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STRUCTURE OF ERRORS IN CONDUCTING FORENSIC MOLECULAR-GENETIC EXPERTISE

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Summary. Identification expertise is one of the most complex types of expertise and, according to global standards such as DVI-Interpol, involves several parallel types of investigation aimed at confirming the result. Forensic molecular genetic testing is considered the «gold standard» of identification studies, as the high discriminatory power of this method allows results to be obtained with a high degree of certainty. However, due to errors at various stages of the expert's work, it can sometimes produce erroneous results that are inconsistent with other parallel investigative methods.

The aim of the study was to determine the frequency and causes of errors leading to erroneous results of molecular genetic forensic examination in the Ivano-Frankivsk Scientific Research Forensic Centre of the Ministry of Internal Affairs of Ukraine from 2019 to 2024.

Materials and methods. A retrospective study of 4595 conclusions of forensic molecular-genetic expertise from 2019 to 2024 at the Ivano-Frankivsk Scientific Research Forensic Center of the Ministry of Internal Affairs of Ukraine was conducted.

Results and discussion. When analysing the reasons for obtaining erroneous results, it was found that human error and contamination were the most frequent causes throughout the study period. Technical problems, sample mix-up and others were less frequent.

Conclusions. The indicators and error structure presented in this study are useful for improving the quality and control of the performance of forensic molecular genetic expert testimony, as well as contributing to the formation of an open research culture and helping to find ways to minimise errors. However, it is important to remember that they are not relevant in the context of a specific study. It is also worth considering the possibility of the presence of specific undisclosed errors in a particular case. It is also important to clearly indicate the possibility of DNA transfer, etc. Forensic statistical models, including Bayesian networks, can be useful to account for various uncertainties and to demonstrate their impact on the probative value of forensic molecular genetic expert testimony.

Keywords: Personal identification, DNA, objects of biological origin, biological information, forensic molecular genetic expert opinion.

Introduction. Identification expertise is one of the most complex types of expertise and, according to global standards such as DVI-Interpol, involves several parallel types of investigation to confirm the result. Molecular genetic forensic expertise is considered the «gold standard» of identification studies, as the high discriminatory power of this method allows results to be obtained with a high degree of certainty. However, due to errors at various stages of its execution, it sometimes produces erroneous results that are inconsistent with other parallel investigative methods. This is a significant problem both from an economic point of view, as each molecular genetic expert opinion is quite expensive and requires the use of expensive reagents as well as specially trained personnel, and from a legal point of view, as it leads to delays in court proceedings and the inability to make the right decision, which has another socially negative aspect – public distrust of the investigating authorities, the prosecution and the court [1, 2].

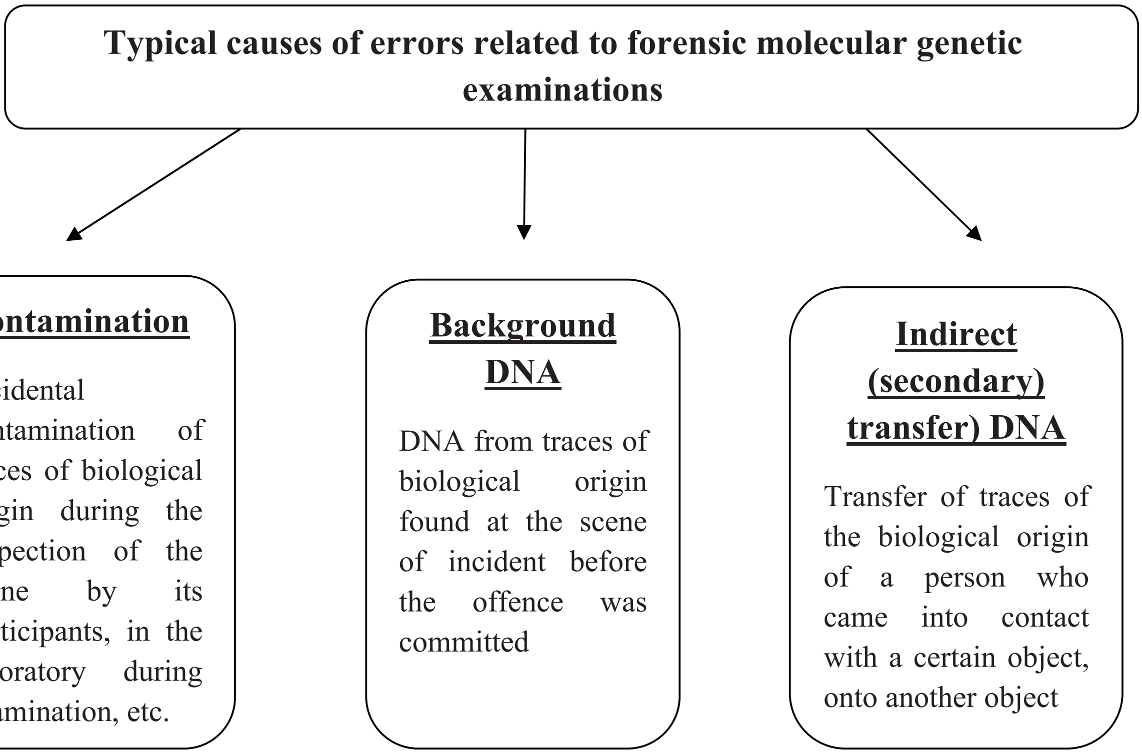
Among the errors leading to erroneous results in forensic molecular genetic testing, three main groups can be distinguished, namely

