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EMPOP 20 YEARS

HIFS
HUNGARIAN INSTITUTE
FOR FORENSIC SCIENCES

Preliminary Programme

12th Haploid Markers 2023

May 18-21, 2023 | Budapest, Hungary

PRELIMINARY PROGRAMME

WEDNESDAY | 17.05.2023

13.00-15.00	**WORKSHOP** **Processing Y chromosome related casework** Sascha Willuweit, Lutz Roewer
15.30-17.30	**WORKSHOP** **Casework experience with mtDNA: reporting of evidence, haplogrouping and ancestry estimation** Walther Parson
19.00-22.00	**WELCOME GET-TOGETHER PARTY**

THURSDAY | 18.05.2023

08.00-12.30	**Registration / Poster Exhibition / Seminar/Lunch**
08.30-12.30	**WORKSHOP** **Forensic Database Advisory Board** FDAB
09.00-10.00	**Presentation of the report (including Ethical Challenges and Recommendations)**
10.00-10.15	**Short survey of participants**
10.15-10:30	**COFFEE BREAK**
10.30-11.45	**Discussion:** • Type of data and identifiability • When should we assume vulnerability? • Legacy data • Data without consent • What should a good informed consent form and information sheet look like? • Elements of informed consent for international data sharin
11.45-12.00	**Concluding remarks**
12.30-13.00	**PROMEGA LUNCH SEMINAR**
13.15-13.45	**OPENING CEREMONY**
	POPULATION GENETICS I. **Chairs:** Lutz Roewer, Francesc Calafell
13.45-14.15	**A global analysis of matches and mismatches between human genetic and linguistic histories** Chiara Barbieri

14.15-14.30	**The universal Y-SNP database: from a few to a lot and beyond; how to bring it all together** Arwin Ralf
14.30-14.45	**Combining autosomal ancestry with X and Y AIMs: the VISAGE Enhanced Tool for Appearance and Ancestry** Jorge Ruiz-Ramírez
14.45-15.00	**Population analysis of complete mitogenomes for 334 samples from El Salvador** Francesc Calafell
15.00-15.15	**Finnish Y chromosome sequencing data suggests dual paths of N1a1 into Finland** Annina Preussner
15.15-15.30	**Novel Y chromosomal STRs set demonstrates high resolution of male lineages in North Eurasian human populations** Vadim Stepanov
15.30-15.45	**Optimalization of ancient deep Y haplogroup calling** Emil Nyerki
15.45-16.00	**Assessment of automated tools for mitochondrial haplogroup prediction** Kimberly Sturk-Andreaggi
16.00-16.15	**Sequencing the Lebanese Mitogenome and Y-SNPs: Variants, Haplogrouping and Databasing** Mirna Ghemrawi
16.15-16.45	**COFFEE BREAK / POSTER SESSION**

HUMAN IDENTIFICATION

Chairs: Marta Diepenbroek, Andreas Tillmar

16.45-17.00	**Klessin 1945 - history seen through forensics' eyes** Marta Diepenbroek
17.00-17.15	**Haploid markers aid in the identification of victims of World War II** Charissa van Kooten

17.15-17.30	**Ancestry analysis of highly degraded remains to assist the identification of fallen Australian service members** Elaine Cheung
17.30-17.45	**Applications of massively parallel sequencing for unidentified and missing persons casework: An Australian perspective** Kelly Grisdale
17.45-18.00	**When a country exceeds one continent – genetic biogeographical ancestry analysis of remains found at the former Stalag II D prisoner-of-war camp** Maria Szargut
18.00-18.15	**Maternal Lineages of Gepids from Transylvania** Alexandra Gînguță

FRIDAY | 19.05.2023

	TECHNOLOGY I. **Chairs:** Walther Parson, Charla Marshall
09.00-09.30	**Mitochondrial DNA in the Age of SNPs** Charla Marshall
09.30-09.45	**MITOBOOK: A work management tool for mtDNA analysis** Cibeles Serna Menor
09.45-10.00	**MITOMETRICS: Studying mitochondrial heteroplasmy along hair shafts** Vania Pereira
10.00-10.15	**mtDNA casework through MPS using Reverse Complement PCR and DNAxs as a routine tool** Natalie Weiler
10.15-10.30	**MPS mitochondrial DNA mixture analysis and Haploid markers based biogeographical investigation; criminal case examples.** Jord Nagel
10.30-10.45	**Comparison and evaluation of commercially available whole mitochondrial genome massively parallel sequencing workflows** Bethany Forsythe
10.45-10.55	**Discrimination of monozygotic twins using mtDNA heteroplasmy through probe capture enrichment and massively parallel sequencing** Atif Adnan
10.55-11.05	**Mitochondrial DNA Sequencing from Unbuffered Formalin Fixed Tissues: A Preliminary Study** Kangana Aggarwal
11.05-11.30	**COFFEE BREAK / POSTER SESSION**
	TECHNOLOGY II. **Chairs:** Sascha Willuweit, Maarten Larmuseau
11.30-11.50	**Advancing forensic SNP typing: Insights from an interlaboratory study of the FORCE panel** Andreas Tillmar

