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***E.C.A. Newsletter**

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Editor of the E.C.A. Newsletter:

Konstantin MILLER
Institute of Human Genetics
Hannover Medical School, Hannover, D
E-mail: miller.konstantin@mh-hannover.de

Editorial committee:

J.S. (Pat) HESLOP-HARRISON
Genetics and Genome Biology
University of Leicester, UK
E-mail: phh4@le.ac.uk

Kamlesh MADAN
Dept. of Clinical Genetics
Leiden Univ. Medical Center, Leiden, NL
E-mail: k.madan@lumc.nl

Mariano ROCCHI
President of the E.C.A.
Dip. di Biologia, Campus Universitario
Bari, I
E-mail: mariano.rocchi@uniba.it

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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 4.
Please contact us (mariano.rocchi@uniba.it) if you wish to share an interesting news item or a pertinent article.

President's Address

Dear ECA members and friends,

I am happy to announce the next ECA conference:

The 15th European Cytogenomics Conference will be held in **Leuven, Belgium**, **29 June - 1 July, 2025**. Here are some details:

Innovative Format
We are evolving the conference format to include a series of **pre-conference workshops** designed to provide hands-on experience and in-depth knowledge on specialized topics.

Program Highlights
Several eminent scientists have agreed to contribute their expertise in various fields of cytogenomics, complemented by presentations in developing areas.

The meeting covers all aspects of chromosome and genome biology as well as clinical cytogenomics. The scientific sessions cover **technological advances** in long and short read sequencing, in situ sequencing, methylation analysis, multi-omics, single cell omics, cfDNA analyses; **fundamental aspects of genome biology** including centromere organization and evolution; telomeres and genome aging, animal and plant cytogenomics, structural variation, chromatin structure, the origins and evolution of aneuploidy in cancers and chromosomal disease mechanisms; microplastic genome toxicity; **clinical progress** including constitutional and acquired cytogenetics; preimplantation and prenatal diagnosis; AI in cytogenomics and medicine.

Permanent Working Group workshops will include presentations on topical issues, large project outcomes, and introductions to cytogenomic websites and databases.

Participants are invited to present their findings as posters, with some selected for presentation during the conference sessions and workshops. There will be many opportunities for early-career scientists to make presentations and be involved in discussions.

Registration
Registration details and early bird discounts will be available soon on our conference website (https://www.e-c-a.eu/EN/). Be sure to secure your spot early to take advantage of these offers.

I would like to take this opportunity to remind you about the two courses that are managed by ECA.

The 17th Goldrain Course in Clinical Cytogenetics takes place in the Goldrain castle in South Tyrol, Italy, **20-26 August, 2024**. The course was founded by Prof. Albert Schinzel and since last year is supported and organized by ECA. Scholarships are offered to cover registration and accommodation fees. There are no more places available for this year; stay tuned for next year (http://www.biologia.uniba.it/SEC/).
For further details, please contact Prof. Albert Schinzel (schinzel@medgen.uzh.ch) and myself (mariano.rocchi@uniba.it).

The Nîmes course (European Diploma in Classical and Molecular Cytogenetics) is scheduled for **24-30 March 2025**. Registration closes on January 31, 2025; details can be found at http://www.biologia.uniba.it/SEC/. ECA is offering two scholarships for the course, covering registration and accommodation fees. For more information and registration, please contact Prof. Jean-Michel Dupont (jean-michel.dupont@aphp.fr) and/ or Prof. Thierry Lavabre-Bertrand (thierry.lavabre-bertrand@umontpellier.fr).

Kind regards,

Mariano Rocchi
E.C.A. President

In memoriam: Maj Hultén

The prominent and internationally renowned clinical geneticist Maj Hultén died on May 29, 2024 at the age of 91. She was awarded an honorary membership of the E.C.A. in 2011 in recognition of her major contribution to meiotic studies and the mechanisms of origin of genetic disease as well as for running a major genetic diagnostic service for many years. Maj was an esteemed member of and a contributor to the E.C.A.

Maj Hultén was born on August 10, 1932 in Lund, a small university town in the southern part of Sweden. Already as a child she was fascinated by the unusual looking children that lived in a nearby institution, and wondered what could cause such problems. She later decided to study psychology and education at the University of Stockholm, and in addition genetics - which at that time mainly concerned bacteria, fruit-flies, plants and statistics.

