

20th ISFG CONGRESS - SEPTEMBER 9 to 13, 2003 - ARCACHON-BORDEAUX - France

Tuesday September 9

10:00 am - 6:00 pm	Registrations
2:00 - 4:30 pm	Forum on DNA Databases. <i>Chair: Peter D. Martin</i>
5:00 - 6:00 pm	Opening ceremony
6:00 pm	Welcome reception offered by the City Ha

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Wednesday September 10

New Technologies and SNP Analysis

8:30 - 10:15 am	Poster Installation
8:30 - 9:15 am	"Methodologies for SNP typing" - <i>Ann-Christin Syvanen</i>
9:15 - 10:15 am	Oral presentations - Session 1
	O-01 A DNA microarray system for forensic DNA analysis - <i>A-M. Divne and M. Allen</i>
	O-02 Detection of genetic variation by MALDI-TOF mass spectrometry: Rapid SNP genotyping using the GENOLINK system - <i>D. Niemeyer, E. Petkovski, T. Elssner, K. Fahr, D. Peters, T. Wenzel, and M. Kostrzewska</i>
	O-03 Development of SNP microarray for supplementary paternity testing - <i>P. Ellonen, M. Levander, I. Ulmanen and M. Lukka</i>
	O-04 Multiplex Y chromosome SNP genotyping using MALDI-TOF MS - <i>J. Mengel-Jørgensen, J.J. Sanchez, C. Børsting, F. Kirpekar, N. Morling</i>
10:15 - 10:45 am	Coffee break – Poster session and Industrial exhibition
10:45 - 12:00 am	Oral presentations - Session 2
	O-05 Analysis of nuclear STR markers using Pyrosequencing Technology - <i>A-M. Divne and M. Allen</i>
	Selecting Single Nucleotide Polymorphisms for Forensic Applications - <i>C. Phillips, M. Lareu, M. Brion, B. Sobrino, A. Carracedo, C. Boersting, F. Kirpekar, J. Mengel-Jørgensen, J. Sanchez, N. Morling, D. Syndercombe Court, K. Balogh, M. Bogus, K. Bender, P.M. Schneider</i>
	O-06 Selection and use of SNP markers for human identification and paternity analysis in Koreans - <i>Hwan Young Lee, Myung Jin Park, Ji-Eun Yoo, Ukhee Chung, Gil-Ro Han, and Kyoung-Jin Shin,</i>
	O-07 SNPs: Tools for individual identification - <i>E. Petkovski, C. Keyser-Tracqui, D. Niemeyer, R. Hienne and B. Ludes</i>
	O-08 SWaP SNPs and Mirror SNPs: multiplex genotyping of a rare subset of SNPs enables the analysis of mixtures - <i>N. Anwar, K. Elliot, T. Harding, P. Rowan and B. McKeown</i>
	O-09 Whole genome amplification - the solution for a common problem in forensic casework? - <i>P.M. Schneider, N. Naveran, K. Balogh, M. Bogus, K. Bender, M. Lareu and A. Carracedo</i>
12:00 am - 1:00 pm	Poster session
1:00 - 2:00 pm	Lunch

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Wednesday September 10

New Technologies and SNP Analysis

- 1:00 - 2:00 pm ISFG Working Party meetings
- 2:00 - 2:45 pm "Linkage disequilibrium - Population Genetics, Genetic Epidemiology, and Forensic Genetics" - *Max Baur*
- 2:45 - 4:00 pm Oral presentations - Session 3**
- O-11 Non Binary Single Nucleotide Polymorphism Markers - *C. Phillips, M. Lareu, A. Salas, A. Carracedo*
- O-12 Population Studies Using SNP Typing – How Important Is Detailed Sample Origin Information? - *C. Thacker, C. Harrison, M. Brion, C. Phillips, P. Sanchez-Diz, D. Ballard, A. Carracedo and D. Syndercombe Court*
- O-13 Characteristics of mutations among alleles at the D5S818 locus analyzed using a tightly linked SNP marker. - *M. Edwards and R. Allen*
- O-14 Cytochrome P450 2D6 genotyping of fatal intoxications using Pyrosequencing - *AL. Zackrisson, P. Holmgren, AB. Gladh, J. Ahlner and B. Lindblom*
- O-15 Correlation between the ultra rapid metabolizer genotype for cytochrome P450 CYP2D6 and the consumption of methadone - *K. Bender, A. Koch, J. Becker und C. Rittner*

