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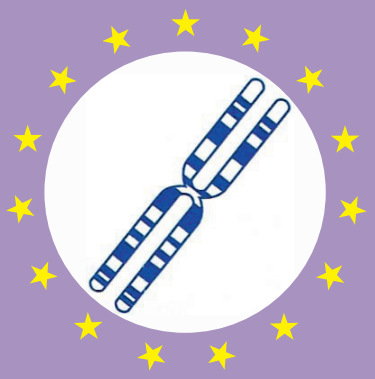

E.C.A. NEWS LETTER

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E.C.A. Newsletter

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No. 51 January 2023

Contents	*Page*

E.C.A. on Facebook

As mentioned in earlier Newsletters, E.C.A. is on Facebook.
You will find announcements of interesting articles, related to cytogenomics or to biology in general, and also pictures and stories from social events related to E.C.A. and its members. Also our E.C.A. conferences will be covered on Social Media.
You can see the weekly posts and announcements via the direct link

https://www.facebook.com/Cytogeneticists/ or on the updated E.C.A. website **http://www.e-c-a.eu/**

You will find a selection of interesting Facebook posts in this Newsletter starting at page 6.
Please contact us (mariano.rocchi@uniba.it) if you wish to share an interesting news item or a pertinent article.

President's Address

Dear friends,

First of all, Happy New Year!

I started my letter of January 2022 with: "We last saw each other in 2019 [in Salzburg]. Then Covid came along, and we entered a tunnel, confident that we would soon see the light at the end of the tunnel". I am glad to say that the end of the tunnel now appears to be real and we will have the long-awaited opportunity to meet in person this year. As already announced, our biennial conference will be held in Montpellier, 1 to 4 July 2023; see https://www.e-c-a.eu/EN/UPCOMING-CONFERENCES.html.
The program is almost complete and you will hear more about it soon.
Other ECA activities are also finally being held in person. The Nîmes course is scheduled to take place from 20 to 26 March 2023. Registration closes on 15 February 2023; see https://www.e-c-a.eu/EN/European-Advanced-Postgraduate-Course-in-Classical-and-Molecular-Cytogenetics-2023.html
The E.C.A. offers two scholarships for the course, covering the registration and accommodation fees. For further information and registration, please send an e-mail to Prof. Jean-Michel Dupont (jean-michel.dupont@aphp.fr)
and/or to Prof. Thierry Lavabre-Bertrand (thierry.lavabre-bertrand@umontpellier.fr)
The Goldrain Course in Clinical Cytogenetics, organized by Prof. Albert Schinzel in the Goldrain castle (South Tyrol, Italy) was held in person already last summer. It was, as always, a great success. By the end of the course, however, it appeared that it might be the last because until now it has been organized and run almost entirely by Prof. Schinzel alone and he felt it was becoming too difficult to sustain it further on his own. So, considering the importance of the course, the ECA decided to look for a solution. Prof. Schinzel, Prof. Dupont, Prof. Miller and I met in Milan on November 12, 2022 and as a result, a solution has been found. In Bari, where I live, a non-profit association has been created (Scuola Europea di Citogenetica; European School of Cytogenetics) to provide administrative and organizational support, thus ensuring that the Goldrain course will continue (see https://www.e-c-a.eu/files/downloads/16th-Goldrain-flyer.pdf).
The E.C.A. offers two scholarships to cover the registration and accommodation fees. Additional scholarships will be provided by the E.S.H.G. (European Society of Human Genetics). For further information please write to Prof. Albert Schinzel (schinzel@medgen.uzh.ch).
The flyers with details of the Nîmes and Goldrain courses can be found at the end of this Newsletter.

This Newsletter also contains the ECA posts that have appeared on its Facebook page since the previous issue of the newsletter (https://www.facebook.com/Cytogeneticists).
These are announcements/summaries of interesting articles, related to cytogenomics and to biology in general. Your contributions are welcome (please contact mariano.rocchi@uniba.it).

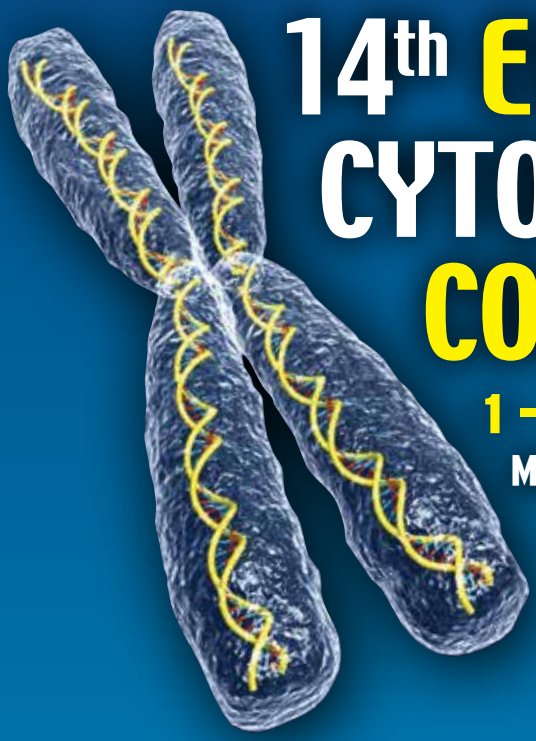
Wishing you again a happy 2023,

Kind regards,

Mariano Rocchi
E.C.A. President




European Cytogeneticists Association



14th EUROPEAN CYTOGENOMICS CONFERENCE

1 - 4 July 2023

MONTPELLIER - FRANCE

www.eca2023.org

INVITED SPEAKERS

Alex Hoischen, Sweden
Anna Lindstrand, Sweden
Antonio Capalbo, Italy
Antonio Rausell, France
Bekim Sadikovic, Canada
Brankica Mravinac, Croatia
Brunella Franco, Italy
Caroline Schluth-Bolard, France
Eva R. Hoffmann, Denmark
Folker Spitzenberger, Germany
Giacomo Cavalli, France
Johan den Dunnen, Netherlands
Karen Temple, UK
Lars A. Forsberg, Sweden
Lyn Chitty, UK
Malgorzata I. Srebniak, Netherlands
Michael E. Talkowski, USA
Matthiue Rouard, France
Nicolas Chatron, France
Orsetta Zuffardi, Italy
Robert-Jan H. Galjaard, Netherlands
Sarah McClelland, UK
Tony Heitkam, Germany

IMPORTANT DATES

February 27, 2023 Monday
Deadline for Abstract Submission

March 20, 2023 Monday
Notification of Acceptance

April 3, 2023 Monday
Deadline for Early Registration

14th European Cytogenomics Conference – Preliminary Program

Opening lecture Aneuploidy in the Maternal Germline	Eva R. Hoffmann	Denmark
Plenary session 1 - **Mosaicism: from Preimplantation Embryos to Aging**		
1. Mosaicism in Preimplantation Embryos	Antonio Capalbo	Italy
2. Mosaicism in Prenatal Diagnosis: from NIPT to Amniocytes Investigation	Malgorzata I. Srebniak	Netherlands
3. Hematopietic Loss of Chromosome Y and Higher Mortality in Men	Lars A. Forsberg	Sweden
Plenary session 2 - Cancer Cytogenomics		
1. Replication Stress Generates Distinctive Landscapes of DNA Copy Number Alterations and Chromosome Scale Losses in Cancer	Sarah McClelland	UK
2. Whole-Genome Duplication Shapes the Aneuploidy Landscape of Human Cancers	Uri Ben-David	Israel
Concurrent Session 3 - Recent Advances in Cytogenomics		
1. Optical mapping to karyotype	Alex Hoischen	Netherlands
2. Artificial Intelligence in Cytogenetics	Antonio Rausell	France
Concurrent Session 4 - **Beyond Genome Sequencing: the Epigenetic Signature**		
1. DNA Methylation Episignatures Associated with Large Structural Copy Number Variants: Clinical Implications	Bekim Sadikovic	Canada
2. Multi-locus imprinting disorders	Karen Temple	UK
Plenary session 3 - Clinical Cytogenomics		
1. Complex Genomic Rearrangements: an Underestimated Cause of Rare Diseases	Anna Lindstrand	Sweden
2. Distal Germ-Line Deletions in Mosaic With Copy-Neutral Loss of Heterozygosity: Something to Be Considered in Genetic Counselling	Orsetta Zuffardi	Italy
3. From Gene Disruption to Missense Variants: how different Types of Variants Influence the X-Linked Inheritance Model	Brunella Franco	Italy