– at the pre-laboratory stage, related to violations of the rules for collection, transport and storage of biological material intended for forensic molecular genetic testing,

– at the laboratory stage, including technical errors and so-called «human errors»;

– at the post-laboratory stage, mainly related to the human factor, such as misinterpretation of research results [3].

The most typical causes of investigative, expert and judicial errors in DNA analysis are contamination (contamination of objects with the DNA of individuals who have worked with traces), the extraction of objects containing DNA that was left before the event under investigation and is not related to it (background DNA), and the detection at the scene of the crime of DNA that has accidentally arrived there by indirect transfer, when the DNA of a third party first arrives on a certain object (clothing, money, household items, etc.) and is then brought to the scene of the crime by other individuals (Fig. 1).



Typical causes of errors related to forensic molecular genetic examinations

Contamination

accidental contamination of traces of biological origin during the inspection of the scene by its participants, in the laboratory during examination, etc.

Background DNA

DNA from traces of biological origin found at the scene of incident before the offence was committed

Indirect (secondary) transfer) DNA

Transfer of traces of the biological origin of a person who came into contact with a certain object, onto another object

Fig. 1. Typical Causes of Errors Associated with Conducting Forensic Molecular-Genetic Expertise.

The experience of expert practice in recent years indicates the existence of certain problems in the organisation of proper expert support for criminal proceedings. The emergence of negative «chain reactions» is caused, first of all, by the improper collection of traces of biological origin during the examination of the crime scene, i.e. disregard of the rules of sterility, negligent handling of the preparation of materials, which, in turn, leads to contamination of traces of biological origin and sometimes prevents biological expertise. Therefore, during the examination of the scene of the incident, which includes the collection of objects of biological origin, it is necessary to comply with the requirements aimed at minimising the biological contamination of the objects and promptly sending them to laboratories [4-6]. This applies both to the personnel directly carrying out the examination of the scene of the incident and to other persons present in the area where the examination is being carried out [7-9]. Equally important are the efforts made by laboratory staff to eliminate errors at the laboratory and post-laboratory stages.

In view of the above, it is important to study and search for ways to solve the problems associated with the collection and preservation, examination of objects of biological origin and interpretation of the obtained results of molecular genetic research [10]. The specificity of biological trace information is that objects remain on objects of the material environment as a result of both contact and non-contact interaction. The introduction of biological material can occur during conversation, laughing, coughing, when objects are contaminated with cellular material, as a result of touching the face or other exposed areas of the body, or through contact with objects such as mobile phones, pens, glasses, etc. Such incidental generation of biological traces may result in contamination of items with biological material from individuals participating in investigative activities and loss of trace information due to improper handling of carrier objects.

The aim of the study was to determine the frequency and causes of errors leading to erroneous results of forensic molecular genetic examination in the Ivano-Frankivsk Scientific Research Forensic Centre (IFSRFC) of the Ministry of Internal Affairs of Ukraine in 2019-2024.

Materials and methods. A retrospective statistical study of 4568 conclusions of forensic molecular genetic expertise in the period 2019-2024 at the IFSRFC of the Ministry of Internal Affairs of Ukraine was conducted. The frequency of negative conclusions of forensic molecular-genetic examination due to various errors occurring at the stage of organisation and conduct of examination of the crime scene, collection, transport and storage of objects of biological origin was determined.

Results and discussion. It was found that in 2019-2024 at the IFSRFC of the Ministry of Internal Affairs of Ukraine 4568 forensic molecular-genetic expert opinions were submitted for execution, of which 4226 expert opinions were conducted, and the results of 662 of them were found to be erroneous (Fig. 2).

