Description for the general public

The industrial activity of humans results in producing and releasing into the environment numerous toxic substances including dioxins. Dioxins are by-products of herbicide and fungicide industry, chlorine and paper industry as well as color metal production and recycling. Municipal waste incineration, car traffic and cigarette smoking are also a significant source of dioxins. As a result they are present in air, soil, water as well as in plant and animal cells. 2,3,7,8-tetrachlorodibenzo-p-dioxin (TCDD) is the most potent dioxin. Most of the exposure of the general population to 2,3,7,8-TCDD is from food**.** Due to its lipophilic character, TCDD has the ability to bio-accumulate in fat tissue. It was found that TCDD action results in broad spectrum of pathologies including disturbances of immune, neural, and endocrine functions. In the reproductive system, TCDD affects spermatogenesis, steroidogenesis, growth of ovarian follicles and ovulation as well as implantation and embryo development. It is also the cause of endometriosis, miscarriages, and diminished fertility. TCDD affects the ability of granulosa cells to produce steroids, but the results are inconsistent. The extreme chemical and biological stability of dioxins as well as lack of effective detoxication mechanisms in animals, result in a long half-life in both the environment (25-100 years) and living organisms (7-10 years in humans). Among the examined animal species there are tremendously large differences in sensitivity to TCDD. TCDD lethal dose 50% (LD_{50}; causing death of 50% of the treated animals), varies from 0.6 μg/kg body weight in the guinea pig to 5000 μg/kg in the hamster. The hamster is the most resistant among all examined animal species whereas TCDD sensitivity of the pig has not been examined due to ecological and economic issues. In the present project, we intend to find differences in the mechanisms responsible for TCDD-induced toxicity between the hamster and the pig. Specifically, we plan to identify genes, expression of which will be changed in hamster granulosa cells (CHO line) treated with TCDD, and then to compare the gene expression profile of TCDD-treated CHO cells with that of porcine granulosa cells (AVG-16 line). To meet this goal, high-throughput, next generation sequencing technology will be used to reveal the transcriptomes of porcine and hamster granulosa cells, both treated or untreated (control) with TCDD. Previous studies reported TCDD-induced changes with regard to a limited number of genes. The obtained results will help in better understanding: 1/ molecular mechanisms of TCDD mechanism of action and TCDD metabolism in two different mammalian species and 2/ the molecular mechanisms underlying different susceptibility to TCDD of the examined species.