Concurrent Session 5 - Clinical Cytogenomics 2		
1. Structural Variants in Clinical Practice Using Short Read WGS	Nicolas Chatron	France
2. Chromoagensis: From Diagnosis to Genetic Counselling	Caroline Schluth-Bolard	France
Concurrent Session 6 - Animal and Plant Cytogenomics I		
1. Comparative Genomics and Tools for Studying Chromosome Evolution	Matthieu Rouard	France
2. Coleopteran Satellite Profiles: Chromosomal and Sequence Organization	Brankica Mravinac	Croatia
Plenary session 4: Nuclear Organization and Disease		
1. The Role of 3D Genome Organization in The Regulation of Gene Expression and Cell Fate	Giacomo Cavalli	France
2. Spatial Organization of Transcribed Eukaryotic Genes	Irina Solovei	Germany
Concurrent Session 7 - Animal and Plant Cytogenomics II		
1. Adding a Chromosome Perspective to Plant Genomics: Making Sense of Retained Retroviruses, Moving Retrotransposons and Expanding Satellite DNAs	Tony Heitkam	Germany
Concurrent Session 8 - Accreditation, Quality Control and Education		
1. The New ISO 15189 Standard Medical Laboratories	Folker Spitzenberger	Germany
2. Sequence-based Nomenclature and the Novelties to Come in the Next ISCN Version	Johan den Dunnen	Netherlands
Plenary session 5 - Prenatal Diagnosis and preimplantation		
1. Genome-Wide Noninvasive Prenatal Testing: Follow-Up Results of the TRIDENT-2 Study	Robert-Jan H. Galjaard	Netherlands
2. Fragmentomics and Non Invasive Prenatal Screening (NIPS)	Joris Vermeesch	Belgium
3. Prenatal Diagnostic Yield and Pitfalls Through Arrays, Exome, and NIPT	Lyn Chitty	UK
Closing keynote: The Landscape of Structural Variation Across Diverse Global Populations and Developmental Disorders	Michael E.Talkowski	USA

Literature on Social Media

E.C.A. is now also present on Social Media. Here are announcements of interesting articles that we have posted on Facebook. The articles and news items are related to cytogenomics or to biology in general. If you have relevant articles that you would like to share, please contact mariano.rocchi@uniba.it.

RARE DE NOVO TERMINAL DELETIONS THE RESCUE OF UNFAVORABLE ZYGOTIC IMBALANCES?

A recent review article (Eur J Hum Genet, by Zuffardi et al.[1]) examines the evidence which suggests that many *de novo* unbalanced structural rearrangements are not representative of the genomic constitution of the zygote but are rather the result of modifications of genomic imbalances that are incompatible with embryonic development. It has long been known that a cell with trisomy can undergo a rescue process, which can result in a cell with 46 chromosomes with segmental or complete uniparental disomy. More recently, it has been demonstrated that both unbalanced *de novo* translocations and small supernumerary chromosomes may result from modifications of an entire supernumerary chromosome. The article, in addition to reviewing this evidence, focuses on distal *de novo* deletions that could result from the breakdown of an isodicentric chromosome present in a zygote, which, despite having 46 chromosomes, has in fact an almost complete functional trisomy. The authors underline how the rescue events of the deletion can, through somatic recombination with the normal homolog, create errors of interpretation if adequate methodologies are not used to highlight segmental disomies. Furthermore, the dicentrics break and the resulting products, which lack telomeres, undergo repeated breakage-fusion-bridge cycles. This can lead to the production of a variety of rearrangements such as unbalanced translocations and ring chromosomes, which can then be present in the embryo but more frequently in the placental cells.

[1]https://www.sciencedirect.com/science/article/pii/S1769721222001136?via%3Dihub

RARE VARIANTS IN DOMINANT GENES CAUSING MILD PHENOTYPIC CONSEQUENCES

It is well known that monogenic variants can display different effects in different individuals.
In a paper which appeared in Nature Biotechnology in 2016 Chen et al.[1] reported results of exome analysis of 874 genes in 589,306 individuals. Unexpectedly, they found 13 "normal" adults harboring mutations for 8 severe Mendelian conditions, with no clinical manifestation of the indicated disease.
A very similar task was performed by Kingdom et al. (Am J Hum Genet *in press*) who took advantage of the UK Biobank (UKB) to investigate phenotypes associated with rare protein-truncating and missense variants in 599 monoallelic DDG2P genes (clinically curated Developmental Disorders Gene2Phenotype Database) by using whole-exome-sequencing data from ~200,000 individuals and rare copy-number variants overlapping known developmental disorders loci by using SNP-array data from ~500,000 individuals.
They suggest that (1) many genes routinely tested within pediatric genetics have deleterious variants with intermediate penetrance that may cause lifelong sub-clinical phenotypes in the general adult population; (2) clinical studies may overestimate the penetrance of such rare variants, while population cohorts like UKB are likely to underestimate the penetrance as a result of ascertainment bias toward healthy individuals.

[1] https://www.nature.com/articles/nbt.3514
[2]https://www.sciencedirect.com/science/article/pii/S0002929722002178?via%3Dihub

LOH AND GENE CONVERSION

Most tumor-suppressor (TS) genes have been identified through Loss of Heterozygosity (LOH) in cancer cells. SNP-microarrays is the ideal technique to detect LOH, confirmed by Comparative Genome Hybridization (CGH). Occasionally, however, copy neutral loss of heterozygosity are detected, resulting from different mechanisms, such as mitotic recombination. The homozygosity of a mutation in a TS gene can also result from gene conversion (Wikipedia).
In a recent paper in Genome Research, Takahashi and Innan[1] report the development of an algorithm to detect somatic gene conversion from short-read sequencing data. They analyzed 6,285 cancer patient samples and found 4,978 instances in which the homozygosity of the mutation of the TS gene had

resulted from gene conversion. This figure represents the 14.8% of the total LOH mutations detected in their samples.

[1] https://genome.cshlp.org/content/32/6/1017

LOSS OF CHROMOSOME Y AND HIGHER MORTALITY IN MEN

Genomic differences between men and women lead to differential susceptibility to some diseases. Lidia Larizza, a former president of the E.C.A., outlined the difference in susceptibility to Covid-19 (see NL 46[1]). One of the most debated differences is the lifespan, which is higher in women than in men. Evolutionary pressures on grandmothers have been invoked, because they are more useful for the fitness of grandchildren.
Now, an article in Science by Sano et al., 2022 presents evidence that hematopoietic loss of the Y chromosome leads to cardiac fibrosis and heart failure. The results perfectly match the idea that heart failure is more common in men than in women. It could also help explain the difference in lifespan.

