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Processing of experimental data for the separation of chromatographic signals of tetracycline group antibiotics by mathematical modeling

© **Aisylu Z. Mukharlyamova**,*+ **Aleksandr M. Saifutdinov**, **Elvira R. Rakhmetova**, **Aygul G. Mukhammetshina, Aynaz Z. Gaynullin, Alena Yu. Likhacheva**, and **Igor M. Fitsev**
Federal Center for Toxicological, Radiation and Biological Safety (FSBSI «FCTRBS-RRVI»). Nauchny Gorodok-2. Kazan, 420075. Republic of Tatarstan. Russia. E-mail: fitzev@mail.ru

*Supervising author; +Corresponding author
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Abstract

Antibiotics belonging to the classes of sulfonamides, amphenicols and tetracyclines, such as tetracycline, oxytetracycline and chlortetracycline, are used to control infectious diseases of honeybees. In addition, tetracycline group antibiotics can be added directly to plants during flowering. Contamination of the flower with high concentrations of antibiotics entails the risk of transferring antibiotic residues to honey. Consequently, these antibiotics persist as contaminants in honey, and the determination of these drugs in honey samples is of great importance.

Tetracyclines have a broad spectrum of activity against gram-positive and gram-negative bacteria. The basic structure of tetracyclines consists of a hydro-naphthacene framework containing four rings. Due to their possible toxic or allergic reactions and the possibility that pathogens may become resistant to these drugs, much attention has recently been paid to tetracyclines.

For the detection of residual quantities of antibiotics in food products increasingly requires reliable analytical methods. The main method for determining tetracycline group antibiotics is the method of high-performance liquid chromatography, but the micro-quantities of their residual concentration and unsatisfactory chromatographic conditions, under which peaks may overlap, as well as insufficient sample preparation conditions, under which matrix components may overlap, make quantitative calculations difficult when using this method.

This article describes a method for calculating the initial value of intesiveness and peak width using mathematical modeling. Based on the analysis of real chromatographic data, the applicability of this method for the quantitative determination of tetracycline group antibiotics is shown.

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