collection of analytical information was checked as the final QC step, including background signal, corner signal, number of presence/absence calls and the expression values of housekeeping genes. The intra- and inter-group reproducibility was also evaluated. If a sample was found to be damaged, it was replaced by one of the two remaining fragments. The QC information is not open to the public. During the course of the 10-year project, two kinds of kits were used in the biotin-labeled cRNA synthesis procedure. These kits were the BioArray High Yield RNA Transcription Labeling Kit (Enzo Diagnostics, Farmingdale, NY, USA) and the GeneChip® IVT Labeling kit (Affymetrix, Santa Clara, CA, USA). For rat and human samples, the Rat Genome 230 2.0 Array and the Human Genome U133 Plus 2.0 Array were used, respectively. The probe set information is obtained from the Affymetrix support materials page, including gene names and identifiers in other representative databases. The probe set information is typically updated once a year. Gene expression analysis, including data QC processes, was performed according to an SOP, which for the most part followed the procedures supplied by the respective kit manufacturers.

Metadata in Open TG-GATEs

The metadata in the database includes the code for each GeneChip and corresponding data such as test compound name, dosage and body weight, as well as hematological and biochemical data (Table 1). The metadata files are stored in 'Attribute.tsv' for each compound. Peer-reviewed histopathological findings and topography information are also provided in Open TG-GATEs and the archived site (http://dbarchive.biosciencedbc.jp/en/open-tggates/download.html). Food consumption data is available only from the archived site.

Pathology images and annotation

The liver and kidney sections were stained with H&E (hematoxylin and eosin) and mounted on glass slides. Images of the sections were converted to digital pathology images using ScanScope AT (Aperio Technologies Inc., CA, USA). The digital images were saved and stored in .svs format, which consists of TIFF format files with associated sample dimensions and other relevant values. The pathological information is composed of histopathological finding, topography and grade. These curated data were originally annotated by each contract research organization and the data were subsequently peer-reviewed by the pathologists of the TGP member companies. The annotation was conducted based on a 'Pathology Glossary', a consensus controlled vocabulary for histopathological findings for liver and kidney (http://toxico.nibio.go.jp/open-tggates/doc/pathology_parameter.pdf), which was originally assembled by NIHS. Representative cropped pathology images were assembled in a pdf ('3. Histopathology photograph collection/list of histopathology findings' at http://toxico.nibio.go.jp/english/seika.html). Unfortunately, the XY positions of the cropped images from the full-size digital pathology image were not recorded.

DISCUSSION

The term toxicogenomics appeared in publications starting in the late 1990s (10). The concept was expected to enhance the determination of chemical toxicity by improving the prediction and understanding of the mechanisms of toxicity. Before the initiation of TGP, Iconix Pharmaceuticals, Inc. (11), had developed its own toxicogenomics database. This dataset is currently available to the public as the DrugMatrix database of the National Toxicology Programs of the National Institute of Environmental Health