During her final year in 1955, she had to make a special three months project and managed to get Professor Albert Levan to be her supervisor. In his lab, beautiful spreads of human chromosomes were made by the visiting scientist Dr Joe-Hin Tjio. Maj was invited to look at them under the microscope and was immediately hooked. She decided to study medicine, hoping that Medical Genetics would one day become a discipline, where the study of chromosomes would play an important part. In 1974, she defended her thesis "Cytogenetic aspects of human male meiosis" at Karolinska Institutet in Stockholm, and soon thereafter moved to Great Britain to fill the post of Clinical Director of the West Midlands Regional Genetics Laboratory and Consultancy Service, where she stayed from 1975 to 1997.

From 1991, Maj devoted a lot of her time to UNIQUE - Rare chromosome disorder support group, as a board member and Chief Medical Advisor. The aim of this group is to promote awareness of the effects of chromosome disorders, not only for the medical and scientific societies, but also for the patients and their families. Maj enthusiastically chaired the E.C.A Permanent working group on Meiosis, sharing her vast knowledge of the basic principles as well as the latest news on the subject with anyone who wished to participate.

Maj's research was devoted to studies on patterns of meiotic recombination in human males and females; she continuously incorporated novel technology as it developed over the years. She was appointed honorary professor in Medical Genetics and Reproductive Genetics at the University of Birmingham in 1989. After her retirement in 1996 she moved her activities to the University of Warwick where she was also an honorary professor; finally she became professor emeritus at Karolinska Institutet in 2010. In her last active years her main interest was chromosomal mosaicism. "Trisomy 21 mosaicism: we may all have a touch of Down syndrome" was the ingenious title of one of her last works.

Maj was a very talented, colorful, challenging, inspiring and funny person who was not afraid to express her opinions - few who met her will forget her.

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.

MEIOTIC CROSSOVERS AND ANEUPLOIDIES IN PGT

Meiotic crossovers are important not only in generating diversity but also also for ensuring the correct segregation of chromosomes. The relationship between the lack of meiotic crossovers and aneuploidies has been investigated using different approaches. Ariad et al. (1) derived sex-specific recombination landscapes using sequencing data from 18.967 preimplantation genetic testing for aneuploidy. Their methodological approach is able to exploit even relatively low-coverage sequencing (<0.05×). Note that monosomic chromosomes or uniparental isodisomy are phased by default. They found a reduced total length of the female genetic map in trisomies compared with di-somies, as well as chromosome-specific alte-rations in crossover distributions. In addition, their data indicate chromosome-specific propen-sities for different mechanisms of meiotic error.

[1]https://genome.cshlp.org/content/early/2024/01/17/gr.278168.123.long

HLA FUNCTIONAL DIVERSITY AND HIV

As a simple evolutionary rule, the higher an individual's heterozygosity, the better! In particular, HLA heterozygosity is linked to better outcomes of HIV infection, possibly because it allows the immune system to present a wider range of HIV-related elements to fight the virus. However, not all combinations of gene versions are equally effective in presenting these elements. Viard et al. (1) moved forward and created a measure called "functional divergence" to quantify how well different combinations of gene versions work together in presenting viral elements. They found that greater functional divergence in certain combinations was associated with slower progression to AIDS and better control of viral load. This measure predicts the effectiveness of the immune response at the level of specific viral elements, rather than just looking at the overall diversity of the genes.
The findings might also have implications for responses to other infections, vaccinations, immunotherapy, and other diseases where having diverse gene versions provides an advantage.

[1]https://www.science.org/doi/10.1126/science.adk0777

RISK OF MULTIPLE SCLEROSIS INHERITED FROM STEPPE PASTORALIST

A recent study on ancient DNA by Barrie et al. (1) suggests that genetic variants associated with the risk of multiple sclerosis (MS) were introduced to Europe approximately 5,000 years ago by herders, known as the Yamnaya, migrating from western Eurasia. These variants, which increased in prevalence over time, are **believed** to have conferred an evolutionary advantage, possibly by helping ancient populations combat pathogens. The study compared ancient DNA from Mesolithic and Bronze Age samples, as well as Medieval genomes, with modern DNA from the U.K. Biobank. The researchers propose that the MS-associated variants may have protected Yamnaya herders from diseases carried by their livestock. While these variants may have been advantageous in the past, they are now linked to an increased risk of MS, possibly due to changes in disease dynamics and advancements in healthcare over the millennia. The findings contribute to understanding the historical origins of MS and the impact of ancient migrations on genetic diversity in western Eurasia.
This is an additional example of “mismatch diseases”. As humans have transitioned from hunter-gatherer societies to modern, industriali-

zed societies, certain genetic variants that provided advantages in the past may now contribute to health issues in the current context.

