ForumDNA, a custom-designed Laboratory Information Management System

C. Karlsson*, S. Holgersson

National Laboratory of Forensic Science, S-581 94 Linköping, Sweden

Abstract

ForumDNA is a Laboratory Information Management System (LIMS) developed to support DNA analyses. This is integrated with a case handling system. The systems are custom designed by Ida Infront in collaboration with the National Laboratory of Forensic Science in Sweden. The platform is called iiPax 2 and the database is an object database. The system has several advantages in comparison with manual handling, e.g. in terms of quality assurance, the simplicity by which case information is collected as well as time saving aspects.
© 2003 Elsevier Science B.V. All rights reserved.

Keywords: Laboratory Information Management System; LIMS; DNA analysis

ForumDNA is a Laboratory Information Management System (LIMS) developed to support DNA analyses. This is integrated with a case handling system. The systems are custom designed by Ida Infront in collaboration with the National Laboratory of Forensic Science in Sweden. The platform is called iiPax 2 and the database is an object database. The system has several advantages in comparison with manual handling, e.g.:

- Information is registered once.
- Transfer of information is accurate.
- Access to information is fast.
- Seeking and overview of information is flexible.
- Actions and changes in the system are registered in log files.
- Reports are created in Microsoft Word.
- Methods can be added and changed in a register.
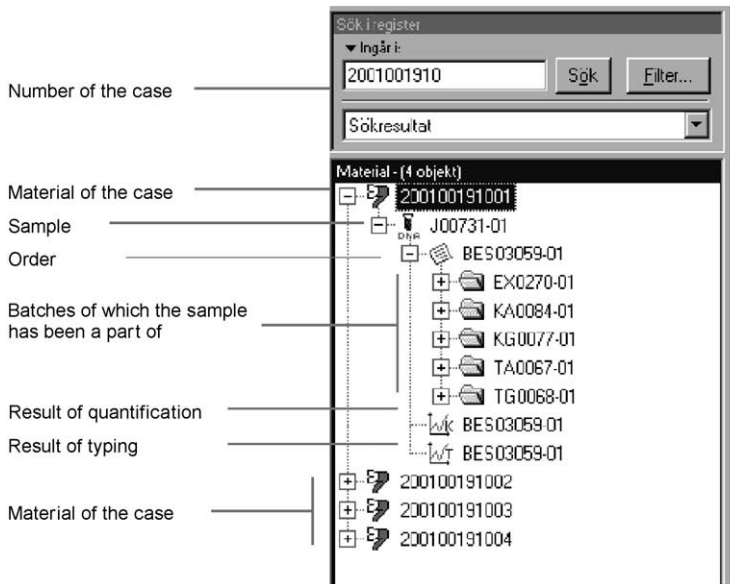
---

* Corresponding author.

Fig. 1. Display of the tree structure of some of the objects of a case in ForumDNA.
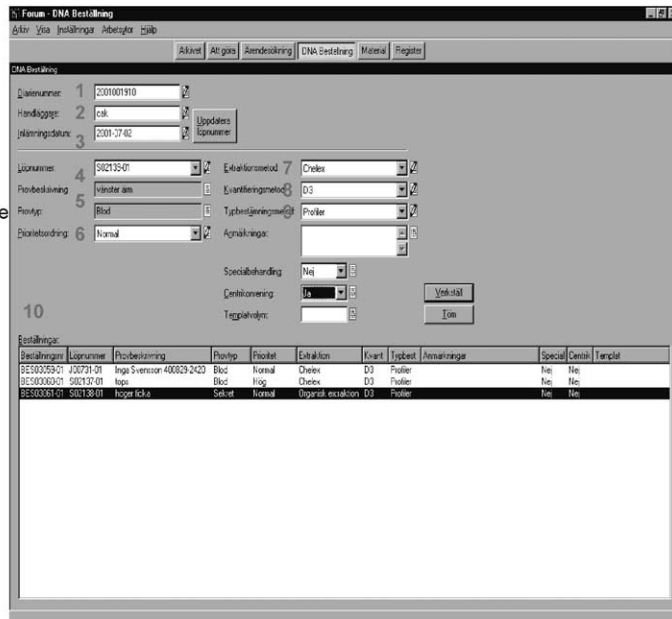

Fig. 2. An order of a DNA analysis. The order includes, e.g. the choice of methods of extraction, quantification and typing. During analysis, the order is the central object and it has a lifecycle determining how the sample is to be processed.

- Staff working with the DNA analyses has an excellent overview of the workload.
- Reporting officers have an excellent overview of all samples in a case.

Taken together, ForumDNA saves a lot of time and improves the quality of information.

New cases are registered electronically as well as all material, reference samples and questioned samples. These objects are created before the analysis. During the analysis, new objects are created, e.g. positive control, negative control, batch, quantification result and typing result. The objects in the database have references to each other and can be displayed in a tree structure, Fig. 1. When a DNA analysis is to be performed, another object, the order, is created in LIMS, Fig. 2. This order includes the choice of methods of extraction and typing and also the level of priority.

All information of each object can easily be searched for and seen in the system. During the DNA analysis, all samples to be analysed can be overviewed. The samples are sorted in the overview by different status of analysis and methods. One can also see, e.g. how many samples of each method there are and the oldest date of order. During analysis, the order is

Description of the material / Description of the sample / Number of the material	Number of the sample / Type of the sample / Number of order	Result (quant). / Conc. / In-hibition	Results of the typing in AmpFISTR Profiler										Date of decision / Status of analysis / Genotype or mixed DNA
			AM	D3	VW	FG	TH	TP	CS	D5	D13	D7	
- Blood-sample from Inga Svensson 400829-2420 200100191001	J00731-01 Blood BES03059-01	1,250 0	X	15 16	14 19	24 26	6 10	8 9	12	8 13	13	10	2001-07-02 Finalised Genotype
1 A swab swab 200100191002	S02137-01 Blood BES03060-01	0,250 0	X	15 16	14 19	24 26	6 10	8 9	12	8 13	13	10	2001-07-02 Finalised Genotype
2 A pair of jeans right pocket 200100191003	S02138-01 Saliva BES03061-01	0,750 25											2001-07-02 Waiting for typing
3 A T-shirt left sleeve 200100191004	S02139-01 Blood BES03062-01												2001-07-02 Waiting for quantification

Fig. 3. Summary of results includes, e.g. all samples, their orders, quantification and typing results. The status of analysis and the date the last step was performed are also shown.

the central object and it has a lifecycle determining how the sample is to be processed. When creating a batch, batches of samples with the same method are suggested by the system. If needed, the batch can be changed or rearranged manually. After each step in the analysis, a batch is reported and an individual decision can be made on each sample, e.g. repeat the amplification, make a new quantification and stop the analysis. Results of each sample are also registered when the batch is reported. If a fault has occurred, e.g. the wrong method of extraction was chosen in the system, there is a possibility to correct it. When a DNA analysis is finalised, an electronic message is sent to the reporting officer. A summary of all results in the case can then simply be created including all samples, their orders, quantification and typing results, as shown in Fig. 3. This summary also includes the status of analysis of each sample and a date when the last step was performed. With this information, an estimation of remaining time of analysis can easily be done. When all orders in the case have been finalised, a statement is written, all materials are included in the report automatically, and the case is closed.