[1] https://www.e-c-a.eu/files/downloads/Newsletters/NL46-July-2020.pdf
[2] https://www.science.org/doi/10.1126/science.abn3100

COMPLEX GENOMIC REARRANGEMENTS AND RARE DISEASES

In the past, several Mendelian genetic diseases have been identified because the gene in question was interrupted due to a chromosomal breakpoint. Recent developments in sequencing and mapping technologies have provided several new tools for analyzing complex genomic rearrangements, which can harbor the etiology of rare diseases.
A publication by Schuy et al.[1] (Trends in Genet) specifically analyzes the relationship between rare diseases and complex genomic rearrangements (CGRs), defined as "structural variants (SV) that host more than one breakpoint junction and / or comprise structures consisting of several of a SV in cis ". CGRs "also include structural rearrangements that have at least three cytogenetically visible breakpoints." The paper lists pros and cons of different technological approaches, aimed at implementation in a clinical cytogenomics laboratory. It also critically analyzes the data available in the literature. The article appears to be a further step in the trend "from cytogenetics to cytogenomics" that A. Lindstrand, the leader of the group, undertook in 2019 (Genome Medicine[2]).

[1] https://www.cell.com/trends/genetics/fulltext/S0168-9525(22)00145-7?_returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0168952522001457%3Fshowall%3Dtrue
[2] https://genomemedicine.biomedcentral.com/articles/10.1186/s13073-019-0675-1

X-CHROMOSOME GENE VARIANTS AND THEIR IMPACT ON SPERMATOGENIC FAILURE

The authors of a study that appeared in 2013 (Mueller et al. 2013, Nature Genetics[1]) showed that some ampliconic genes on the X chromosome are primarily expressed in testicular germ cells and are functionally connected to sperm production. These results suggested that the X-chromosome, like the Y-chromosome, is crucial for male fertility. Consequently, the X chromosome has become a good candidate for discovering new genetic causes of spermatogenic failure. Nevertheless, the current list of causes is not that long; even with the use of high-throughput sequencing technologies, the number of X-chromosome gene variants associated with male infertility remains low (reviewed by Houston et al. 2021, Human Reproduction Update[2]).
In a recent article published in the American Journal of Human Genetics (Riera-Escamilla et al. 2022[3]), the authors present an analysis of the whole set of X chromosome protein-coding genes in a huge population of infertile patients. Specifically, a total of 2,354 men with idiopathic non-obstructive azoospermia (absence of sperm in the ejaculate) or cryptozoospermia (fewer than 100,000 sperm per milliliter of ejaculate) have been screened using whole exome sequence analysis. The main objective of the article was to identify new monogenic anomalies associated with severe spermatogenic defects.
This article makes one realize the importance of some crucial steps in this kind of study, such as variant filtering and the application of different strategies of gene selection and prioritization. The authors identified 21 novel gene anomalies linked to severe spermatogenic failure. Importantly, the 21 candidate genes were found to be crucial for spermatogenesis-related pathways.
The results presented in this paper emphasize the importance of the X chromosome in the etiology of male infertility by doubling the number of X chromosome genes associated with severe spermatogenic

defects. From a clinical perspective, these results will contribute to the development of gene panels addressed to the diagnosis of male infertility.

[1] https://www.nature.com/articles/ng.2705
[2] https://academic.oup.com/humupd/article/28/1/15/6366465?login=false
[3] https://www.cell.com/ajhg/fulltext/S0002-9297(22)00260-9

LACTASE PERSISTENCE REVISITED

The lactase genomic domain is the region of the human genome that shows the strongest selection pressure in northwestern European populations and in the Maasai from Kenya (Schlebusch et al. 2013[1]). The peaks of homozygosity for lactase persistence are impressive. The simple interpretation was that the continued ability to digest lactose after weaning constitutes a strong selective advantage for people who have access to milk.
A recent paper by Evershed et al.[2] in Nature, reports that the situation is more complex. They looked at the use of milk in Europe (analysis of milk fat residues in ceramics) and the mutations responsible for the persistence of lactase (ancient genomes) starting from ~7000 years ago and found that the use of milk was widespread also among populations with intolerance to milk. Their interpretation is that positive pressure of natural selection for lactase tolerance became very strong in periods of famine or pestilence, when lactose-intolerant individuals would have been more likely to die.
See also News & Views[3] in the same issue of Nature.

[1] https://www.nature.com/articles/ejhg2012199
[2] https://www.nature.com/articles/s41586-022-05010-7
[3] https://www.nature.com/articles/d41586-022-02067-2

ARTIFICIAL KARYOTYPE MODIFICATION

YAC, Yeast Artificial Chromosomes, (later supplanted by BACs) were popular at the very beginning of the human genome project. While it is relatively easy to manipulate the yeast karyotype, it is much more difficult to perform chromosome engineering in higher eukaryotes.
Acrocentric (Robertsonian) fusions are not a rare event in humans, and, very occasionally, homozygous individuals have been reported as a result of consanguineous marriages. In the wild, chromosomal fusions during evolution have led to a reduced chromosome number in several populations, such as mice and other mammals (e.g., sheep and goat with 54 and 60 chromosomes respectively). In *Homo sapiens*, chromosome 2 is the result of a telomere-telomere fusion of two ancestral chromosomes, which correspond to chromosomes 12 and 13 in chimpanzee.
Wang et al. (Science) have used DNA editing technology to create two types of heterozygous and homozygous mice with terminal fusions of chromosomes.
The first type of the fusion is between chromosomes 1 and 2, and the second is between chromosomes 4 and 5. The fusions did not appear to affect chromatin conformation and stem cell differentiation. The developmental trajectory in the two cases, however, was very different. Normal homozygous offspring were possible only in the second case (4/5 fusion).

[1] https://www.science.org/doi/10.1126/science.abm1964

PREIMPLANTATION EMBRYOS AND GLUCOCORTICOIDS

Glucocorticoids are used to improve the success rate in assisted reproductive technology (ART) cases. Zhao et al.[1] (Genome Res.) have done an i*n vitro* study of the effects of very early glucocorticoid treatment, in 7-day human embryos.
The rationale for the study was that early embryonic environments can have profound effect on development trajectories in the fetal period and in adult life. They found that glucocorticoid treatment produced no changes in morphology, blastocyst size or cellular composition. However, they report profound molecular changes at the level of gene expression, DNA methylation and small RNAs. Their obvious conclusion is that caution is recommended because of the possible consequences associated with the use of adjuvants and additives in ART and infertility treatment.
[1] https://genome.cshlp.org/content/early/2022/09/16/gr.276665.122.long

ENHANCER REDUNDANCY

The 1000 Genome Project[1] found that in an analyzed population of 2504 individuals, 240 genes were inactivated, suggesting that these were "dispensable". The most likely interpretation of these results is redundancy, i.e. the existence of other genes with identical or similar function.

Lin et al. (Science[2]) analyzed the enhancers of the well-studied *MYC* locus as a model system. *MYC* enhancers are organized in two clusters, one of which is far away (~1Mb) from the other.
The authors found that, when pairs of enhancers from the same cluster were perturbed, the effect on MYC expression (and, therefore, on cell proliferation) was relatively mild. By contrast, when the perturbed pair contained one enhancer from each cluster, the reduction in *MYC* expression and cell proliferation was much more drastic.
The interpretation is that the system functions as a protection against mutations because the possibility that distant clusters are affected by the same mutational event is low. A kind of well-designed redundancy.
See also the comment in News&Views (Science September 15, 2022).

