

The DuPont Company, Haskell Laboratory for Toxicology and Industrial Medicine, Newark, Delaware, USA

- All models were constructed using Advanced Continuous Simulation Language (ACSL).
- The primary models were tested against available laboratory and worker exposure data for acceptability.
- The initial model was a non-physiological, 2-compartment model (Figure 2).
- The lung and dermal compartments are included to accommodate potential exposure via these routes, but the primary focus of the work is on the oral route of exposure.
- While the liver is not a site of PFOA metabolism, it is described as a separate model compartment since it is a reported toxicity target in some animal species and may represent a source of significant protein binding.
- Physiological and chemical specific data input into the model are shown in Table 1.
- Sixty data compared against model simulations in Figures 4 and 5 were obtained from the literature.

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graph TD
    A[Noncompartmental Analysis] -- Data --> B[2-compartment Model]
    B -- Data --> C[PBPK Model]
    C --> D[Compare to Data]
    D --> E{Sufficient?}
    E -- Y --> End(( ))
    E -- N --> F{Data Gaps?}
    F -- Y --> G[Experiment]
    G -- Data --> C
    F -- N --> C
  
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Parameter	Variable	R ²	Human
Body Weight	BW (kg)	450	70
Body Surface	BSA (m ²)	1.8	1.73
Cardiac Output	CO (L/hr)	6.6	310
Blood Flow (mL per cardiac output)			
Skin	QDC	5.8	5.8
Brain	QDC	7	7
Spleen Perfused	QDC	2.8	2.8
Liver Perfused	QDC	52	52
Kidney	QDC	18.1	17.5
Uterus	QDC	14.3	27.7
Tissue Volumes (mL body weight)			
Brain	VDC	3.4	19
Fat	VDC	30	7
Spleen Perfused	VDC	4.7	5.7
Liver	VDC	5	6
Kidney	VDC	0.4	0.7
Uterus	VDC	2.5	3.4
Radical Coefficients			
Blood → A	PB	10	10
Skin → Blood	PD	10	10
Brain → Blood	PD	10	10
Spleen → Blood	PD	10	10
Uterus → Blood	PD	10	10
Rapid → Blood	PD	10	10
Kidney → Blood	PD	10	10
Liver → Blood	PL	10	10
Metabolic Constants			
Metabolic Rate	VMA (μmol/L)	0	0
Mechanics Constant	KM (μmol/L)	0	0
Protein Binding Constants			
Brain Binding Rate	VMA ₁ (μmol/L)	0	0
Uterus Binding Rate	VMA ₂ (μmol/L)	0.1	0.1

Body lumped into single storage compartment

The diagram illustrates a compartmental model of the human body. It consists of several interconnected compartments represented by boxes. The compartments are arranged vertically from top to bottom: Alveolar Space, Lung Blood, Dermal Input, Fat Tissue Group, Slowly Perfused Tissue Group, Rapidly Perfused Tissue Group, Kidney, Liver, and Oral Input. Arrows indicate the flow of substances between these compartments, with labels indicating the type of flow or compartment. For example, CP (Capillary Pressure) flows from Alveolar Space to Lung Blood, and CC (Capillary Concentration) flows from Lung Blood to Alveolar Space. Other flows include CV (Capillary Volume) from Lung Blood to Dermal Input, CVD (Capillary Volume Distribution) from Dermal Input to Fat Tissue Group, CFS (Capillary Flow) from Fat Tissue Group to Slowly Perfused Tissue Group, CYS (Capillary Flow) from Slowly Perfused Tissue Group to Rapidly Perfused Tissue Group, CK (Capillary Flow) from Rapidly Perfused Tissue Group to Kidney, and CL (Capillary Flow) from Kidney to Liver. The Oral Input compartment is at the bottom, with an arrow pointing up to the Liver compartment.

Time (hours)	ugm in blood, female rat
10	30
10	20
10	15
10	12
20	0.8
20	0.7
160	0.02
160	0.01

Figure 1 is a semi-logarithmic plot showing the decline of *p,p'*-DDE concentration in female rats over time. The y-axis is labeled "ppm in blood, female rat" and ranges from 0.01 to 100 on a logarithmic scale. The x-axis is labeled "Time (hrs)" and ranges from 0 to 180 on a linear scale. The data points, represented by open circles, show a rapid initial decline from approximately 10 ppm at 0 hours to about 1 ppm at 24 hours, followed by a slower, more linear decline on the log scale, reaching approximately 0.2 ppm at 180 hours. A solid line represents the fitted exponential decay model.

Time (hrs)	ppm in blood, female rat
0	10
2	10
4	10
6	10
8	10
10	10
12	10
14	10
16	10
18	10
20	10
24	1
28	1
32	1
36	1
40	1
44	1
48	1
52	1
56	1
60	1
64	1
68	1
72	1
76	1
80	1
84	1
88	1
92	1
96	1
100	1
104	1
108	1
112	1
116	1
120	1
124	1
128	1
132	1
136	1
140	1
144	1
148	1
152	1
156	1
160	1
164	1
168	1
172	1
176	1
180	1

- The two-compartment model simulates the general trends in the rat data. It is not satisfactory, however, for predictive uses.
- The preliminary PBPK model performs better than the two-compartment model, but includes many estimated or "fit" parameter values. One function of this investigation was to identify the data gaps in the existing literature. Table 2 lists the relevant areas and their relative importance to the modeling effort.
- The human data in the literature at this time are not complete enough for modeling purposes. Most of the human data are taken from monitoring of production workers and thereby lacks any exposure information. In addition, there is no associated "event" on which to base a time-dependent estimate of human blood concentrations of PFOA are generally below 35 ppb.

While protein binding has been noted in the literature, there is no information available to quantify the binding parameters. A binding term is included in the preliminary PBPK model but the values used have no physical significance at this point.

[illegible]

- Determine key tissues from mass balance data and literature.
- Identify target proteins in key tissues.
- Determine branched chain effects.
- Check for the presence of non-protein (e. g. lipid) interactions.

Quantitation of Model Parameters

- Calculate stability, stoichiometry and kinetic parameters of PFOA interaction with applicable proteins and biomolecules.
- Determine differences in binding of proteins with linear and branched PFOA

- Classical compartmental modeling was not sufficient to describe PFOA kinetics in mammalian systems.
- A preliminary rat PBPK model was developed.
- Data gaps were identified and a pathway for further model development presented.

Future Directions

- Conduct Mass Balance, Adsorption, Distribution and Elimination studies in male and female rats.
- Characterize the rate, extent and type of PFOA binding in rats and human systems.
- Develop model descriptions for the human.
- Include quantitative protein binding terms into rat and human PBPK models.
- Use model to simulate the plasma kinetics, uptake, distribution and elimination of PFOA in humans.