Table 1. The column names and example data in attribute file are shown

Category	Column names	Values	Category	Column names	Values
Metadata of experiments	BARCODE	003017644018	Hematology data of individual animals	Plat(x10_4/μl)	143.6
	ARR_DESIGN	Rat230_2		WBC(x10_2/μl)	16.4
	EXP_ID	0040		Neu(%)	17
	GROUP_ID	01		Eos(%)	3
	INDIVIDUAL_ID	1		Bas(%)	1
	ORGAN_ID	Liver		Mono(%)	16
	MATERIAL_ID	B		Lym(%)	63
	COMPOUND_NAME	acetaminophen		PT(s)	12.1
	COMPOUND Abbr.	APAP		APTT(s)	13.7
	COMPOUND_NO	00001		Fbg(mg/dl)	207
	SPECIES	Rat		ALP(IU/l)	877
	TEST_TYPE	*in vivo*	Biochemical data of individual animals	TC(mg/dl)	104
	SIN_REP_TYPE	Single		TG(mg/dl)	83
	SEX_TYPE	Male		PL(mg/dl)	172
	STRAIN_TYPE	Crj:CD(SD)IGS		TBIL(mg/dl)	0.29
	ADM_ROUTE_TYPE	Gavage		DBIL(mg/dl)	0.04
	ANIMAL_AGE(week)	6		GLC(mg/dl)	196
	SACRI_PERIOD	3 h		BUN(mg/dl)	17
	DOSE	0		CRE(mg/dl)	0.3
	DOSE_UNIT	mg/kg		Na(meq/l)	141
	DOSE_LEVEL	Control		K(meq/l)	6.7
Physiologcial data of individual animals	TERMINAL_BW(g)	209.5		Cl(meq/l)	102
	LIVER(g)	10.548		Ca(mg/dl)	10.9
	KIDNEY_TOTAL(g)	1.886		IP(mg/dl)	12.1
	KIDNEY_R(g)	0.94		TP(g/dl)	5.6
	KIDNEY_L(g)	0.946		RALB(g/dl)	3.6
Hematology data of individual animals	RBC(x10_4/μl)	581		A/G	1.8
	Hb(g/dl)	12.6		AST(IU/l)	83
	Ht(%)	38.2		ALT(IU/l)	50
	MCV(fl)	65.7		LDH(IU/l)	128
	MCH(pg)	21.6		GTP(IU/l)	2
	MCHC(%)	32.9	Cell viability data for in vitro experiments	DNA(%)	NA
	Ret(%)	7.6		LDH(%)	NA

Abbreviations for hematology and biochemical items. RBC:red blood cell count, Hb:hemoglobin, Ht:hematocrit value, MCV:mean corpuscular volume, MCH:mean corpuscular hemoglobin, MCHC:mean corpuscular hemoglobin concentration, Ret:reticulocyte, Plat:platelet count, WBC:white blood cell count, Neu:neutrophil, Eos:eosinophil, Bas:basophil, Mono:monocyte, Lym:lymphocyte, PT:prothrombin time, APTT:activated partial thromboplastin time, Fbg:fibrinogen, ALP:alkaline phosphatase, TC:total cholesterol, TG:triglyceride, PL:phospholipid, TBIL:total bilirubin, DBIL:direct bilirubin, GLC:glucose, BUN:blood urea nitrogen, CRE:creatinine, Na:sodium, K:potassium, Cl:chlorine, Ca:calcium, IP:inorganic phosphorus, TP:total protein, RALB:albumin, A/G:albumin globulin ratio, AST:aspartate aminotransferase, ALT:alanine aminotransferase, LDH:lactate dehydrogenase, GTP:γ-glutamyltranspeptidase.

Sciences (https://ntp.niehs.nih.gov/drugmatrix/index.html). Other toxicogenomic and related databases are also available, including Chemical Effects in Biological Systems (12) and the Comparative Toxicogenomics database (13).

The Open TG-GATEs was developed in an effort to be a 'gate' to a new frontier beyond toxicogenomics and other fields. Therefore, the gene expression data is stored in the CEL format in order to allow users to select suitable methods (14–16) to covert CEL files to numerical data. At the same time, this file type may render the data difficult to analyze for users unfamiliar with Affymetrix data analysis. To address this challenge, Nystrom *et al.* have made the data available as a second-party web service called Toxygates (17). The Toxygates site is administered independently from Open TG-GATEs and offers data analysis functionality using preprocessed data obtained from Open TG-GATEs (Figure 2).

To date, one of the major barriers in computational toxicology has been the limited number of public toxicity datasets upon which computational models could be built (18). After the Open TG-GATEs and DrugMatrix data were made available to public, the challenge has become focused on data mining. In addition to data mining, validation will be required at some stage. There are two ways to validate analyses, results or models using Open TG-GATEs data. One way is to (re)-produce the gene expression data using the same experimental conditions and procedures described in this paper. Another way is to use the Drug-