

EDITORIAL

Introduction to the Special Issue on Forensic Genetics: Non-Human DNAAntonio Amorim^{1,2,*}

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Summary: A brief overview of the current state of the art of non-human DNA in forensics is provided, followed by a synopsis of the articles included in this special issue. Future perspectives are outlined, carrying convincing evidence for the expansion of the forensic use of non-human DNA.

Keywords: DNA, genetics, forensic, non-human.

OVERVIEW

Forensic Genetics is now recognized as an example to follow by the sister forensic disciplines [1]. The growth and success of Forensic Genetics has been amply demonstrated employing biological material of human origin. Extension to the forensic examination of non-human DNA lagged behind, but it is now intensively researched and has already provided spectacular and innovative results. This growth can be assessed, for instance, through the number of presentations devoted to non-human DNA in the last International Society for Forensic Genetics Congress (21 out of 317; proceedings soon to be published in *Forensic Science International: Genetics Supplement Series*) or by browsing the most recent issues of the leading journals in the field [e.g., 2-5]. Moreover, a comprehensive and authoritative handbook has been recently published [6].

Therefore, instead of trying to summarize the contributions from non-human genetics to forensics, I will just recall a few aspects that I repute as specific for this area.

First of all, it is now widely acknowledged that criminals - who are more and more aware of the possibilities of human identification - have become extremely cautious and sophisticatedly avoid leaving their own biological traces in the crime scene. However, they face a much more difficult task when trying to prevent 'transfer' or 'associative evidence' pieces such as carrying the victim's pet hairs which therefore behave as a 'silent witness' testifying the criminal's link to the crime scene [7].

A second topic, is the question of taxonomic identification (e.g., for the control of illegal trade). The possibility of forensic application requires a sound knowledge of the molecular systematics of the involved taxa. The enormous research effort implied must be shared with biologists in general (zoologists, botanists, microbiologists), and in particular with conservationists and other wild life specialists [4, 8].

Food traceability and fraud, namely on genetically modified foods and their production, is another group of emerging applications, for which a growing market is already showing up [9].

However, microbiological forensic genetics seems to be the most innovative and promising area, from individual profiling of the host by its fauna or flora to the tracing of infectious agents used in biological warfare or terrorism [10, 11] and - I dare to speculate - to a future stage in which microbial sharing between individuals would be used as associative evidence between perpetrator and victim of a sexual offense.

All these facts and prospects were considered sufficient to justify this special issue of 'The Open Forensic Science Journal'. This volume collects a small but significant number of contributions, providing updated reviews and a broad collection of examples of utmost impact and quality. I do hope that this endeavor will be useful to the forensic community and will foster new developments in the emerging field of non-human DNA.

ARTICLES SYNOPSIS

Dog (*Canis familiaris*), the most common domestic animal, being involved in manifold forensic situations (as a victim, a perpetrator or a link between a suspect and a crime scene) is - not surprisingly - overrepresented in this issue. Three

contributions were dedicated to it: van Asch and Pereira provide a comprehensive review of canine short tandem repeat genotyping whereas Smalling *et al.* present us the exciting and promising results of a research on the geographic differences in mtDNA distribution among domestic dog populations. About the first I will highlight two important points which are not restricted to canids: the urgent need for standardization and quality control improvement in non-human DNA forensics and the difficulties involved in distinguishing domestic and wild specimens. Concerning Smalling *et al.* contribution, I dare say that, apart from the extensive dataset now provided, the authors' analyses have demonstrated that not only in humans, but also in dogs, mtDNA phylogeography can be useful in forensics and the probable geographic origin of a dog can be inferred from its mtDNA. Parra *et al.* paper although using also dogs as a model, discusses a rather general issue: the choice of microsatellite markers in forensic typing, alerting for the consideration of mutation rate.

As any expert in forensic genetics painfully knows, mtDNA is in many cases the only genetic material that can be successfully amplified from the so called challenging (vestigial or degraded) samples. This simple fact explains its popularity in forensics and amply justifies the inclusion in this issue of the review authored by Pereira *et al.* In my view their highly valuable contribution, rooted in a solid experience in the field, and encompassing a wide range of species, can save a lot of work to any expert entering the subject as well as providing for the first time, to my knowledge, a comparative framework for translating experience from a specific taxon to another.

