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Suggestions for the Preliminary Definition of a Current Background Profile of Polychlorodibenzodioxin (PCDDs) and Polychlorodibenzofuran (PCDFs) Congeners in Serum Samples

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Introduction

The congener specific polychlorodibenzodioxins (PCDDs) and polychlorodibenzofurans (PCDFs) distribution in human body is a function of bioavailability processes needed to cross the biological membranes. The blood is the destination of major distribution of chemicals into the body. This matrix appears the most important to interpret the concentration levels determined in terms of toxicity or to link them to the interpretation of temporal and spatial trends.

Theoretical and Experimental

The distribution of PCDD and PCDF congeners in human serum samples may vary according to the source(s) of exposure encountered by the subjects, but food is the main source and the variable levels of these contaminants in human tissues reflect the differing levels of contamination in different foods. In breast milk samples, the congeners from possible different dietary patterns appear to correspond to the widespread combustion profile [1]. However, the precise extent of the aforesaid variation is not known but would be extremely useful when assessing background contamination profiles. These in turn could help in monitoring the efficacy of measures aimed at reducing environmental levels of PCDDs and PCDFs, such as those established in the Stockholm Convention on Persistent Organic Pollutants [2]. There are 17 PCDD and PCDF congeners of toxicological relevance usually determined in human tissues and they exert their toxicity via a common mechanism of action [3]. Their presence in all environmental and human matrices is determined by high resolution gas chromatography coupled with high resolution mass spectrometry (HRGC-HRMS). The database we used comprises a sub-selection of subjects enrolled in a number of bio-monitoring research projects completed in different Regions of Italy over the last three years. This preliminary sub-selection was based only on an evaluation of the possible sources of exposure and did not consider the age of subjects as a weighting factor; this will be included in future reports on these researches in this area. All the samples were collected from hypothetical background areas. One hundred matrices (each being a pool of ten subjects) were analyzed. This preliminary investigation was performed using Principal Component Analysis [4].

Results and Discussion

Table 1 shows the Principal Component (PC) loadings with their variability estimates. The dataset is described by just two Principal Components, suggesting that the potential sources of exposure do not influence greatly the separation of samples. In Table 1, only one component takes into account the major variance quote (66.7%) which confirms that the prevalent congeners mark this variance quote of the dataset. Therefore, these congeners can be supposed to constitute a background profile. Except the OctaCDD and 1,2,3,4,6,7,8-HeptaCDF, all of them have loadings higher than 0.3.

The loading value of OctaCDD is border-line, but this congener is usually determined in all tissues. This value could depend on steric hindrance associated with molecule size [4]. To our knowledge, the half-life of this congener has not been experimentally determined although it has been calculated using models. Much shorter half-lives than usual have been reported for several PCDDs and PCDFs, including OctaCDD in breast-fed infants, but the data were calculated by models [5]. The congeners with the highest scores (Table 1) of the first PC appear to derive from general combustion source(s) [7], such as indicated previously. These congeners include 1,2,3,7,8-PeCDD, 1,2,3,4,7,8-HxCDD, 1,2,3,6,7,8-HxCDD, 1,2,3,4,6,7,8-HpCDD, 2,3,4,7,8-PeCDF, 1,2,3,4,7,8-HxCDF and 1,2,3,6,7,8-HxCDF. PC2, however, is dominated by 1,2,3,4,6,7,8-HeptaCDF, which appears to constitute an industrial fingerprint, suggesting that the database contains samples with a specific contamination source: these samples account for a quotient of variance of 11.1%. To define a background profile, the variability of the database should be reduced because the subjects should be not exposed to certain sources such as specific foods with a high lipid content and/or oily fish. Lifestyle variations, such as the use of pharmaceuticals [8], can affect the bioavailability of such compounds and therefore influence the determination of a background

	PC1	PC2
eigenvalues	6.7	1.1
percent of variance (%)	66.7	11.1
cumulative percentage (%)	66.7	78.02
Log[pg1,2,3,7,8-PeCDD/g lb]	0.316	-0.150
Log[pg 1,2,3,4,7,8-HxCDD) /g lb]	0.327	-0.245
Log[pg 1,2,3,6,7,8-HxCDD/g lb]	0.350	-0.236
Log[pg 1,2,3,7,8,9-HxCDD/g lb]	0.310	-0.178
Log[pg 1,2,3,4,6,7,8-HpCDD/g lb]	0.333	0.153
Log[pg OCDD/g lb]	0.297	0.009
Log[pg 2,3,4,7,8-PeCDF) /g lb]	0.349	-0.073
Log[pg 1,2,3,4,7,8-HxCDF) /g lb]	0.333	0.223
Log[pg 1,2,3,6,7,8-HxCDF) /g lb]	0.358	0.167
Log[pg 1,2,3,4,6,7,8-HpCDF) /g lb]	0.121	0.850

Table 1: Principal Component (PC1 and PC2) loadings with variance quote estimations.

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profile. However, the samples in Figure 1 (sample scores) are clustered around the centre of the graph, indicating low variability among the samples. This method could be improved by including a further selection of data covering all the factors potentially involved, including latent, exogenous and endogenous variables.

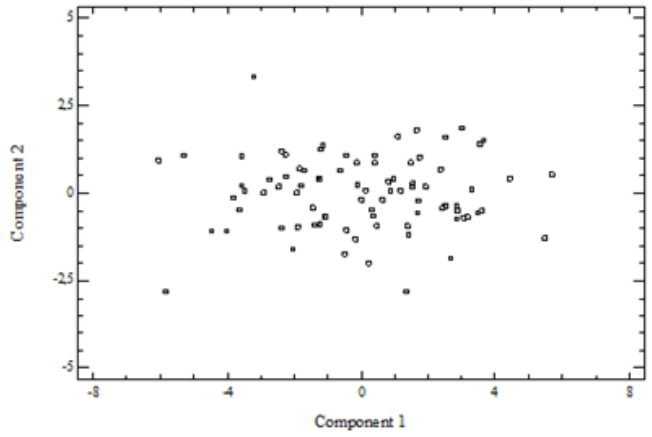

Figure 1: Scatterplot of sample scores.

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