Annex 8.2 Human Tissues (WEOG3 report)

Quality assurance and quality control QA/QC and data treatment

During the work to assemble data on POPs in human tissue, a data treatment procedure has been conducted to harmonize data. This was achieved by setting up a process of quality assurance and quality control (QA/QC) practices. The overall aim of these processes was to get a common standard for the data to ensure comparability within and between data sources. Differences between data sources in their respective standards (i.e. units and systematics of compound names) had to be accounted and corrected for. Changes in detection and quantification limits over time and differences between labs preclude the robustness of trends, especially in the case where large proportion of samples being reported below detection limit (DL) or quantification limit (QL).

All data collected were. assembled in a primary dataset that contained all raw data from each data source. Separate primary datasets were created for breast milk and human blood data using variables presented in Table 5.2.2 (human milk) and Table 5.2.3 (human blood). After a series of data treatment steps and selection of data (substances and population cohorts) to improve comparability of data, final datasets for breastmilk and human blood were produced. These final datasets were then used for analysis of trends and patterns of POPs in human tissue.

Unit standardization

Units used in different data sets were standardised by adjusting concentration values so that, as far possible, each group of substance has the same unit to ensure comparability between data sources. For breast milk samples, ng/g lipid weight (ng/g lw) were used for most of the substances except for PFASs where ng/mL was used. For blood samples, concentrations expressed both on lipid-weight as well as wet-weight basis were used and are presented separately. In cases where concentrations were expressed based on fresh weight volume (*e.g.* ng/mL) concentrations were calculated to fresh weight (*e.g.* ng/g) using a standard density of 1.025 g/ml (Sniegoski and Moody 1979 and https://www.aqua-calc.com/page/density-table/substance/blood-blank-plasma). This calculation was done for all cases except for PFASs that were based on fresh weight volume (ng/mL).

Detection limit / Quantification limit

In the case where concentration values were accompanied by detection limits (DL) or quantification limits (QL), they were added to the dataset. If concentration values were reported as below ("<") the DL or QL (defined by data source), they were calculated as half the reported concentration value (i.e. half the DL or QL) for the inclusion into the final dataset as median values. If no information was provided whether the "<" concentration was based on either DL or QL, the data were treated as below DL. If only DL or QL was reported, the final dataset was updated with QL according to equation1 and DL according to equation 2, respectively.

QL=DL*3.3 Equation 1.

DL=QL/3.3 Equation 2.

TEQ

For dioxins/furans and dl-PCB in breast milk, units were accompanied by a toxicity equivalence (TEQ) variable. Different TEQs were used in the data and were part either of the unit name or in accompanied metadata. Concentrations of dioxins/furans and dl-PCB with units that did not contain any information on TEQ were handled separately from other data. No calculations of TEQ concentrations or summary or individual concentrations and dioxins/furans and dl-PCB were done.

Continental classification

Countries were grouped in continents (Europe (Austria, Belgium, Denmark, Faraoe Islands, Finland, France, Germany, Greece, Greenland, Iceland, Ireland, Israel, Italy, Luxembourg, Netherlands, Norway, Spain, Sweden, Switzerland and Turkey), Australasia (Australia and New Zeeland) and North America (USA and Canada)) based on the country origin of each observation in the dataset.

Data information and sample information

The variable gives information if the concentration value represents an individual measurement of a sample or aggregated data (mean, median, min/max, percentiles). Aggregated data corresponds to individual data observations that have been treated and replaced by group observations in the summary statistics. The variable “Sample information” gives information if the sample concentration value is derived from analytical results from a pooled sample or from samples taken from an individual mother.

Matrix

Matrix gave information about the specimen analysed for each reported concentration. For breast milk, only breast milk was used but in the case for human blood information on plasma, serum or blood were indicated. In the summary and analysis of blood data trends and patterns, data on plasma and serum were evaluated together.

Primapara and age

When available in the data sources, the proportion of primapara as well as age of mothers have also been included. The effect from these factors on the concentration of POPs in breast milk have been well established where primapara mothers have relatively higher concentrations of POPs and that mothers accumulate POPs with age. Primapara is given as a percentage between 0 (no primapara in sample) or 100 (all primapara in sample). The proportion primapara could also

be given a value between 0 and 100 if there were information available on the proportion of primapara in the sample.

The age of the mother was also included for each observation if this was available in the data source, either as the age of an individual mother or as a mean age for aggregated data or for a pooled sample.

Gender and cohort information

Variation in blood POPs concentration is also affected by gender as well as lifestyle, feeding habits and socio-cultural factors. In several data sources the sampling design have been stratified based on age groups, regions, or specific population cohorts. In cases where information about gender or cohort groups were added in the data sources this was added to the dataset. In case the information about gender or cohort information had an impact on the trend analysis, this was noted in tables or figures.

Quantity

For aggregated data, the number of observations was used in the statistical measure reported as the "quantity" in blood dataset. Data sources that contained non-aggregated data (i.e. individual data of individual or pooled samples) in the primary dataset were calculated as medians for each year and substance in the data harmonization to the final dataset (partly even aggregated for different chosen age groups, see Final blood dataset). In this case, "quantity" represents the number of observations used to calculate each median concentration.

Detection / Number BDL and BQL

The "detection" parameter were included for some data and describe the relative proportion of observations below detection limit (BDL) or below quantification limit (BQL) in concentrations reported as central tendencies (i.e. if 100 samples were used in central tendency and 10 samples were measured BDL the "detection" were 10%). In cases where central tendencies were calculated from non-aggregated data, the number of observations reported as below detection limit (BDL) or below quantification limit (BQL) in the populations was summed up as the "number BDL" or "number BQL". From these values, the "detection" parameter was calculated as a proportion relative to the number "quantity" in the final dataset. The variable "detection" indicates the relative number of samples that were reported as BDL or BQL.

Summary statistics in results table

In the summary statistics for substances in this report central tendencies (average and median), standard deviation (SD), min and max were reported per continent and if possible, also on national level based on the concentration values in the final dataset for breast milk or human blood. The number of observations (n) used in the final dataset for the summary statistics of each

substance and geographic region was indicated in tables. In those cases, where information was available for the number of observations that were BDL or BQL in the final dataset this was indicated also in the summary statistics table.