[1] https://www.nature.com/articles/s41586-023-06618-z

GENOMIC HETEROZYGOSITY - LOWER RISK OF OSTEOARTHRITIS

A recent post stated "As a simple evolutionary rule, the higher an individual's heterozygosity, the better!" The post referred to a paper illustrating the relationship bezygosity and better outcomes of HIV infection (1). In a paper which appeared in BMC Genomics, Gill et al. (2) investigated the association between osteoarthritis (OA) and genomic heterozygosity. The research involved end-stage knee and hip OA patients, as well as healthy controls from Newfoundland and Labrador, (Canada) with validation from the Arthritis Research UK Osteoarthritis Genetics (arcOGEN) consortium database. DNA analysis revealed an inverse relationship between OA and genomic heterozygosity, indicating that reduced heterozygosity is a risk factor for developing OA.
This brings to mind an article from 2019 (3), with a self-explanatory title: "Genome-wide analysis indicates association between heterozygote advantage and healthy aging in humans".

[1] https://www.science.org/doi/10.1126/science.adk0777
[2] https://bmcgenomics.biomedcentral.com/articles/10.1186/s12864-024-10015-9
[3] https://bmcgenomdata.biomedcentral.com/articles/10.1186/s12863-019-0758-4

TOWARDS CONVERSATIONAL DIAGNOSTIC ARTIFICIAL INTELLIGENCE (AI)?

The title is exactly the title of a paper which appeared in arxiv.org (1) by Tu et al. (by Google Research), but without the question mark.
The paper received positive feedback from Nature on January 12, 2024 (2). However, concerns have been raised by the World Health Organization, warning about the potential risks of Medical AI for less affluent nations. This cautionary note was highlighted in a report by Nature on January 18 (3).
The need for feedback on outcomes was stressed in an article which appeared in JAMA (4).
Undoubtedly, AI's role in medicine will continue to be a significant focus, akin to its impact in other fields.

[1] https://arxiv.org/abs/2401.05654
[2] https://www.nature.com/articles/d41586-024-00099-4
[3] https://www.nature.com/articles/d41586-024-00161-1
[4] https://jamanetwork.com/journals/jama/fullarticle/2814610?utm_campaign=articlePDF&utm_medium=articlePDFlink&utm_source=articlePD

X-INACTIVATION AND AUTOIMMUNE DISEASES

Women account for around 80% of all cases of autoimmune disease. A Cell paper (1) explains why.
Xist long non-coding RNA (lncRNA) is expressed only in females to randomly inactivate one of the two X chromosomes to achieve gene dosage compensation. Xist ribonucleoprotein (RNP) complex, comprising numerous autoantigenic components, is an important driver of sex-biased autoimmunity. The study was performed on mice, but the authors found important confirmation in humans, where human female patients with autoimmune diseases displayed significant autoantibodies to multiple components of XIST RNP. Thus, a sex-specific lncRNA scaffolds ubiquitous RNP components to drive sex-biased immunity.

[1] https://www.cell.com/cell/fulltext/S0092-8674(24)00002-3?_returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0092867424000023%3Fshowall%3Dtrue

MOSAIC LOSS OF Y CHROMOSOME (LOY)

It has been known for many years that loss of the Y chromosome in males is associated with aging (1).

In a recent article Wilson et al. (2), using single-cell RNA and ATAC sequencing (Assay for Transposase-Accessible Chromatin with high-throughput sequencing sequencing) studied gene expression and Y loss in the kidney. Gene expression analysis revealed that a subset of kidney cells acquire a proinflammatory transcription profile, that these damaged cells have the greatest percentage of LOY, and their presence predicts future decline in kidney function.
Furthermore, they suggest applying their approach to other tissues.

[1]https://link.springer.com/article/10.1007/s00439-017-1799-2
[2]https://genomebiology.biomedcentral.com/articles/10.1186/s13059-024-03173-2

A HISTRORICAL REVIEW OF STRUCTURAL VARIANT DISCOVERY

Evan Eichler played a significant role in advancing the understanding of structural variants during the sequencing era. However, the exploration of structural variant discovery predates this era, commencing with cytogenetics.
In a recent paper (1), Eichler conducts a retrospective analysis of this narrative, emphasizing the current breakthrough achieved through the use of state-of-the-art long-read sequencing. He highlights the fact that we are now on the brink of achieving comprehensive variant detection across all forms of genetic variation using a single assay.
Some of these steps have been personally illustrated by Eichler during our past ECA conferences.

