

PRELIMINARY PROGRAM OF THE 13TH INTERNATIONAL CONGRESS ON HAPLOID MARKERS

Day 1 (Wednesday) - May 21, 2025

11:00 - | Participant Registration

12:00 – 13:30 | Workshop 1: **Walther Parson, Innsbruck, Austria** (*EMPOP FAQ Workshop*)

13:30 - 13:45 | Coffee Break

13:45 - 15:15 | Workshop 2: **Sascha Willuweit, Berlin, Germany** (*YHRD FAQ Workshop*)

20:00 - 22:30 | Welcome Party

Day 2 (Thursday) - May 22, 2025

08:00 - | Participant Registration

09:00 - 09:10 | Opening Address

09:10 - 09:30 | **Lutz Roewer, Berlin, Germany** Haploid Markers Workshops 1996-2025 - A Special Experience

09:30 - 10:15 | **KEYNOTE SPEAKER: Michael Krawczak, Kiel, Germany** 30+ years later: The Y-STR Match Probability Problem Revisited

10:15 - 11:00 | **SESSION 1: Y-STR ANALYSIS AND MATCH PROBABILITY IN FORENSIC GENETICS**

10:15 - 10:30 | **Dion Zandstra, Rotterdam, Netherlands** MATCH-Y: A Software for Pedigree-based Calculation of Y-STR Match Probabilities

10:30 - 10:45 | **Mikkel Meyer Andersen, Aalborg, Denmark** MITOFREQ: A Novel Approach for Mitogenome Frequency Estimation from Top-Level Haplogroups and SNVs

10:45 - 11:00 | **Amke Caliebe, Kiel, Germany** Number of Y-STR Matches and Degree of Relatedness Between Matching Males - Results from Evolutionary Simulations

11:00 - 12:00 | *Coffee Break and Poster Session*

12:00 - 13:30 | **SESSION 2: ADVANCES IN HAPLOID MARKER APPLICATIONS**

12:00 - 12:15 | **Arwin Ralf, Rotterdam, Netherlands** Bringing Out the Big Guns: Whole Genome Sequencing for Male Relative Differentiation and Male Identification Using Y-Chromosome

- 12:15 - 12:30 | **Alessia Riem, Torino, Italy** Liquid-based Cytology Samples as a Source for Y-STR Profiling in Sexual Assault Cases
- 12:30 - 12:45 | **David Ballard, London, United Kingdom** Application of Digital PCR as a Triaging Tool within a Mitochondrial DNA Analysis Workflow
- 12:45 - 13:00 | **Martin Bodner, Innsbruck, Austria** Y-STR Nomenclature is Not Old Hat
- 13:00 - 13:15 | **Peter Resutik, Zurich, Switzerland** Open-source Nextflow Pipeline for Comprehensive Whole mtDNA Genome Analysis
- 13:15 - 13:30 | **Vladimir Bajić, Berlin, Germany** mtDNA “Nomenclutter” and its Consequences on the Interpretation of Genetic Data

13:30 - 14:30 | *Lunch Break*

14:30 - 16:45 | **SESSION 3: FORENSIC APPLICATIONS AND CASEWORK EXPERIENCE**

- 14:30 – 14:45 | **Anna Lemalu, Auckland, New Zealand** The Implementation of Y-STR DNA Profiles in a Crime Sample Databank - the New Zealand Perspective
- 14:45 – 15:00 | **Rijad Konjhodžić, Sarajevo, Bosnia and Herzegovina** Identification of Forensically Significant SNPs Across the Entire Mitochondrial Genome in the Population of Bosnia and Herzegovina
- 15:00 - 15:15 | **Diana Hall, Lausanne, Switzerland** Inferring Biogeographic Ancestry with Haplotype Markers: The Case of DIP-STRs
- 15:15 - 15:30 | **Thomas Krahn, Berlin, Germany** Applying Y chromosome Methods to a 200-Year-Old Matching Haploblock on Chromosome 3

15:30 - 16:30 | *Coffee Break and Poster Session*

- 16:30 - 16:45 | **Le Wang, Beijing, China** Loci Screening and Genotyping Panel Development of 1338 Microhaplotypes for Accurate Identification of Kinship Within the 3rd Degree
- 16:45 - 17:00 | **Milica Keckarević Marković, Belgrade, Serbia** Y-STRs in Casework - Distinguishing Relatives in Crime Scene Samples
- 17:00 - 17:15 | **Viktorija Belakaposka Srpanova, Skopje, North Macedonia** DNA Profiling in Homicide Investigations: Unveiling the Truth Through Forensic Evidence
- 17:15 - 18:15 | *Discussion and Daily Conclusions, Poster Session*