11.50-12.05	**A combined procedure of WGA and hybrid capture-based MPS enables to genotype 1.2 K identity-informative SNPs from sub-nanogram templates** Kyoung-Jin Shin
12.05-12.20	**Early noninvasive prenatal paternity testing with markers designed for forensic DNA mixture resolution** Diana Hall
12.20-12.30	**Developmental validation of the MGIEasy Signature Identification Library Prep Kit, an all-in-one multiplex system for forensic applications** Yicong Wang
12.30-13.45	**LUNCH / POSTER SESSION**
12.30-12.45	**QIAGEN SEMINAR**
	TECHNOLOGY III. **Chairs:** Athina Vidaki, Arwin Ralf
14.00-14.20	**Epigenetic aging of the human Y-chromosome in sperm** Athina Vidaki
14.20-14.35	**A Y-chromosomal MSRE/MDRE multiplex assay for the detection of semen** Jessica Rothe
14.35-14.50	**Real Time Y Chromosome Enrichment with Nanopore Sequencing** Thomas Krahn
14.50-15.05	**RM Y-STRs: where do we stand and where are we heading next** Dion Zandstra
15.05-15.20	**Design and development of novel single multiplex system incorporating 26 rapidly mutating Y-STRs; 26 RM Yplex** Rashed Alghafri
15.20-15.35	**Developmental validation of a high-resolution panel genotyping 639 Y chromosome SNP and InDel markers based on next-generation sequencing** Le Wang

15.35-15.50	**A novel multiplex of 12 multicopy Y-STRs for forensic application** Lei Shang
15.50-16.05	**Postmortem prevalence of seminal stains and detectability of Y-haplotypes** Viktor Poór
16.05-16.15	**Uniq Typer™ Y-10 Genotyping System: Genetic Variation In Southern Africa** Maria Eugenia D'Amato
16.15-16.45	**COFFEE BREAK / POSTER SESSION**
	STATISTICS **Chairs:** Amke Caliebe, Martin Zieger
16.45-17.05	**The discrete Laplace method in court** Martin Zieger
17.05-17.20	**Weight of evidence of Y-STR matches computed with the discrete Laplace method: Impact of adding a suspect's profile to a reference database** Mikkel Meyer Andersen
17.20-17.35	**Haploid marker data analysis using the STRAF 2 software** Alexandre Gouy
17.35-17.50	**The importance of relatedness in Y chromosomal match probability** Amke Caliebe
17.50-18.05	**Towards probabilistic genotyping for Y-STR profiles** Maarten Kruijver
18.05-18.20	**Is the marker-specific average mutation rate the appropriate parameter for computations in forensics and population genetics?** Nadia Pinto
18.20-18.35	**Recombulator-X: a fast and user-friendly tool for estimating X chromosome recombination rates in forensic genetics** Serena Aneli
20.00-24.00	**SOCIAL EVENING**

SATURDAY | 20.05.2023

POPULATION GENETICS II.

Chairs: Horolma Pamjav, Marcin Wozniak

09.00-09.20	**Combining haploid markers with in-depth family trees to enhance investigative genetic genealogy** Maarten Larmuseau
09.20-09.35	**Uniparental genetic diversity of three Hungarian-speaking isolated communities in the Carpathian Basin** Noémi Borbély
09.35-09.50	**Comparison of Iranian and Mongolian Populations Based on Y-STR Haplotypes Using Machine Learning Methods** Atefeh Joudaki
09.50-10.05	**Increasing the resolution of Latin American haplogroup Q sub-lineages using massively parallel sequencing** Zehra Köksal
10.05-10.15	**Unraveling the history of East Marshal Street Well through ancestry inferences** Filipa Simão
10.15-10.45	**COFFEE BREAK / POSTER SESSION**
10.45-11.00	**Mitochondrial DNA analysis in the United Arab Emirates populations** Reem Mheiri
11.00-11.15	**Y-chromosomal landscape in Serbian population groups originating from the Balkan Peninsula** Milica Mihajlovic
11.15-11.30	**Unexpected findings at the Amelogenin sex test in forensic paternity/kinship analysis: insights from a 13-year case history** Elena Chierto
11.30-11.45	**Canine mitochondrial investigation for breed determination** Federica Giangasparo

11.45-11.55	**Genetic polymorphisms of 23 Y-STR loci in Romanian population** Raluca Dumache
11.55-12.15	**WRAP-UP DISCUSSION AND CLOSING**
12.45-14.15	**FAREWELL LUNCH**