[1] https://www.cell.com/cell/fulltext/S0092-8674(24)00004-7?_returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0092867424000047%3Fshowall%3Dtrue

THE INTRIGUING STORY OF EPAS1 IN HUMAN GROUPS LIVING AT EXTREME ALTITUDES

In 2014 Huerta-Sanchez et al. (1) reported a study on altitude adaptations in Tibetans. The study confirmed previous studies that the *EPAS1* gene variant was subjected to Darwinian selection. The authors noted, intriguingly, that this variant was present in Denisovans (cousins of Neanderthals), thus hypothesizing that the variant was an introgression event.
But how did Denisovans acquire this adaptation? Did they also dwell at high altitudes? The answer arrived in 2019 when Chen et al. (2) unearthed a Denisovan mandible in the Tibetan Plateau (3.280m). While standard DNA sequencing was unusable, cutting-edge proteomic technologies (liquid chromatography and tandem mass spectrometry) revealed that the same protein variant found in Tibetans was present in the mandible. This finding strongly supported the hypothesis of Denisovan inheritance.
A recent article published in *Science Advances* (3) reports that a different variant of this same *EPAS1* gene is present in Andean highlanders living up to above 4.000 m.
Science comment: “The mutation in the same gene allows two different groups of humans to thrive at extreme altitudes”.

[1] https://link.springer.com/article/10.1007/s10577-007-1208-0
[2] https://www.nature.com/articles/s41586-019-1139-x
[3]https://genomebiology.biomedcentral.com/articles/10.1186/s13059-023-02912-1

UNDERSTANDING THE ROLE OF TRANSPOSABLE ELEMENTS IN THE HUMAN GENOME

In the beginning, the human genome was sharply divided between gene-coding sequences, which comprised just ~2%, and the rest, apparently non-functional junk DNA composed mostly of transposable elements (TEs). This prevailing perspective has served as the primary objection to sequencing the entire human genome.
Gradually, perspectives changed. The ENCODE consortium, aptly called the Encyclopedia of DNA Elements, revealed that approximately 20% of our genome is made up of regulatory elements, and that at least 25% of these regulatory elements are TE or derived from them. “At least” indicates that the annotations concern nearly intact TE

elements, with the more degenerate ones (the older ones) being particularly difficult to identify. In this respect, the availability today of hundreds of sequenced animal genomes can prove extremely helpful. In fact, the reconstruction of the evolutionary history of an unknown sequence can be crucial to identify it as a TE-derived sequence. This is exactly what Matsushima et al. reported in a recent article in Cell Genomics (1). They discovered previously unannotated degenerate TEs by analyzing multiple reconstructed ancestral genomes from hundreds of species. They achieved a 10.8% increase in coverage compared to the most recent annotation.

In this context it is worth reporting a paradigmatic example in which tracing the evolutionary history of TE elements has brought to light lost pieces of the recent history of our genome.

Imagine that a phrase from an ancient book has been erased in all surviving copies of the book. No one can even imagine the manipulation until the original, lost book containing the phrase is found.

Let's go back to the human genome. Homologous-nonallelic recombination (HNAR) can also occur between TE elements, particularly *Alu*. Indeed, Song et al. (2), studying a population of 54,000 subjects, identified 47 duplications and 40 deletions mediated by *Alu*/*Alu* HNAR. The deletions were easily identified as such because they were in a heterozygous state in the population.

In their 2006 publication, Sen et al. (3) argued that a deletion resulting from HNAR between *Alu* elements could go unnoticed once it became fixed in the population. To uncover these occurrences, the researchers conducted a comparative analysis between the human and chimpanzee genomes. They revealed 492 instances of such deletions, spanning a total of 400 kb. Notably, a majority of these deletions (295 out of 492) impacted known or predicted genes, providing evidence for potential evolutionary implications.

[1] https://www.sciencedirect.com/science/article/pii/S2666979X24000247

[2] https://genome.cshlp.org/content/28/8/1228.abstract

[3] https://www.sciencedirect.com/science/article/pii/S0002929707600159

BATS, VIRUSES AND INTROGRESSION

One hypothesis about the origin of COVID-19 is that the virus was transmitted by bats. Bats are known to harbor large numbers of such viruses and to tolerate them. Why does this happen? In a recent paper in Cell Genomics Foley et al. (1) try to explain why.