Day 3 (Friday) - May 23, 2025

- 09:00 - 09:45 | **KEYNOTE SPEAKER: Pablo Carrion, Leipzig, Germany** Ancient Markers: How Ancient DNA Reveals the History of Uniparental Markers in the 1st Millennium CE Balkan Peninsula

09:45 - 11:15 | **SESSION 4: POPULATION AND EVOLUTIONARY GENETICS**

- 09:45 - 10:00 | **Paolo Francalacci, Cagliari, Italy** Reassessing Y Chromosome Diversity with the T2T Human Genome Reference
- 10:00 - 10:15 | **Zehra Köksal, Copenhagen, Denmark** Introducing the Y-Chromosomal Ancestral Reference Sequence Y-ARS
- 10:15 - 10:30 | **Francesc Calafell, Barcelona, Spain** Mitogenomes in East African Populations Show Extreme Levels of Phylogenetic Diversity
- 10:30 - 10:45 | **Vanja Tanasić, Belgrade, Serbia** Genetic Variability of Roma Population in Serbia: The Perspective from Uniparentally Inherited Markers
- 10:45 - 11:00 | **Khushboo Gautam, Ahmedabad, India** A Comprehensive Portrait of Y-STR Diversity of Sindhi Indian Populations and Comparison With Worldwide Populations
- 11:00 - 11:15 | **Milica Mihajlović Srejić, Belgrade, Serbia** Y-chromosomal Landscape of Haplogroup I-P37.2 in Serbian Population Groups Originating from the Balkan Peninsula
- 11:15 - 13:00 | *Coffee Break and Poster Session*
- 13:00 - 14:00 | *Lunch Break*
- 14:00 - 14:45 | **KEYNOTE SPEAKER: Jodi Irwin & Lara Adams, Washington, USA** Validation and Implementation of Next Generation Sequencing for Mitochondrial DNA Casework in a High-Throughput Forensics Laboratory
- 14:45 - 16:00 | **SESSION 5: EMERGING TECHNOLOGIES**
- 14:45 - 15:00 | **Nicole Huber, Innsbruck, Austria** From MITOTREE to MITOLEAF: Advancing Open Science in Mitochondrial DNA Phylogenetics
- 15:00 - 15:15 | **Lourdes Prieto, Madrid, Spain** MPS in mtDNA Analysis: Looking for Missing Amplicons
- 15:15 - 15:30 | **Lei Feng, Beijing, China** Haploid Markers Testing in Hair Protein
- 15:30 - 15:45 | **Chiara Saccardo, Verona, Italy** Unusual Tri- and Tetra-allelic Patterns Revealed by Massive Parallel Sequencing at the DYS385a/b and DYF387S1 Loci
- 15:45 - 16:00 | **Jing Liu, Beijing, China** Testification of Two SNP-Array-Based Genealogy Algorithms Using Extended Han Chinese Pedigrees and Recommendations for Improved Performance in Forensic Practice
- 16:00 - 16:45 | *Coffee Break and Poster Session*
- 16:45 - 18:00 | **SESSION 6: CASEWORK AND STATISTICAL APPROACHES IN FORENSIC GENETICS**
- 16:45 - 17:00 | **Kris van der Gaag, The Hague, Netherlands** oYSTER: Improving Y-Common Ancestor Time Estimations for DNA Kinship Analysis

- 17:00 - 17:15 | **Marija Vuković, Belgrade, Serbia** Application of the Male Pedigree in the Analysis of Mutation Events in a Serbian Deep-Rooted Pedigree Based on 30RM Y-STR Markers
- 17:15 - 17:30 | **Vania Pereira, Copenhagen, Denmark** Mitometrics: Incorporation of Heteroplasmic mtDNA Profile Mismatches in Likelihood Ratio Calculation
- 17:30 - 17:45 | **Xue Bai, Beijing, China** Development and Validation of 9-Dye Multiplex System
- 17:45 - 18:00 | **Martha Diepenbrock, Munich, Germany** Quo Vadis, BGA? A Reflective Assessment of the Status of Forensic Predictions of Biogeographical Ancestry
- 18:00 - 18:30 | Discussion and Daily Conclusions
- 20:00 - 02:00 | Socializing and Networking Event
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Day 4 (Saturday) - May 24, 2025

- 10:00 - 12:15 | **Final Panel Discussion:** The Future of Forensic DNA Databases
- 12:15 - 12:45 | Closing Remarks