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Thursday September 11

Mass Disaster Victim Identification and Forensic Casework

8:30 - 9:15 am

"DNA testing as the primary tool for the victim identification effort after the World Trade Center terrorist attack." -
Mechthild Prinz

9:15 - 10:15 am

Oral presentations - Session 4

- O-16 The Use of a Single Nucleotide Polymorphism (SNP) Marker Panel for Human Identification from Compromised Biological Specimens - *E. Anguiano, C. Barceleau, R. Giles, and J. Baisch*
- O-17 Searching DNA profiles to identify victims in a mass disaster - *C. Brenner*
- O-18 DNA identification of the victims of the Linate air crash of October 8th, 2001 - *A. Piccinini, M. Capra, F. Betti and C. Cattaneo*
- O-19 Large-Scale Comparative Genotyping and Kinship Analysis: Evolution in Its Use for Human Identification in Mass Fatality Incidents and Missing Persons Databasing - *B. Leclair*

10:15 - 10:45 am

Coffee break – Poster session and Industrial exhibition

10:45 - 12:00 am

Oral presentations - Session 5

- O-20 Use of Laser Capture Microdissection to isolate sperm - *K. Elliott, D.S. Hill, C. Lambert, T.R. Burroughes and P. Gill*
- O-21 An Easily-Automated, Closed-Tube Forensic DNA Extraction Protocol using a Thermostable Proteinase - *D. Moss, S.-A. Harbison and D. J. Saul*
- O-22 Discrepant results of samples taken from different tissues of a single individual - *EM Dauber, G Dorner, M Mitterbauer, S Wenda, I Faé and WR Mayr*
- O-23 Genetic investigation of historical and modern burned corpses - *N. von Wurmb-Schwark, M. Harbeck, E. Simeoni, M. Oehmichen*
- O-24 Origin of DNA Profiles from Body Fluid Stains - *C. Peel*
- O-25 Genetics and Other Forensic Tools for Attribution of Microbiological Agents - *B. Budowle*

12:00 am - 1:00 pm

ISFG General Assembly

1:00 - 2:00 pm

Lunch

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Thursday September 11

Mass Disaster Victim Identification and Forensic Casework

2:00 - 2:45 pm "Population substructure: effects in interpretation" - *Ranajit Chakraborty*

2:45 - 4:00 pm Oral presentations - Session 6

- O-26 A Comparison of Adjustment Methods to Test The Robustness of an STR DNA Database Comprised of 24 European Populations - *Peter Gill, Lindsey Foreman, John S. Buckleton, Christopher M. Triggs Heather Allen*
- O-27 Assigning individuals to ethnic groups based on 13 STR loci - *X. Fosella, F. Marroni, S. Manzoni, A. Verzeletti, F. De Ferrari, N. Cerri, S. Presciuttini*
- O-28 Between country comparison of a large Caucasian STR database collected as part of the Standardisation in DNA Profiling (STADNAP) project - *D Syndercombe Court and the EDNAP Group*
- O-29 FINEX and FAMILIAS: two programs for analysis of defective identification cases - *M. Dobosz, P. Mostad, R.G.Cowell, V.L. Pascale*
- O-30 Germline Mutations at 15 STR Loci in the Chinese Population - *W.M. Tang and M.Y. Law*