A step back: introgression refers to the movement of genes from one species to another through backcrossing. In this way each species can take advantage of the beneficial variants developed by the other species. Some human populations took advantage of the variants present in Neanderthals, who had much more time to adapt to the Northern Hemisphere, through backcrossing. Here are just two examples: variants of the genes for keratin filaments that confer resistance to cold inherited from the Neanderthals (2); the *EPAS1* variant present in Tibetans, inherited from the Denisovans, which made them capable of tackling high altitudes (3) (see the recent post on *EPAS1*).

Several closely related bat species frequently share a cave, at the entrance of which they gather during the mating season (the phenomenon is called swarming). This is an opportunity for multiple crossings or introgressions, leading to the accumulation, in each species, of the most efficient variants capable of coping with a wide variety of viruses.

[1] https://www.sciencedirect.com/science/article/pii/S2666979X23003348?via%3Dihub

[2] https://www.nature.com/articles/nature12961

[3] https://www.nature.com/articles/s41586-019-1139-x

EXPANDING GENOMIC RESEARCH TO INCLUDE ETHNIC MINORITIES REVEALS GREATER HUMAN DIVERSITY

The UK Biobank project is one of the largest human population genomic studies, done on 500,000 individuals. However, approximately 88% of these are people of European ancestry.

A similar project is underway in the United States ("All of us" project). The researchers have recently published their first results in Nature (1,

1b). The number of people included in this publication (245,000) is less than half of that in the UK Biobank study, but 46% of them belong to minority ethnic groups. The ethnic minorities have contributed substantially to the total of 275 million new genetic variants.

These results parallel the recent data on Australian indigenous people (2, 2b). The number of individuals analyzed is very small (159 individuals), but demographic history, including early divergence from the Papua New Guinea (about 47,000 years ago) and Eurasian groups, has generated a substantial percentage of variation that is not observed in global reference panels or clinical datasets

Please note: 'b' in the references refers to a comment by NATURE (under 'news') on the original article; it also constitutes a good summary.

[1] https://www.nature.com/articles/s41586-023-06957-x
[1b] https://www.nature.com/articles/d41586-024-00502-0
[2] https://www.nature.com/articles/s41586-023-06831-w
[2b] https://www.nature.com/articles/d41586-023-04006-1#:~:text=Indigenous%20Australian%20communities%20have%20the,genomes%20are%20from%20Indigenous%20Australians.

EVOLUTION OF HUMAN CENTROMERS

The first complete sequence of the human genome (telomere-to-telomere, T2T) (1) made use of long-reads technologies. Even these technologies, however, are not yet able to completely resolve the haploid arrangement of the centromeres of a diploid cell line. Indeed, the authors used a complete hydatidiform mole which, being the duplication of a human male haplotype, greatly simplified the task.

Many other human genomes have since been sequenced T2T, but centromeres had to be deliberately excluded from the analysis. As a result, whereas the precise variability of the euchromatic part of the human genome is continuously being refined, no progress has been made regarding the centromeres.

In an article published online in Nature (2), a sequence of the T2T genome of a second hydatidiform mole was published, focusing on the comparison of the centromeres of the two sequences. Additionally, samples of primate centromere sequences were also analyzed. The centromeres have been found to be the most rapidly evolving regions in primates and humans in particular. These results substantiate the evidence obtained from FISH experiments many years ago (3).

[1]https://www.science.org/doi/10.1126/science.abj6987?url_ver=Z39.88-2003&rfr_id=ori:rid:crossref.org&rfr_dat=cr_pub%20%200pubmed
[2]https://www.nature.com/articles/s41586-024-07278-3
[3]https://www.sciencedirect.com/science/article/abs/pii/088875439580048Q?via%3Dihub

LENGTH OF HUMAN TELOMERES

Short telomeres cause age-related disease and long telomeres predispose to cancer". This is the first sentence of the abstract of a recent article published by Karimian et al. in Science (1). As highlighted in earlier posts, the "trade-off" situation is quite common in biology.

Using long-read sequence technology, the authors obtained unprecedented information on telomeres of 147 individuals. The main finding is that specific telomere length is conserved across individuals. Furthermore, the telomeres of 4q, 12q and 3p are the longest, while those of 17p, 20q and 12p are the shortest, and these differences are already present at birth.