[1] https://pubmed.ncbi.nlm.nih.gov/26432246/
[2] https://www.science.org/doi/10.1126/science.abk3512

AGING AND AGE REVERSAL

Yamanaha in 2006 (Cell) reported the induction of pluripotent stem cells from mouse fibroblast. Since then, huge amount of resources have been invested in finding remedies for aging. This article in MIT Technology Review takes stock of the situation.

[1]https://www.sciencedirect.com/science/article/pii/S0092867406009767?via%3Dihub
[2]https://www.technologyreview.com/2022/10/25/1061644/how-to-be-young-again/?utm_source=Nature+Briefing&utm_campaign=1d73b0342c-briefing-dy-20221026&utm_medium=email&utm_term=0_c9dfd39373-1d73b0342c-44083589

ANCESTRAL MAMMALIAN KARYOTYPE

The availability of data on a large number of mammalian species that have been sequenced has allowed the computational reconstruction of the ancestral karyotype of mammals (Damas et al., PNAS 2022[1]). The hypothetical mammalian ancestor is supposed to have had 19 pairs of chromosomes. Some syntenic regions were very large, as large as an entire chromosome. These data suggest that the synteny conservation was subject to a strong evolutionary constraint that lasted for over 300 million years.

[1]https://www.pnas.org/doi/abs/10.1073/pnas.2209139119?url_ver=Z39.88-2003&rfr_id=ori%3Arid%3Acrossref.org&rfr_dat=cr_pub++0pubmed

ROLE OF 3D GENOME ANALYSIS IN THE DIAGNOSIS AND THERAPY OF LEUKEMIA AND CANCER

In a recent paper in Nature[1] Xu *et al*. explore the relationship between three-dimensional (3D) chromatin structure and related methylation alterations in acute myeloid leukemia (AML). The authors conclude that changes in DNA methylation and 3D genome structure may provide subtype-specific clues for understanding and treating the disease.
The study was based on a variety of approaches through which profiles of chromatin organization compartments, topologically associating domains, and chromatin loop features in the context of other genomic alterations were analyzed in more than two dozen AML cases.
The analyses have highlighted that genetic subtypes of AML differ in chromatin organization features, with recurrent chromatin loops showing specific enhancer or silencer activity on promoters in the diverse myeloid tissue malignancies.
The AML-related genome organization and expression effects appear to be somewhat reversed in the presence of hypomethylating agents, such as 5-azacytidine or decitabine or in cells with lower-than-usual levels of genes coding for DNA methyltransferase enzymes. The results suggest that treatment with an HMA may achieve therapeutic efficacy, at least partly, through restoring normal chromatin architecture and opening new mechanism-based therapeutic approaches to improve treatment outcomes in AML and other cancers.

[1] https://www.nature.com/articles/s41586-022-05365-x

POLYPLOIDY IN ANIMALS

Redundancy in data storage is a safe rule that you learn when your computer breaks down (see RAID5[1]). This is also true in living organisms. The most likely explanation for the fact that each of us has ~200 non-functional (homozygous) genes is that they are redundant[2]. Polyploidy can be considered a redundant state of the genome. It is relatively common in plants and "Plants with double genomes might have had a better chance to survive the Cretaceous–Tertiary

extinction event" (PNAS)[3]. A larger quiver of arrows certainly comes in handy.
Polyploidization is much rarer in animals than in plants. Kyle T. David, in PNAS[4], analyzes the biogeographical dataset distribution of polyploidy in amphibians, ray-finned fishes, and insects. He found that polyploidy correlates with newer and more extreme environments and may indicate the role of genome duplication in facilitating adaptation. As mentioned, a larger quiver of arrows is definitely beneficial.

[1] https://en.wikipedia.org/wiki/RAID
[2] https://www.nature.com/articles/nature15394
[3] https://www.pnas.org/doi/abs/10.1073/pnas.0900906106
[4] https://www.pnas.org/doi/10.1073/pnas.2214070119

MICRODELETION-MICRODUPLICATION SYNDROMES

Microdeletion and microduplication syndromes (MMS) often involve intellectual disability, autism spectrum disorders, dysmorphic features and/or multiple congenital anomalies. The recurrent ones have been characterized quite well. However, there is no available comprehensive resource for the many rare non-recurrent MMS.
In their paper in BMC Genomic Data, Wetzel and Darbro provide a comprehensive list of MMS that have been reported in the medical literature to date, sorted by their genomic location.
This centralized and well detailed resource could be of help to those who are involved in clinical genomic testing.

[1]https://bmcgenomdata.biomedcentral.com/articles/10.1186/s12863-022-01093-3

REJUVENATION

It is difficult to understand the causes of aging. Accumulation of mutations appears to be the most valid explanation. An indirect proof is provided by the observation that the difference in lifespan between different species is correlated to the difference in their mutation rate (see post of July 13, 2022, Mutation Rate and Lifespan).
It is known that the Cnidarian *Turritopsis dohrnii* maintains its high rejuvenation potential (up to 100%) in the post-reproductive stages, i.e. it is immortal. Its congener *Turritopsis rubra* is not immortal.
Pascual-Torner et al.[1] (PNAS) compared the genomes of these two species in search of an explanation for the difference. They have not come up with a definitive answer, but they have identified a number of genes and a number of differences in their expression that will help solve the problem.
In this context, see also the post of November 16, 2022, Aging and Age reversal.

[1]https://www.pnas.org/doi/abs/10.1073/pnas.2118763119?url_ver=Z39.88-2003&rfr_id=ori%3Arid%3Acrossref.org&rfr_dat=cr_pub++0pubmed

NUCLEAR LOCATION FORETELLS CHROMOSOME ANOMALIES

It is well known that chromosomes occupy distinct territories inside the nucleus, and that this arrangement is not random. However, the origin and the biological impact of this topographic setting is far from being fully understood.
The study by Sjoerd Lkaaseen et al.[1]: "Nuclear chromosome locations dictate segregation error frequencies" published in Nature sheds light on the consequences of the topographic location inside the nucleus on chromosome segregation. The authors nicely demonstrate that peripheral chromosomes need more time to congress to the metaphase plate, and that this delayed timing is correlated to an increase in frequency of non-disjunction.
Hence, they provide evidence linking 3D positioning of chromosome territories and frequency of segregation error for different chromosome pairs which may play a role in genome evolution during development and tumorigenesis.
These results are in line with the observation that absence of clustering of chromosomes at the interface between the two pronuclei after fecundation is associated with a delayed congression because of greater distance to the metaphase plate, an increase in the number of lagging chromosomes, segregation errors and micronuclei formation (T. Cavazza *et al*[2]., *Cell* 184, 2860 (2021).