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Friday September 12

Y Chromosome and mtDNA Studies

8:30 - 9:15 am	"The Y chromosome: population structure and forensic applications" - <i>Mark Jobling</i>
9:15 - 10:15 am	Oral presentations - Session 7
	O-31 29 Y-chromosome SNP analysis in European populations - <i>M. Brión, A. Blanco-Verea, M. Lareu, A. Carracedo</i>
	O-32 Development of a Male-Specific, 12-Locus Fluorescent Multiplex - <i>B. E. Krenke, P. M. Fulmer, K. Driftmier Miller, C. J. Sprecher, S. Lupton</i>
	O-39 Sequence analysis of the complete mitochondrial genome - <i>M. Nilsson, U. Gyllensten, M. Allen</i>
	O-43 Measuring by fragment analysis the proportion of length variants in samples carrying lenght heteroplasmy at the Homopolymeric C-Stretch in mitochondrial HVII region - <i>L. Prieto, M. Montesino, A. Rodríguez-Monge, C. García, E. García, E. Rivas, A. Salas</i>
10:15 - 10:45 am	Coffee break – Poster session and Industrial exhibition
10:45 - 12:00 am	Oral presentations – Session 8
	O-35 Y-Chromosomal Microsatellite Mutation Rates: Differences in Mutation Rate Between and Within Loci - <i>B. Myhre Dupuy, M. Stenersen, A.G. Flønes T. Egeland and B. Olaisen</i>
	O-36 Y-STR typing by SNaPshot minisequencing in degraded forensic samples - <i>N. Siebert, B. Hoste</i>
	O-37 Y-STRs Analysis in Japanese using Liquid Bead Array Technology - <i>Masaki Hashiyada, Masayuki Nata, Toshio Nagashima</i>
	O-38 The highly discriminating Y-STR DYS464: a reasonable extension of the minimal Y-STR haplotype? - <i>B. Berger, H. Niederstätter, A. Brandstätter, W. Parson</i>
	O-33 Multiplexed Assays for Evaluation of Y SNP Markers in U.S. Populations - <i>P.M. Vallone and J.M. Butler</i>
	O-34 How much more should the Y-STR Haplotype Reference Database increase to reach a pragmatic saturation level? - <i>L. Pereira, A. Amorim</i>
12:00 am - 1:00 pm	Poster session
1:00 - 2:00 pm	Lunch

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Friday September 12

Y Chromosome and mtDNA Studies

1:00 - 2:00 pm	EDNAP/ENFSI meeting
2:00 pm	Poster removal
2:00 - 2:45 pm	"mtDNA: Phylogeography" - <i>Martin Richards</i>
2:45 - 4:00 pm	Oral presentations – Session 9
O-40 Validation of semi automated quality assessment of mitochondrial control region sequence data by PHRED and Sequencher - <i>E. Sørensen, E.M. Rasmussen, B. Eriksen, H.J. Larsen, N. Morling</i>	
O-41 Analysis of SNP-variation in the coding region of mitochondrial DNA - <i>A. Coene, N. Vanderheyden, A. Gilissen, J.-J. Cassiman, R. Decorte</i>	
O-42 Beyond HV1 and HV2 - identification of valuable mitochondrial SNP positions - <i>W. Branicki, T. Kupiec, P. Wolańska-Nowak, A. Parys-Proszek, G. Ba</i>	
O-44 EMPOP – The EDNAP mtDNA Population Database Concept for a new generation, high-quality mtDNA database - <i>W. Parson, A. Brandstätter, M. Pircher, M. Steinlechner, R. Scheithauer</i>	
O-45 Is selection at mtDNA really a major concern? - <i>L. Pereira, A. Amorim</i>	

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Saturday September 13

9:00 - 10:30 am	Oral presentations and roundtable discussion - Session 10 (including further presentations to be announced) Interpretation of mixtures and low copy number DNA profiles in crime case. <i>Chair: Peter Gill</i> O-46 Expert systems to interpret mixtures and low copy number DNA profiles - <i>Peter Gill</i>
10:30 - 11:00 am	Coffee break – Industrial exhibition
11:00 am - 12:30 pm	Oral presentations and roundtable discussion - Session 11 (including further presentations to be announced) Quality management. <i>Chair: Niels Morling</i> O-47 Results of the 2003 Paternity Testing Workshop of the English Speaking Working Group - <i>B.T. Simonsen, N. Morling</i> O-48 eDNA, networking software tailored for identity testing laboratories. - <i>Robert W. Allen,, Kent Harman, and Allan Sieker</i>
12:30 pm	Closing ceremony