[1]https://www.science.org/doi/10.1126/science.ado0431?url_ver=Z39.88-2003&rfr_id=ori:rid:crossref.org&rfr_dat=cr_pub%20%200pubmed

SKEWED X-INACTIVATION

In mammalian females one of the two Xs is inactivated in early embryogenesis. This explains how gene expression is balanced between XX females and XY males (the Lyon hypothesis, Mary Lyon, 1961)[1]. The inactivation randomly affects the maternal or the paternal X and is then clonally transmitted. So, it is expected that in 50% of the somatic cells the maternal X and in the other 50% the paternal X is active. Example of active and inactive X-linked gene is shown in

Figure 1A. In individuals carrying more than two Xs, all except one are inactivated (see Figure 1B). We now know that a gene, *XIST,* mapping at Xq13, is responsible for the inactivation of the X and that about 20% of genes on the X escape inactivation. We also know that in ~25% of the females the pattern of X-inactivation is skewed. In some cases, as in carriers of X/autosome translocations, the normal X is inactive in all cells, and is most likely a result of cell selection. Assessing the presence of biased inactivation is not simple. Fadra et al. 2024[2] have published an effective method for estimating the X inactivation status. They suggest that it can be useful in cases of females presenting with possible rare inherited disorders, and, of course, for determining X-skew in common X-linked disorders.

[1] https://www.nature.com/articles/190372a0
[2]https://bmcgenomics.biomedcentral.com/articles/10.1186/s12864-024-10240-2

UNLOCKING THE GENETIC SECRETS OF MALE INFERTILITY BY EXOME SEQUENCING

In previous posts within this forum, we highlighted the potential of exome sequencing in understanding the genetic etiology of male infertility ("Male Infertility 07/03/2022" and "How to Select a Shortlist of Genetic Markers for Male Infertility? 15/01/2021"). In a new study published in The American Journal of Human Genetics1, the authors delve into this question, analyzing 638 genes linked to male infertility in a group of 521 men with primary spermatogenic failure, including men with congenital hypogonadotropic hypogonadism (CHH).
Pathogenic and Likely pathogenic variants were uncovered in 12.3% of patients, regardless of their specific infertility conditions like azoospermia or oligozoospermia. This figure rose to 17% in the CHH group, a previously unreported result in this patient cohort. From the gene perspective, the study identifies disease-causing variants in 6% of the analyzed genes, including variants in genes not previously associated with male infertility. Some individuals even harbored multiple gene variants, adding more complexity to the puzzle. In another layer of the study, findings revealed that men with genetic infertility face a fourfold higher risk of early-onset cancer compared to the general population.
Overall, this study demonstrates, once again, the value of exome testing in male infertility diagnosis and management. With one in eight men receiving a molecular diagnosis, it's clear that genetic insights are pivotal in guiding personalized treatment strategies and early detection of potential health risks.

[1] Lillepea et al., Toward clinical exomes in diagnostics and management of male infertility, The American Journal of Human Genetics (2024), https://doi.org/10.1016/j.ajhg.2024.03.013

EXPERIMENTAL ANEUPLOIDY IN CANCER

Oncogene or suppressor gene mutations are well studied in cancer. Less is known about aneuploidies because they are less tractable in experimental procedures. Watson et al., in a paper in Nature Genetics (1), have tried to fill this gap. They used normal mammary and renal epithelial cells, immortalized by forcing overexpression of telomerase. They then triggered aneuploidies by disrupting mitosis using reversine.
The complex results were extensively analyzed. The general conclusion the authors propose is that "intrinsic, tissue-specific proliferative effects underlie tumor copy number patterns in cancer".
In News&Views Guscott and McClelland (2) comment on the strengths and weaknesses of the work, and make suggestions for further experimental developments.

[1] https://www.nature.com/articles/s41588-024-01665-2
[2] https://www.nature.com/articles/s41588-024-01742-6

TELOMERE LENGTH AND HEALTH

Shortening of telomeres has been associated with cellular aging, and longer telomeres were initially reported to predict lifespan (1). Studies in animals show that the rate of shortening is probably more important.

Taking advantage of telomere length data in the UK Biobank, Moix et al. (2) delineate a comprehensive view of "causes, consequences, and mediating effects of telomere length variation on human health". Interestingly, the paper takes into consideration also lifestyle, and socio-economic factors.

The equally complex relationship between telomere length and tumors was not included in this paper. In another recently published paper, DeBoy et al. (3) report that "Telomere-lengthening germline variants predispose to a syndromic papillary thyroid cancer subtype".