[1] https://www.nature.com/articles/s41586-022-04938-0
[2] https://www.sciencedirect.com/science/article/pii/S0092867421004920X

Educational External Quality Assessment (EQA) and competency programs for the global genetics community

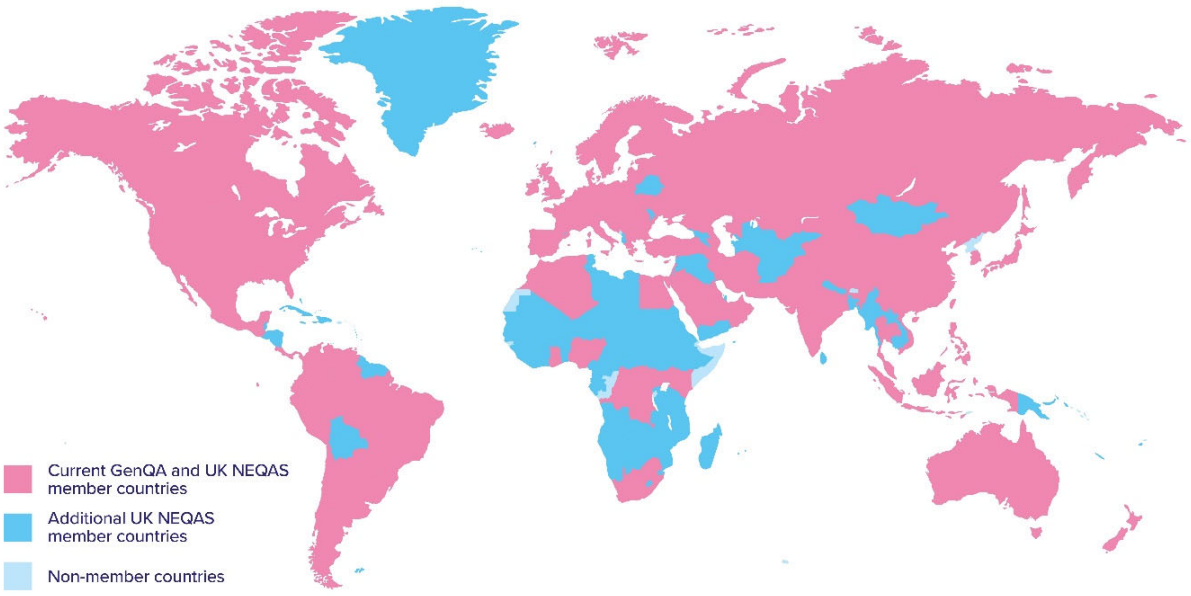
Ros Hastings, Fiona Morgan, Mark Sales, Katrina Rack, Melody Tabiner, Sandi Deans.

After the unprecedented last two years dealing with the effects of the COVID-19 pandemic, GenQA continues to respond to participant demand and the global expansion of genomic testing. There is so much work undertaken behind the scenes at GenQA that we thought we would share some of it with you.

Background

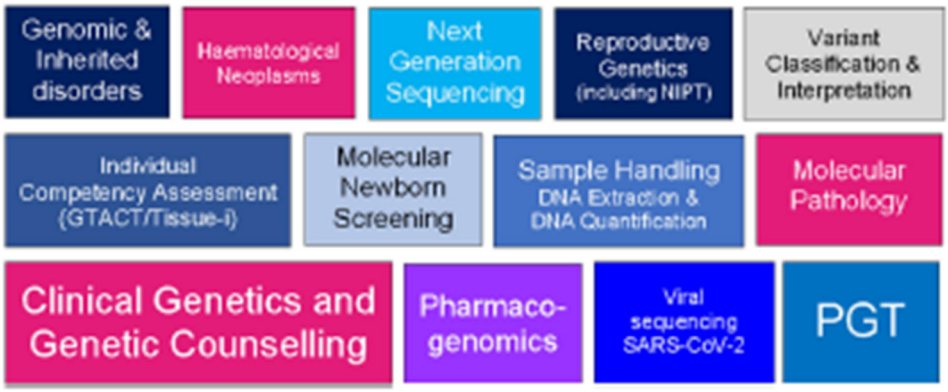
GenQA is the sole global external quality assessment provider to cover the entire clinical genomics service, from patient counselling, sample preparation, testing processes, results interpretation, and reporting. We also offer individual competency testing.

With our extensive level of expertise, we are able provide 119 unique EQAs during 2023 encompassing all aspects of the sample/patient journey, from sample reception through to reporting, and even genetic counselling for a vast range of genomic disciplines. This gives us greater flexibility in providing genomic EQAs to both small specialist laboratories and larger facilities, whilst also catering for clinical geneticists and laboratory-based staff with our individual competency assessments. Wherever you or your laboratory/ clinical genetics centre is based, we can support you by providing relevant EQAs reflecting the rapidly expanding repertoire of genomic tests. We are proud to be meeting the needs of the genomics community across the world with currently 87 countries participating and submissions in English, French, German, Italian, Polish, Portuguese and Spanish supported.



Updating our comprehensive repertoire

Genomic medicine is evolving at a rapid pace and our comprehensive range of EQAs and individual competency assessments are continuously developed to ensure delivery of a service that is fit for purpose. EQAs are continuously modified to follow clinical pathways for specific clinical indications to reflect the change to testing strategies in laboratories. We are keeping pace with the implementation of new and evolving technologies such as liquid biopsy testing, non-invasive prenatal testing (NIPT), large gene next generation sequencing (NGS) panels, optical genome mapping (OGM) and whole genome/ exome sequencing. Our vast scientific knowledge, with the support of our expert assessors, ensures that we encourage best practice and improvements with the clinical laboratory sector at all levels.



EQAs cover 13 different disciplines, and have been expanded to address the challenge of variant interpretation (SNVs and CNVs in the pre/postnatal and somatic setting). The ISCN Accuracy EQA is another example of a new development which addresses the challenges of using standardised nomenclature for constitutional, neoplasia, FISH, region-specific, array and NGS case scenarios. Following both the variant classification and ISCN EQAs, a unique GenQA workshop or FOCUS is webinar was provided to discuss the expected results and inform participants which parameters or rules are appropriate when interpreting the results. The next ISCN workshop will be held in London, UK in March 2023. Attendance is free for GenQA ISCN Accuracy participants. To register your interest, please email info@genqa.org.

New pilot EQAs

GenQA continuously strive to expand their EQA repertoire, by introducing new pilot EQAs and updating the format of current EQAs, in response to advances to genomic testing strategies. Pilot EQAs are generally focussed on new and upcoming tests that laboratories are introducing and GenQA acts on participant feedback. There will be ten new pilots offered in 2023 covering preconception carrier screening, endometrial tumour testing, Optical genome mapping, extended pharmacogenomics testing and NIPT for *RHD* status to name a few. For a complete list of EQAs currently available go to www.genqa.org/EQA

Education and Scientific support

GenQA provide individual educative feedback tailored to your laboratory, as well as general recommendations to improve your performance and quality. Our participants receive a detailed EQA Summary report for each EQA in which they participate. This includes a summary of the findings from the EQA, guidance on improvements to their testing processes and/or clinical reports (if required) and reference to current professional guidelines and standards. EQAs often include educational cases to raise awareness of challenges which maybe encountered by laboratories. These cases are discussed in depth in the EQA Summary report.

We also provide several participant scientific meetings and workshops throughout the year, as well as presenting our work at many international conferences. Throughout 2022 GenQA provided 11 free online FOCUS ON webinars, which covered many different aspects of genomic diagnostics including:

- Meiotic segregation,
- Genomic testing for chronic lymphocytic leukaemia (CLL),
- Variant classification,
- NIPT,
- ISCN,
- Reporting guidelines,
- Quality.