POSTER SESSION

PP01	**Screening of highly discriminative microhaplotype markers for individual identification and mixture deconvolution in East Asian populations** An-Quan Ji
PP02	**Analysis of paternal and maternal lineages in Serbian Roma population** Vanja Tanasic
PP04	**Massively parallel sequencing of 124 SNPs of the Precision ID Identity panel in the Qatari population** Waad Al-Dosari
PP05	**Gender-biased ancestry and gene flow in Brazilian Quilombos** Masinda Nguidi
PP06	**Population data and forensic parameters for 12 X-chromosome short tandem repeats in South Africa** Kgothatso Selepe
PP07	**The effect of geographical database subsets for forensic applications: an mtDNA example from Mexico** Martin Bodner
PP08	**Estimation of mutation rates and relative differentiation rate for 30 rapidly mutating Y-STRs in Serbian father-son pairs** Marija Vukovic
PP09	**Analysis of determining if two male samples are from the same family** Liping Yuan
PP10	**Analysis of 50 Y-STRs enables nearly full discrimination between unrelated males from the African continent** Chiara Della Rocca
PP11	**Inter-ethnics differences in the discrimination power of Y-STRS in Iran are due to urbanization level and clan structuring** Mogge Hajiesmaeil
PP12	**Inferring ancestry of Second World War (WWII) victims through YHRD database search** Irena Zupanič Pajnič

PP13	**A Comprehensive Portrait of Y-Chromosomal Variation of Bangladeshi Populations** Mahamud Hasan
PP14	**The genetic paternal ancestry of South American populations** Julyana Ribeiro
PP15	**The role of haploid markers in the identification of war victims** Irena Zupanič Pajnič
PP16	**Kinship testing using X-STR linkage groups on a Tamil pedigree** Sasitaran Iyavoo
PP17	**Genetic genealogical analysis of extensive family pedigrees using a high-density SNP data** Jing Liu
PP18	**Microhaplotypes for solving distant kinship relationships: a nanopore sequencing approach** Jorge Ruiz-Ramírez
PP19	**Age prediction from semen samples through detection of DNA methylation** Lucie Kotková
PP20	**Development of a DIP-STR multiplex panel for NGS analysis** Laura Carrara
PP21	**The power of 8 colors: next generation CE STR analysis** Andrew J. Hopwood
PP22	**An Automated Differential Extraction Solution for use on the Maxwell® System** Stefan Kutranov
PP23	**Evaluating the performance of microhaplotype markers for the analysis of DNA mixtures of up to four contributors** Jorge Ruiz-Ramírez
PP24	**An NGS-based Typing Panel of Human Multi-source Genetic Markers: Development and Validation** Hui Sun
PP25	**Revealing family secrets within identification case?** Ivana Furac

PP26	**Identification of tDMR-MH markers for analysis of body fluid mixtures** Sang Un Park
PP27	**Application of the Massive Parallel Sequencing for mtDNA control region analysis for forensic purposes, using QIAseq Targeted DNA Panel (Qiagen)** Marek Kowalczyk
PP28	**Analysis of mitochondrial DNA from degraded forensic samples using QIAseq Targeted DNA Panel (Qiagen) and Illumina sequencing** Andrzej Sekuła
PP29	**From body fluid detection to human identification: Is mtDNA the missing piece?** Sara C. Zapico
PP30	**An internal verification on the sequencing of mitochondrial DNA control region using Precision ID mtDNA Whole Genome Panel, Ion Chef System and Ion S5™ XL System** Bing Hong Shue
PP31	**mtDNA heteroplasmy detection with the iSEQ100 system (Illumina)** Katarzyna Skonieczna
PP32	**Mitochondrial DNA as a piece of ancestry-inferring puzzle of Second World War casualties** Marcel Obal
PP33	**Design and Validation of new SNaPshot assays for the most common European mitochondrial haplogroups** Kristin Rath
PP34	**Whole Mitochondrial DNA Sequencing for Human Identification with the PowerSeq® Whole Mito System** Andrew Hopwood
PP35	**1,2,3,… 1000 or how many? Assessment of mitochondrial DNA copy number variation between tissues** Jana Naue
PP36	**Ultra-deep Illumina sequencing of PCR products amplified with different polymerases** Katarzyna Skonieczna

PP37	**Sequence polymorphisms of forensic Y-STRs revealed by a 68-plex in-house massively parallel sequencing panel** Ke-Lai Kang
PP38	**Evaluation of the MHSeqTyper47 kit for forensically challenging DNA samples** Chi Zhang
PP39	**Utilizing TSPY Locus Markers to Develop a Sensitive Human Sex Identification Assay** Richard Li
PP40	**A preliminary study on the mechanism of genotype absence at DYS449 locus** Guangshu Staff Ding
PP41	**The successful analysis of DNA from human nails of 5 highly decomposed bodies found in seawater: from Y-ancestry to personal identification** Chiara Della Rocca
PP42	**Confirmed occurrences of duplications, triplications and deletions on the Y chromosome by MPS** Jana Nováčková
PP43	**Validation of new multiplex SNaPshot assays for the Y-chromosomal haplogroups R1a and R1b** Maria Seidel
PP44	**Combination of Y-STR and autosomal DNA analysis in a case of murder** Renata Jankova
PP45	**Complementary Y-STR use in forensic evidence analysis** Ljubica Trajkovska Pavlovska
PP46	**Y-STRs of ForenSeq** Marcin Woźniak

CONFERENCE BUREAU

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