Finally, Araujo's contribution, dealing with the topic of microbial forensics, simultaneously addresses the methodological and technical issues relevant to these immensely diverse organisms and reviews the available evidence concerning their biogeography. In this respect, it must be said that the study of the dispersion patterns of microorganisms is relevant not only to forensics, but to clinical medicine and epidemiology, raising again the urgent need for cooperation between specialists from different disciplines.

CONCLUDING REMARKS AND FUTURE PERSPECTIVES

It seems unquestionable that non-human DNA will gain a considerable share among forensic biological evidence. It is also self-evident that non-human DNA forensic value is currently very far from being fully exploited. Since the use of DNA from human sources is more and more problematic and under more and more restrictive regulations [12, 13], the absence (or at least the much lighter) ethical and legal prohibitions on the use of non-human DNA substantially increase its future evidentiary value.

However, in order to be fully exploited, the forensic use of non-human DNA requires a much more challenging coalition of scientists when compared to the classical human evidence. Indeed, while human forensic genetics was limited to the interaction with human biology and medicine (we must recall its birth as an offshoot of Legal Medicine) what is now required is the cooperation of biologists and geneticists in general. We trust that the scientific community will very soon enlarge these complementary and mutually useful approaches to the benefit of the legal system and the society in general. This TOFSJ Special Issue was intended as a small contribution to this ambitious goal.

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REFERENCES

- [1] Saks, M.J.; Koehler, J.J. The coming paradigm shift in forensic identification science. *Science*, **2005**, *309*(5736), 892-895.
- [2] Chen, J.-W.; Uboh, C.E.; Soma, L.R.; Li, X.; Guan, F.; You, Y.; Liu, Y. Identification of racehorse and sample contamination by novel 24-plex STR system. *Forensic Sci. Int. Genet.*, **2009** (Article in Press DOI: 10.1016/j.fsigen.2009.08.001).
- [3] van de Goor, L.H.P.; Koskinen, M.T.; van Haeringen, W.A. Population studies of 16 bovine STR loci for forensic purposes. *Int. J. Legal Med.*, **2009** (Article in Press DOI 10.1007/s00414-009-0353-0358).
- [4] Marín, J.C.; Saucedo, C.E.; Corti, P.; González, B.A. Application of DNA forensic techniques for identifying poached guanacos (*Lama guanicoe*) in Chilean Patagonia. *J. Forensic Sci.*, **2009**, *54*, 1073-1076.
- [5] Sahajpal, V.; Goyal, S.P. Identification of a forensic case using microscopy and forensically informative nucleotide sequencing (FINS): A case study of small Indian civet (*Viverricula indica*) *Sci. Justice*, **2009** (Article in Press, doi:10.1016/j.scijus.2009.07.002).
- [6] Coyle, H.M. *Nonhuman DNA Typing: Theory and Casework Applications*. Press CRC, **2007**.
- [7] Menotti-Raymond, M.A.; David, V.A.; O'Brien, S.J. Pet cat hair implicates murder suspect. *Nature*, **1997**, *386*, 774.
- [8] Cassidy, B.G.; Gonzales, R.A. DNA testing in animal forensics. *J. Wildl. Manage.*, **2005**, *69*, 1454-1462.
- [9] Ogden, R. Fisheries forensics: the use of DNA tools for improving compliance, traceability and enforcement in the fishing industry. *Fish Fish.*, **2008**, *9*, 462-472.
- [10] Keim, P.; Van Ert, M.N.; Pearson, T.; Vogler, A.J.; Huynh, L.Y.; Wagner, D.M. Anthrax molecular epidemiology and forensics: using the appropriate marker for different evolutionary scales. *Infect. Genet. Evol.*, **2004**, *4*, 205-213.

- [11] Breeze, R.G.; Budowle, B.; Schutzer, S.E. *Microbial Forensics*. Elsevier Academic Press, **2005**.
- [12] Mullard, A. UK DNA database needs overhaul. Nature News (December 08 2008) Available from. <http://blogs.nature.com/news/thegreatbeyond/2008/12/doi:10.1038/news.2008.1288> News.
- [13] The Ethics Group: National DNA Database Annual Report. April **2009**. Available from http://police.homeoffice.gov.uk/publications/forensic-science-regulator/NDNAD_Ethics_Group_2nd_Annu1.pdf?view=Binary

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