Participants who attend a FOCUS ON webinar receive an attendance certificate for their own continued professional development records, and our webinars are also made available at a later date via our GenQA YouTube channel. (www.youtube.com/GenQA)

We have an enormous amount of scientific and diagnostic laboratory experience within the team which is reflected in the number of our peer reviewed publications, poster and platform presentations at many international conferences, workshops, participant meetings and the standard of the EQA Summary Reports provided. GenQA staff present at these events both in the UK and abroad, to further educate scientists, laboratory staff, and clinicians regarding the importance of

external quality assessment. We often have a GenQA stand at conferences and we always welcome attendees to come and say 'hello'. More details can be found at www.genqa.org/events or www.genqa.org/publications

About GenQA

GenQA is a member of the UK NEQAS Consortium, which with over 50 years international quality expertise, offers EQAs in all aspects of medical testing. GenQA itself, operates under the legal entity of Oxford University Hospital National Health Service (NHS) Foundation Trust and is provided from two sites (Edinburgh and Oxford). GenQA's EQAs are accredited to ISO/IEC 17043:2010 by United Kingdom Accreditation Service (UKAS) proficiency testing, and a current list of accredited EQAs can be viewed on our UKAS scope (www.ukas.com.find-an-organisation/) or on our website (www.genqa.org). Our 19 pilot EQAs are not accredited while the logistics and marking criteria are robustly scrutinised.

The UK NEQAS consortium is the commissioned EQA supplier for NHS England funded genomic tests included in the 'National Genomics Testing Directory' since 2019. GenQA provides the majority of these EQAs.

GenQA is a not-for-profit organisation and therefore the fee structure is set to cover costs of running the Scheme. Such fees are annually reviewed to take into account the actual cost of delivery of the service and are often decreased in response to changes in the EQA format e.g., if the number of samples are reduced per distribution. GenQA is fully aware of financial constraints within participating laboratories and endeavours to minimise the cost of EQA participation.

Additional support

For laboratories who are new to external quality assessment or have received a poor performance status in an EQA, GenQA are able to offer tailored support to ensure the laboratory can provide the highest quality of testing. This may take the form of providing additional samples for testing, or review of their testing methodologies. GenQA also offers additional financial support for laboratories from Evolving Economies.

We would be delighted to assist you in your provision of high quality genomic diagnostic testing, so if you require further information regarding any aspect of our EQAs and educational provision, please, please email us on info@genqa.org, or visit our website (www.genqa.org). We are also active via our social media platforms including Twitter (www.twitter.com/GenQA) and Linkedin (https://www.linkedin.com/company/genqa/) where we provide updates and highlights of interesting developments and news in the genomics world.

Call for suggestions for the next version of ISCN

Dear all

The ISCN Standing committee is inviting the genetics community to send their suggestions for required changes to ISCN 2020. All suggestions should be placed on the Forum https://iscn.karger.com (you will need to sign in first) or alternatively you can send them by email to ros.hastings@genqa.org

The ISCN Standing Committee (ISCN SC) is preparing nomenclature for Optical Genome Mapping (OGM) which will be sent out for consultation to the wider genetic community prior to incorporation within the next version of ISCN.

The deadline to submit any changes or additions to ISCN required is the 31st January 2023.

We look forward to hearing from you.

Kind regards
Ros Hastings
ISCN SC Chair

E.C.A. STRUCTURES

E.C.A. BOARD OF DIRECTORS

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COMMITTEE

ECC SCIENTIFIC PROGRAMME COMMITTEE

E.C.A. News

- As required by the statutes, a new committee was elected during the Board meeting in Goldrain in August 2022 (see minutes on page 16).
- The 2023 General Assembly of the E.C.A. with Board elections will take place on 3 July 2023, at 6:30 pm at Montpellier, France.
- Renewal of the Board in 2023: the following members are due for replacement or re-election in 2023 at the General Assembly: S. Artan (Turky), Joan Blanco Rodriguez (Spain), R. Hochstenbach (The Netherlands), K. Miller (Germany), F. Mitelman (Sweden).
- According to the statutes, lists for the board election may be sent to the President until 3 May 2023.
- The E.C.A. has a new address:
  European Cytogeneticists Association, 32 rue Guy Môquet, 92240 Malakoff, FRANCE

E.C.A. Fellowships

- The **E.C.A.** offers two **Fellowships** for each of the following courses:
  European Advanced Postgraduate Course in Classical and Molecular Cytogenetics
  to be held in Nîmes (France) March 2023 (see pages 18-19)
  Goldrain Course in Clinical Cytogenetics
  to be held in Goldrain Castle (South Tyrol, Italy) 22-28 August 2023 (see page 21)
- The fellowships **include the course fees and the accommodation** during the lectures in Nîmes or in Goldrain but **do not include travel expenses** for either of the courses or for accommodation during the practical training for the Nîmes course. Applications with CV, list of publications and a letter of support should be addressed to the appropriate course organizer. The Educational Advisory Council of the E.C.A. will select the successful candidates.
- **European Cytogenomics Conference 2023** in Montellier: Five poster prizes will be awarded to participants who present the best posters on work derived from a thesis or from a degree awarded between 2021 and 2023. In addition, the E.C.A. offers five Fellowships and free registration for early-career researchers presenting posters or talks at the Conference.

MINUTES OF THE E.C.A. GENERAL ASSEMBLY, GOLDRAIN, AUGUST 2022

Minutes of the E.C.A. General Assembly held on 25th August 2022 in the Goldrain Castle, Italy.

All active members were invited to the General Assembly. Six members of the Association were present.

The President Mariano Rocchi opened the Assembly at 18.30 and welcomed those attending.

The voting for board members was closed and the Treasurer and a member of the Association, Dr Soley Bjornsdottir, neither associated with the candidates, were appointed to count the ballots.

The Minutes of the General Assembly meeting held Wednesday 1st September 2021 in the Grand Rosa Hotel, Milan, Italy, and published in the Newsletter NL49 page 14 were approved.

The General Secretary presented the state of the society. Membership was very satisfactory with new members joining. The ECA European Cytogenomics Congress ECC2021 (held before the 2021 General Assembly) online was well-attended and attracted 358 people from 52 countries (86% from Europe), with 146 posters, 9 oral presentations and 17 invited lectures.

The President announced the results of the ballot for election of Board Members. A total of 47 votes (including those received by mail) were received; 47 voted 'yes' and the list comprising Heslop-Harrison, Lavabre-Bertrand, Madan, Pinto Leite and Rieder was duly elected.

The Treasurer reviewed the finances of the ECA. for 2021 and presented working figures showing a modest surplus. The exigencies of the pandemic had not had a serious adverse effect. The reserves of the Association were sufficient to ensure the stability of the Association and in line with the financial policy to cover meetings, courses, and other activities. The General Assembly approved the accounts as presented.

The General Secretary and President thanked the Treasurer for the presentation and for his excellent work as Treasurer noting he had served since 2009 and will not be standing for re-election as Treasurer.

The impact of the Social Media activity organized through the President was recognized and agreed to be valuable. The Facebook page, named Cytogeneticists (https://www.facebook.com/Cytogeneticists) is very active with regular posts of interest to members. The Association Website www.e-c-a.eu with announcements and newsletters has also been kept updated. The outgoing General Secretary agreed to continue as Editor of the Newsletter, and was thanked.

The Association greatly appreciated the 22 years of service from the General Secretary who will not be standing for re-election.

There being no other business, the President closed the General Assembly at 19.00.

MINUTES OF THE E.C.A. BOARD MEETING, GOLDRAIN, AUGUST 2022

Minutes of the E.C.A. Board meeting held on 25th August 2022 in the Goldrain Castle, Italy.