[1] https://www.pnas.org/doi/full/10.1073/pnas.1113306109
[2] https://genomebiology.biomedcentral.com/articles/10.1186/s13059-024-03269-9
[3] https://www.cell.com/ajhg/abstract/S0002-9297(24)00121-6

BACTERIA THAT WRITE NEW GENES

Variability is fundamental to evolving (= surviving). It is provided by mutations and, in almost all eukaryotes, by sexual reproduction that generates infinite new gene combinations.

New genes can emerge almost out of nowhere, but such examples are extremely rare. The production of new genes generally occurs through gene duplication and independent evolution. In some animals (such as elephants) duplication of the olfactory receptor genes has reached a number of ~2,000.

When significantly higher variability is needed, different and exclusively somatic strategies are exploited. An example is the generation of millions and millions of different antibodies by complex somatic recombination. Such a large number of genes would be too heavy to store in a germline genome.

Bacteria use several defense mechanisms to fight invaders (essentially phages). Restriction enzymes and the adaptive CRISPR-Cas systems are among them.

In a paper in the bioRxiv (1), Tang et al. report an unprecedented workflow some bacteria use to create new defensive genes. The title of the paper reads: "De novo gene synthesis by an antiviral reverse transcriptase"; the sub-title of the comment to this paper which appeared in Nature (2) is: "Bacterial defensive systems scramble the standard workflow of life".

RNA viruses use the reverse transcriptase (RT) to convert their RNA genomes into DNA, enabling them to integrate into the genome of the host cell and replicate.

Tang et al. found that in some bacteria (Klebsiella pneumoniae was the one that was studied) an unprecedented RT produces, from a non-coding RNA, a very long in-frame cDNAs consisting of repeated, concatenated sequences with precise junction sequences, without a stop codon.

This newly created gene has been named Neo gene (Never ending open reading frame). The absence of a stop codon explains how the Neo gene has always gone unnoticed (annotators should annotate this detail).

Upon phage infection, this cDNA becomes double-stranded and triggers the expression of a novel protein, which induces cell dormancy, thus protecting the larger bacterial population from the spread of the phage.

This work "adds another layer of complexity to the ways in which protein-coding sequences can be stored in the genome".

The identities and functions of the Neo products remain largely unknown.

The last sentence of Darwin's The Origin of Species says "… from so simple a beginning, endless forms most beautiful and most wonderful have been, and are being, evolved"

[1] https://www.biorxiv.org/content/10.1101/2024.05.08.593200v1
[2] https://www.nature.com/articles/d41586-024-01477-8

AGING AND FITNESS

In 1957, Williams (1) proposed that mutations contributing to aging could be positively selected if they are advantageous early in life, promoting earlier reproduction or more offspring. This antagonistic pleiotropy hypothesis is now a leading theory on the evolutionary origin of aging.

Long and Zang (2) tested this hypothesis by mining the UK Biobank (276,406 individuals).

They found a strong, negative genetic correlation between reproductive traits and life span.

[1] https://onlinelibrary.wiley.com/doi/10.1111/j.1558-5646.1957.tb02911.x
[2] https://www.science.org/doi/10.1126/sciadv.adh4990

THE EXPLORATORY BEHAVIOR GENE

Curiosity is an essential characteristic of Homo sapiens, of scientists in particular: science is curiosity.
Preamble: Lake Tanganyika boasts over 250 cichlid species, each adapted to a specific ecological niche. Scientists have long been fascinated by this extraordinary level of diversification (speciation). Their research has explored various factors driving this phenomenon.
Is curiosity involved in this diversification? Researchers identified a specific genetic variant, an SNP, that appears to be linked to a "curiosity gene". Fishes with this SNP exhibit higher levels of exploratory behavior.
The paper appeared in Science (1). The discovery has aroused considerable curiosity; it is in the spotlight of Trends in Genetics (2). The presence of this gene in humans, as in all vertebrates, further fuels the paper's significance.
If you are of a curious nature: go to YouTube (3)

[1] https://www.science.org/doi/10.1126/science.adj9228
[2] https://www.cell.com/trends/genetics/abstract/S0168-9525(24)00148-3?_returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0168952524001483%3Fshowall%3Dtrue
[3] https://www.youtube.com/watch?v=wRvM6rQFsPU

22q11.2 DELETION AND MENINGOMYELOCELE

The Spina Bifida Sequencing Consortium examined 715 parent-offspring trios. Their paper, which appeared in Science (1), reports six patients with 22q11.2 deletion and meningomyelocele (MM). They calculated that the deletion confers a 23-fold increased risk of MM compared with the general population. In a distinct 22q11.2 deletion cohort the increased risk was of 12-15 fold.
In mice, the knock-out of the Crkl gene, mapping in the minimal deletion interval, was sufficient to replicate neural tube defects, where both penetrance and expressivity were exacerbated by maternal folate deficiency.
In this context it is worth reading the article by Zamariolli et al. (2), whose title is “The impact of 22q11.2 copy-number variants on human traits in the general population”, which took advantage of the 405,324 people composing the UK Biobank.