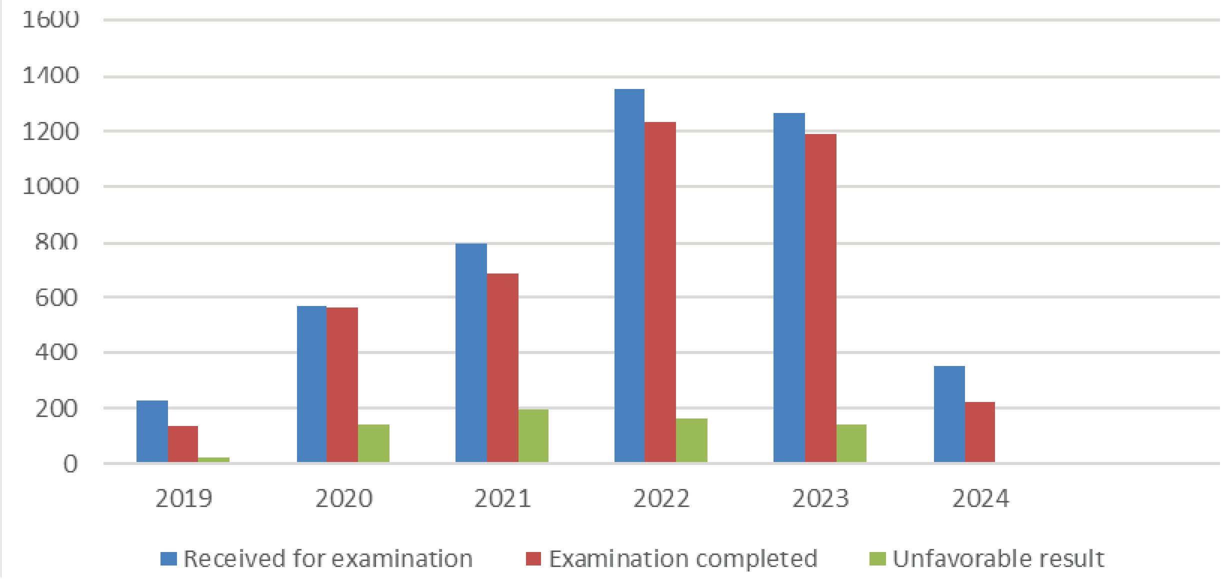


Fig. 2. Frequency of Erroneous Results of Forensic Molecular-Genetic Expertise at the IFSRFC from 2019 to 2024.

In 2019, 230 requests for expertise were received, of which 133 were completed. Negative results were obtained in 19 cases, of which 97 were not achievable due to errors at various stages of the expertise execution.

For the year 2020, 569 requests for expertise were received, of which 565 were completed. Negative results were obtained in 138 cases, of which 4 were not achievable due to errors at various stages of expertise execution.

In 2021, the Department of Biological Research and Records of the Ivano-Frankivsk SRFC received 799 requests for molecular genetic expertise. Of these, 687 were completed, and in 196 cases negative results were obtained, while in 112 cases erroneous results were obtained.

In 2022, 1349 requests for expertise were received, of which 1230 were completed. Of these, 165 expertise requests yielded negative results and 119 could not be completed due to errors encountered at various stages of the research.

It is known that in 2023, 1271 requests for expertise were submitted for examination, of which 1190 were completed, with negative results in 142 cases. In addition, 81 expertise requests could not obtain results due to errors encountered at various stages of the expertise execution.

In the first three months of 2024, 350 expertise requests were received, of which 221 were completed, with 2 negative results. In addition, in 129 cases no results could be obtained due to various errors (Fig. 3).