The Board Members present were:

In person: Jean-Michel Dupont (Outgoing Treasurer), Konstantin Miller (Outgoing General Secretary), Mariano Rocchi (President), Kamlesh Madan (First Vice-President), Pat Heslop-Harrison (Second Vice-President); Via Zoom Videoconference: José M. Garcia-Sagredo, Roberta Vanni, Sevilhan Artan, Juan Blanco, Felix Mitelman.

Apologies and delegations of votes were received from Rosário Pinto Leite, Harald Rieder, Ron Hochstenbach, Thierry Lavabre-Bertrand, Elisabeth Syk-Lundberg.

The President Mariano Rocchi opened the meeting at 19:05 and welcomed those attending.

1. Minutes

The Minutes of the Board meeting held Wednesday 1st September 2021 in the Grand Rosa Hotel, Milan, Italy, and published in the Newsletter NL49 page 14 were approved.

2. Reports

The General Secretary reviewed the outcome of the General Assembly held immediately prior to the Board meeting. The Board was informed about the outcome of the Board Election. The General Secretary presented figures for the Association membership and outcome of the ECC Online Congress.

The list of new members was approved.

3. Committee election

The positions of Officers had been extended from 2021 to 2022 because of the pandemic.

The President, First and Second Vice-Presidents were eligible and willing to be re-elected. The General Secretary reported that he will not be standing for re-election. The Treasurer had agreed to be nominated as General Secretary and would therefore not continue as Treasurer. Thierry Lavabre-Bertrand agreed to be nominated as Treasurer. The Board elected the Officers of the Association as follows:

Mariano Rocchi President
Kamlesh Madan First Vice-President
Pat Heslop-Harrison Second Vice-President
Jean-Michel Dupont General Secretary
Thierry Lavabre-Bertrand Treasurer

Those elected and re-elected accepted the positions and were thanked.

4. ECA registered headquarters

The E.C.A. is a registered Association in France. The Board discussed a change in the registration address within France (domiciliation of the E.C.A.) due to the much increased cost at the present address. The Treasurer Jean-Michel Dupont presented a comprehensive analysis of the options with respect to costs, commitment/ time to change, and locality. The Board agreed to delegate the decision to the Treasurer, taking into account the legal and financial implications.

5. 14th European Cytogenomics Congress ECC2023

Possible venues for the ECC2023 conference were discussed, with seven sites in contention. There were considerable differences in costs and accessibility of the various Centres. Two were considered as "front-runners" and will be followed up bearing in mind complementation with other meetings, local support, accessibility, venues and costs.

6. Miscellaneous

The Board recognized the outstanding contribution of the outgoing General Secretary and thanked him for his remarkable contribution to the Association over the past 22 years. He has guided the Association to become the leading professional society for Cytogeneticists across the world, with enormous impact to all members from all different specialization. His dedication has allowed the Association to prosper with such successful Congresses, courses and Newsletters, and ensured the Governance has met the highest standards.

The next Board meeting is planned in Nimes, France in March 2023 in conjunction with the E.C.A. European Advanced Postgraduate Course in Classical and Molecular Cytogenetics. The next General Assembly will be organized in conjunction with ECC2023.

The President closed the Board meeting at 20.10.

Université de Montpellier
Faculté de Médecine
Montpellier-Nîmes

EUROPEAN CYTOGENETICISTS ASSOCIATION (E.C.A.)
European Advanced Postgraduate Course in Classical and Molecular Cytogenetics

Director: Professor Jean-Michel Dupont, Paris - France

This course was started by Professor Jean Paul Bureau 25 years ago and has been held in Nîmes under his directorship until 2017. It is designed to provide advanced training in constitutional, haematological, and oncological cytogenetics to medical graduates, pharmacists, pathologists, biologists, health professionals and researchers, with an academic qualification. The students will be trained to identify genetic abnormalities for diagnosis and prognosis, and for fundamental and applied research using both classical and molecular cytogenetic techniques. The course is co-organized by E.C.A. and two French Universities.

Registration

You can select either

- Basic diploma : only the lectures and a final online examination
- Advanced diploma : same lectures + 2 months training in a cytogenetic laboratory, and onsite final examination in Paris

For registration, please send a letter of application with your CV to the organizers, Prof. Jean-Michel DUPONT (jean-michel.dupont@aphp.fr) or to Prof. Thierry LAVABRE-BERTRAND (thierry.lavabre-bertrand@umontpellier. fr).
The registration fee to be paid by participants is €884. For payment by institutions and for more information, please contact the organizers.

Accommodation

A **special** price is available for participants in the 4* Vatel hotel close to the course venue (https://www.hotelvatel.fr/en/nimes) . We highly recommend that all participants stay in this hotel where all the lecturers will be hosted in order to promote interactions during the course.

Scholarships

E.C.A. will award two scholarships covering the registration and accommodation fees. The Education Committee of the E.C.A. will select the suitable candidate.
Scholarship will not be awarded to students whose registration is paid by a third party institution

Topics

Technical Aspects: *Classical Cytogenetics:* Cell culture techniques; Chromosome staining methods (Q-, G-, C-, R- banding and high resolution banding); *Molecular Cytogenetics:* Methods and principles of Fluorescence In Situ Hybridization (FISH) and MFISH; Array CGH; Application of Massively Parallel Sequencing to Cytogenetics; Production and use of molecular probes; Database use in Cytogenetics; *Laboratory quality assessment.*

Clinical cytogenetics: *Basics:* Frequency of chromosome disorders; Cell cycle, mitosis and meiosis, gametogenesis; Heterochromatic and euchromatic variants; Numerical chromosome abnormalities; Structural abnormalities: translocations, inversions, insertions, deletions, rings, markers; Risk assessment for balanced abnormalities; X inactivation; numerical and structural abnormalities of the X and the Y; Mosaicism; Chimaeras; ISCN 2020; *Clinical:* Phenotype of common autosomal and gonosomal aneuploidies; Chromosome abnormalities in recurrent abortions; Cytogenetics and infertility; Microdeletion syndromes; Uniparental disomy and its consequences; Genomic imprinting; Genetic counselling and ethical issues in cytogenetics; *Prenatal diagnosis:* Indications, methods and interpretation; Risk assessment for chromosomal abnormalities; Non-invasive methods using foetal nucleic acids and foetal cells in maternal blood; Pre-implantation diagnosis; *Cancer* Cytogenetics: Molecular approach to cancer cytogenetics; Predisposition to cancer, Chromosome instability syndromes; Chromosome mutagenesis; Solid tumors; Clinical application in onco-haematology.

Other topics: Genome architecture; Structure of chromatin; Structure of metaphase chromosomes, Mechanisms of chromosome abberations; Origin of aneuploidy; Evolution and plasticity of the human genome; Animal cytogenetics; Plant cytogenetics.

EUROPEAN CYTOGENETICISTS ASSOCIATION (E.C.A.)

European Advanced Postgraduate Course in Classical and Molecular Cytogenetics

Director: Professor Jean-Michel Dupont, Paris – France

The course is scheduled to be held in Nîmes, France 20-26 March 2023.

2023 Course provisional programme

This approximately 55-hour theoretical part of the course attempts to cover the field of cytogenetics in the broadest sense. The topics can be divided into the following categories:

Technical aspects:

Classical Cytogenetics: Cell culture techniques; Chromosome staining methods (Q-, G-, C-, R-banding and high-resolution banding);

Molecular Cytogenetics: Methods and principles of Fluorescence In Situ Hybridization (FISH) and MFISH; Array CGH; Application of Massively Parallel Sequencing to Cytogenetics; Production and use of molecular probes; Database use in Cytogenetics;

Laboratory quality assessment.

