indicated relatively high toxicity. The lethal concentration LC50 which was received for *A. salina* was 55.4% and the inhibition concentration IC50 which was received for *L. sativa* was 25.8%. Above results indicated the importance of toxicological estimation after enzymatic treatment. The enzymatic treatment was 22.5%. Above results showed the importance of toxicological estimation after enzymatic treatment. The results showed that lignin peroxidase was very expeditious for removal of pentachlorophenol, and the products which were obtained after enzymatic removal indicated relatively high toxicity. The lethal concentration LC50 which was obtained for *Artemia salina* was 50.6% and the inhibition concentration IC50 which was obtained for *Lactuca sativa* was 22.5%. Above results showed the importance of toxicological reckon after enzymatic treatment. The enzymatic treatment was united with photocatalytic treatment for further degradation and toxicity reduction of active textile dyes.

http://dx.doi.org/10.1016/j.copbio.2013.05.159

**The removal of pentachlorophenol with lignin peroxidase as biocatalyst and further removal of pentachlorophenol with Ga2FeSbO7 as photocatalyst**

Jingfei Luan 1, Yanyan Li 1, Zhigang Zou 2

1 State Key Laboratory of Pollution Control and Resource Reuse, School of the Environment, Nanjing University, China
2 Eco-Materials and Renewable Energy Research Center, Nanjing University, China

*E-mail address:* yanyanlyyanyani@sina.com (Y. Li)

This research first indicated the preliminary removal results of pentachlorophenol with lignin peroxidase as biocatalyst. We studied the effect of enzyme load (3.5–130.5 U mL−1), pentachlorophenol concentration (4.5–75.5 mg L−1), reaction time (0–25 min), pH value (1–13), and hydrogen peroxide concentration (15–850 μmol L−1). The results showed that the maximal removal percentage of pentachlorophenol was 83.5% after 12 min of reaction time and the maximal experimental parameters were received as following: hydrogen peroxide 102.4 μmol L−1, enzyme 78.2 U mL−1, pH value 4.5 and pentachlorophenol concentration 46.5 mg L−1. *Lactuca sativa* and *Artemia salina* were used to evaluate the toxicity of the products which formed after enzymatic treatment. The results showed that lignin peroxidase was very expeditious for removal of pentachlorophenol, and the products which were obtained after enzymatic removal indicated relatively high toxicity. The lethal concentration LC50 which was obtained for *Artemia salina* was 50.6% and the inhibition concentration IC50 which was obtained for *Lactuca sativa* was 22.5%. Above results showed the importance of toxicological reckon after enzymatic treatment. The enzymatic treatment was united with photocatalytic treatment for further degradation of pentachlorophenol. Ga2FeSbO7 which crystallized with the pyroclore-type structure, cubic crystal system and space group Fd3m was synthesized by solid state reaction method for the first time. Complete photocatalytic degradation of pentachlorophenol over Ga2FeSbO7 was carried out under visible light irradiation for 20 min. The photocatalytic degradation of pentachlorophenol followed the first-order reaction kinetics. The possible degradation pathway of pentachlorophenol was provided.

http://dx.doi.org/10.1016/j.copbio.2013.05.161

**Modeling of the chemical phase of radiobiological mechanism**

Jiri Barilla 1, Milos Lokajicek 2, Hana Pisačková 2, Pavel Simr 1

1 J.E. Purkinje University in Usti nad Labem, Faculty of Science, Czech Republic
2 Institute of Physics, Academy of Sciences of the Czech Republic

*E-mail address:* Jiri.Barilla@ujep.cz (J. Barilla)

The chemical phase of radiobiological mechanism may play important role in the radiobiological effect of ionizing radiation when the water radicals formed by the densely ionizing ends of secondary charged electrons are mainly responsible for the damage of DNA molecules in living cells. In such a case individual DSBs are formed practically by individual radical clusters generated in the neighborhood of corresponding DNA molecules. We have proposed already earlier mathematical model allowing to study also the influence of different species (radiomodifiers) being present in water medium during irradiation. Now the model has been significantly improved by us when the Petri nets have been made use of. Two parallel processes running in individual clusters before a cluster meets a molecule have been taken into account: corresponding chemical reactions running in a cluster and radical cluster diffusion. The concurrent influence of both the processes may be studied to greater details, which might be helpful in studying all processes influencing final radiobiological effect in individual DNA molecules, and eventually also in cells.

http://dx.doi.org/10.1016/j.copbio.2013.05.162

**Interactions between intronic microRNAs and mRNAs of host genes involved in breast cancer**

Olga Berillo, Anatoliy Ivashchenko

National Nanotechnology Laboratory, al-Farabi Kazakh National University, Almaty, Kazakhstan

*E-mail address:* devolia18@mail.ru (O. Berillo).

MicroRNAs (miRNAs) are short noncoding RNA sequences that suppress translation. Intronic miRNAs coded by host genes. Studying the interactions between miRNAs and mRNAs of these genes will promote the development of novel diagnostic methods. MiRNA sequences were downloaded from the miRBase. RNA hybrid and E-RNA hybrid programs were used to select reliable miRNA binding sites with significance defined at p < 0.0003. The binding sites of 915 intronic miRNAs were studied within the 5’UTRs, CDSs, and 3’UTRs of 193 human host genes, whose encoded proteins were key participants in the progression of breast cancer. Only 11 from these genes were found to be targets for intronic miRNAs (miR-5096, miR-1268b, miR-3129-5p, miR-4308, miR-4447, miR-4534, miR-1273a, miR-1976, miR-1273g-3p, miR-566, and miR-5585-3p) according to our selection criteria. Eleven target genes encoded other intronic miRNAs (miRNAs are indicated in brackets): ARFGAP1 (miR-4326), BCAS1 (miR-4756-3p, miR-4756-5p), CAMK1D (miR-4480, miR-4481, miR-548q), FOXP4 (miR-4641), HUWE1 (let-7f-2-3p, miR-98-3p, miR-98-5p, let-7f-5p), LPP (miR-28-3p, miR-28-5p), NAV1 (miR-1231, miR-5191), SCD5 (miR-575), SKA2 (miR-301a-3p, miR-301a-5p, miR-454-3p, miR-454-5p), TLE3 (miR-629-3p, miR-629-5p), and TMPRSS3 (miR-6508-5p, miR-6508-3p, miR-3197, miR-4760-3p, miR-4760-5p). Disruption of the expression of these genes led to changes in the expression of corresponding miRNAs, which then inhibited the translation of other target mRNAs. The expression of different genes depended on intronic miRNAs, and the features of their interactions with mRNAs were important for the development of novel diagnostic methods.