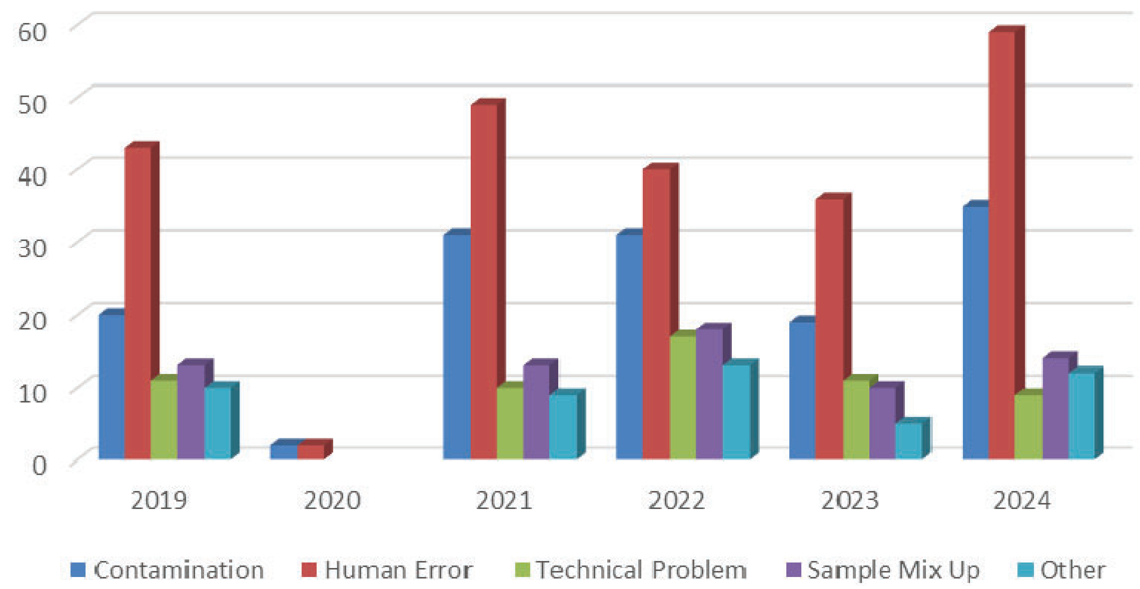


Fig. 3. Structure of Errors in Conducting Forensic Molecular-Genetic Expertise

When analysing the reasons for erroneous results, it was found that human error and contamination were the most common reasons throughout the study period. Technical problems, sample mix-up and others were less frequent.

In 2019, human error occurred in 43 cases and contamination in 20 cases. It is also known that in 2020, errors related to human error (2 cases) and contamination (2 cases) occurred with the same frequency. In 2021, human error occurred in 49 cases and contamination in 31 cases. In 2022, human error occurred in 40 cases and contamination in 31 cases. In 2023, 36 cases were due to human error and 19 to contamination. For the first three months of 2024, human error occurred in 59 cases and contamination in 35 cases (Fig. 3).

The indicators and structure of errors provided in this study are useful for improving the quality and control of forensic molecular genetic expertise, as well as for promoting an open research culture and contributing to the search for ways to minimise them. However, it is important to note that they may not be relevant in the context of a specific investigation. It is also worth considering the possibility of specific undetected errors in a particular case. Forensic statistical models, including Bayesian networks, can be useful in considering various uncertainties and demonstrating their impact on the probative value of forensic DNA analysis results.

Conclusion. The high discriminatory power of the molecular genetic research method allows to obtain unique results. This is particularly useful in forensic medical research, paternity testing and the comprehensive resolution of personal identification issues, in linking suspects to crime scenes or victims, in assisting law enforcement agencies in solving crimes and in bringing perpetrators to justice.. However, it is important to bear in mind the possibility of false results.

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СТРУКТУРА ПОМИЛОК ПІД ЧАС ПРОВЕДЕННЯ СУДОВОЇ МОЛЕКУЛЯРНО-ГЕНЕТИЧНОЇ ЕКСПЕРТИЗИ

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Резюме. Ідентифікаційна експертиза є одним із найскладніших видів експертиз і передбачає відповідно до світових стандартів (наприклад, DVI-Interpol) кілька паралельних видів розслідувань, спрямованих на підтвердження результату. Судову молекулярно-генетичну експертизу вважають «золотим стандартом» ідентифікаційних досліджень, оскільки висока дискримінаційна сила цього методу дозволяє отримувати результати з високим рівнем доказовості. Однак інколи через помилки на різних етапах проведення експертизи отримують її помилковий результат, який не збігається з іншими паралельними методами дослідження.

Метою дослідження було визначити частоту та причини помилок, що призводять до помилкових результатів судових молекулярно-генетичних експертиз з 2019 по 2024 роки в Івано-Франківському науково-дослідному експертно-криміналістичному центрі МВС України.

Матеріал та методи. Здійснено ретроспективне дослідження 4595 висновків судових молекулярно-генетичних експертиз, проведених з 2019 по 2024 роки в Івано-Франківському науково-дослідному експертно-криміналістичному центрі МВС України.

Результати та їх обговорення. Під час аналізу причин отримання помилкових результатів було встановлено, що за весь період дослідження найбільше зафіксовано людських помилок та забруднення. Рідше виникали технічні проблеми, сплутування зразків тощо.

Висновки. Наведені в дослідженні показники та структура помилок є корисними для підвищення якості та контролю за проведенням судової молекулярно-генетичної експертизи, а також сприяють формуванню культури відкритого дослідження та пошуку шляхів їх мінімізації. Однак важливо не забувати, що вони не мають значення в контексті конкретного дослідження. Також варто враховувати можливість наявності в конкретному випадку нерозкритих помилок. Важливо також чітко вказати можливість перенесення ДНК тощо. Судово-статистичні моделі, у тому числі байєсовські мережі, можуть бути корисними для врахування різноманітних невизначеностей та демонстрації їх впливу на доказову силу результатів судової молекулярно-генетичної експертизи.

Ключові слова: ідентифікація особи, ДНК, об’єкти біологічного походження, біологічна інформація, судова молекулярно-генетична експертиза.

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