Clinical cytogenetics:

Basics: Frequency of chromosome disorders; Cell cycle, mitosis and meiosis, gametogenesis; Heterochromatic and euchromatic variants; Numerical chromosome abnormalities; Structural abnormalities: translocations, inversions, insertions, deletions, rings, markers; Risk assessment for balanced abnormalities; X inactivation; numerical and structural abnormalities of the X and the Y; Mosaicism; Chimaeras; ISCN 2020.

Clinical: Phenotype of common autosomal and gonosomal aneuploidies; Chromosome abnormalities in recurrent abortions; Cytogenetics and infertility; Microdeletion syndromes; Uniparental disomy and its consequences; Genomic imprinting; Genetic counselling and ethical issues in cytogenetics.

Prenatal diagnosis: Indications, methods and interpretation; Risk assessment for chromosomal abnormalities; Non-invasive methods using foetal nucleic acids and foetal cells in maternal blood; Pre-implantation diagnosis.

Cancer Cytogenetics: Molecular approach to cancer cytogenetics; Predisposition to cancer, Chromosome instability syndromes; Chromosome mutagenesis; Solid tumors; Clinical application in onco-haematology.

Other:

Genome architecture; Structure of chromatin; Structure of metaphase chromosomes, Mechanisms of chromosome abberations; Origin of aneuploidy; Evolution and plasticity of the human genome; Animal cytogenetics; Plant cytogenetics.

Report of the 15th Goldrain Course in Clinical Cytogenetics 2022

This year the highly coveted Clinical Cytogenetics course overcame the pandemic woes and was held in person at the Goldrain Castle which is nestled amidst the lush green hills of South Tyrol, Italy. Challenging though it was to reach the remote destination, the journey was worth the effort as the attendees were welcomed by sunshine, miles of apple orchards, small rivers and fresh air.

It was an extensive, gruelling and an in-depth 7-day course linking classical, molecular and clinical aspects of genetics. The topics covered a wide range of clinical scenarios (chiefly-prenatal, neonatal and postnatal); technologies such as karyotyping, FISH, QF-PCR, MLPA, oligonucleotide microarrays and sequencing; challenging cases which often arise through complex genetic constitution. This unique course was peppered with hands-on workshops that helped deepen our understanding derived from the lectures. Workshops that help in delineating segregation of chromosomal translocations, interpretation of microarray results, querying databases on the significance of a given variant, and ensuring the highest standards of quality control and reporting are rare to come by. However, the course covered all of these topics under hands-on workshops sessions.

The course also provided an open forum for students to present their rare, challenging and interesting clinical case(s). This was done to encourage students to learn the art of presentation and carry out discussions which can help them in the future. Several students participated in this forum and three students won awards for the best presentation – two received exquisite local South Tyrolean wine and one received a beautiful book on the history and culture of South Tyrol.

A unique feature of this course was the presence of an atmosphere which allowed the attendees and the faculty to interact informally at breakfast, lunch, dinner and coffee breaks. The informal nature of the interaction made it easier to communicate and share ideas and advice effectively. On the 4th day of the course there was an excursion into the mountains that criss-cross the South Tyrol region. The attendees got a chance to let their hair down and enjoy the unblemished natural beauty that graces this region.

I am hugely grateful to all the speakers, especially Prof. Albert Schinzel, who organised the course and made it a grand success for everyone. To sum up, if anyone is seeking to gain an in-depth knowledge and hands-on experience of intersection between dysmorphology, cytogenetics and molecular genetics in a short time span, look no further!

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380015 Ahmedabad, INDIA

16th Goldrain Course in
Clinical Cytogenetics

August 22-28, 2023

European Cytogeneticists Association

SCHLOSS GOLDRAIN
Bildung und Kultur · Formazione e Cultura

DIRECTOR

A. Schinzel (Zurich, Switzerland)

PROGRAMME COMMITTEE

A. Schinzel, M.Rocchi, J-M. Dupont, K. Miller, A. Baumer, E. Klopocki

FACULTY

D. Bartholdi (Berne, Switzerland), A. Baumer (Zurich, Switzerland), P. Benn (Farmington CT, U.S.A.), J.M. Dupont (Paris, France), N. Kurtas (Florence, Italy), E. Klopocki (Würzburg, Germany), K. Madan (Leiden, The Netherlands), K. Miller (Hannover, Germany), R. Pfundt (Nijmegen, The Netherlands), G. van Buggenhout (Leuven, Belgium), M. Vismara (Zurich, Switzerland), J. Wisser (Zurich, Switzerland), O. Zuffardi (Pavia, Italy) and others

LOCATION

Goldrain Castle, Goldrain, South Tyrol, Italy
Website of the venue: **www.schloss-goldrain.it**

COURSE DESCRIPTION

The course is focused on phenotypic findings, mechanisms of origin and transmission, correlations of clinical patterns with chromosomal imbalance and modern ways of diagnosis of the latter. Special attention is paid to an understanding how deletions and/or duplications of chromosomal segments cause developmental defects. The course also addresses the optimal application of the diagnostic possibilities, both pre- and postnatally and including molecular cytogenetic methods for a precise determination of segmental aneuploidy.

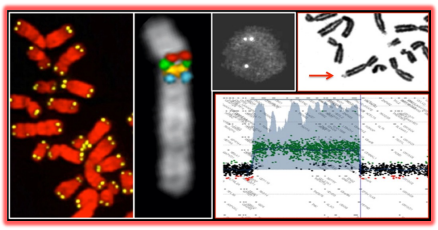
TOPICS

Dysmorphic findings in chromosome aberrations: formation and interpretation – The adult and elderly patient with a chromosome aberration – Follow-up studies in patients with chromosome aberrations – Clinical findings associated with chromosome aberrations – Microdeletion syndromes: clinical pictures – prenatal cytogenetic diagnosis – Mosaics and chimeras – imprinting and uniparental disomy - Epidemiology of chromosome aberrations – Chromosome aberrations in spontaneous abortions and stillborns – Harmless chromosome aberrations – Risk assessment in structural chromosome aberrations Extra small supernumerary chromosomes – Genomic variation: a continuum from SNPs to chromosome aneuploidy – Pre-implantation cytogenetic diagnosis – Ultrasound findings indicative of chromosome aberrations – Ethical issues in the context of cytogenetic diagnosis – Non-invasive prenatal cytogenetic diagnosis.
ISCN - Practical exercises in cytogenetic nomenclature – Accreditation of cytogenetic laboratories - Accreditation of cytogenetic laboratories – Optimal use of available techniques in clinical cytogenetics – NGS – SNP arrays and Array-CGH: principles, technical aspects; evaluation of the results – MLPA - QF-PCR - FISH techniques and their interpretation – Introduction and practical exercises with database for phenotypical and variant interpretation - Students presentation of cases with difficult-to-interpret chromosome aberrations. Introduction to modern genetic editing techniques. - Practical exercises will be offered with the ISCN system for chromosome aberrations and with cytogenetic, genomic, and phenotypical databases.

- *Students will have the opportunity to present their own observations and cytogenetic findings which are difficult to interpret, and*
- *they will also have the opportunity to perform a test at the end of the course.*


2022 course

For further questions please write directly to Albert Schinzel at **schinzel@medgen.uzh.ch**



Full fee is Euro 1600 for a single room or Euro 1450 (VAT included) in a 2-bed-room. It includes tuition, course material, free access to internet during the course, accommodation for 7 nights, all meals, beverages during the breaks and a ½ day excursion.