[1] https://www.science.org/doi/10.1126/science.adl1624
[2] https://www.cell.com/ajhg/fulltext/S0002-9297(23)00005-8?_returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0002929723000058%3Fshowall%3Dtrue

SCIENCE HAS NO DOGMAS

In an earlier post the paper by Klunk et al., published in Nature (1), was reported as a good example of a trade-off between evolution and diseases. The authors analyzed DNA from people living before, during and after Black Death in the London area and in Denmark. They found a strong selection for protective variants, particularly of the gene ERAP2 and suggested that individuals homozygous for this variant had 40% higher chance of survival! The authors concluded: “Finally, we show that protective variants overlap with alleles that are today associated with increased susceptibility to autoimmune diseases…”.
Now, a paper published in Science Advances by Hui et al. (2) reports a similar study in the Cambridgeshire area. They conclude: “we find no evidence of major changes in genetic ancestry nor higher differentiation of immune loci between cohorts living before and after the Black Death”.

[1] https://www.ncbi.nlm.nih.gov/pmc/articles/PMC9580435/
[2] https://www.science.org/doi/10.1126/sciadv.adi5903

CLONAL EXPANSION IN AGING

Replicating tissues accumulate mutations with age. Some mutations can confer a fitness advantage to a stem cell, leading to clonal expansion. The esophagus is the best studied tissue in this respect (1).
The data in the UK Biobank, as is usually the case with Biobank data, comes from blood samples. Berstein et al. (2) mined the 200,618 exomes available in the UK Biobank to identify genes subjected to positive selection. They identified 17 of these genes. Data were validated in 10,837 whole genomes from hematopoietic colonies derived from single cells. The results were correlated with clinical phenotypes, also available at the bank.
The authors note that studies of this kind are scarce, and that other proliferating tissues should be studied.

[1] https://www.nature.com/articles/s41588-021-00957-1
[2] https://www.nature.com/articles/s41588-024-01755-1

RNA AS PESTICIDE

For the most curious: oral RNA (interference) for the… potato beetle.
This paper by E.Stokstad (1), which appeared in Science under "Features", explains how RNA interference works in general, and as a pesticide for the potato beetle. RNA is sprayed on plants and the potato beetle ingests it orally. This terrible beetle is very resilient: "The pest was an early driver of research into chemical pesticides starting in the 1930s. Ever since, it has evolved immunity to one compound after another—now more than 50 pesticides, representing all major types of active ingredients". Darwinian selection.

[1] https://www.science.org/content/article/perfect-pesticide-rna-kills-crop-destroying-beetles-unprecedented-accuracy

TELOMERASE REACTIVATION AND TISSUE REJUVENATION IN MICE

As highlighted in earlier posts, the relationship between telomere length and aging has been extensively studied.
In a paper that appeared in Cell, Shim et al. (1) tested more than 600.000 compounds and found a small molecule acting as an activator of the *TERT* enzyme (*TERT* Activator Compound, TAC) in mice. *TERT* is responsible of the telomere elongation. Administration of TAC in very old mice produces relief from neuroinflammation in the brain, increases neurotrophic factors, stimulates adult neurogenesis; it also preserves cognitive function without obvious toxicity or an increase in cancer risk. The authors conclude that TAC "provide preclinical proof of concept for physiological *TERT* activation as a strategy to mitigate multiple aging hallmarks and associated pathologies".
It is important to note that the mitigation of aging via *TERT* reactivation was reported in 2022 by Jaskelioff et al. (2). However, in that study, the reactivation was achieved through genomic modification of the mice (conditional knock-in), which is obviously not feasible in humans.

[1] https://www.cell.com/cell/abstract/S0092-8674(24)00592-0?_returnURL=https%3A%2F%2Flinkinghub.elsevier.com%2Fretrieve%2Fpii%2FS0092867424005920%3Fshowall%3Dtrue
[2] https://www.nature.com/articles/nature09603

E.C.A. STRUCTURES

E.C.A. BOARD OF DIRECTORS

Joan BLANCO RODRIGUEZ
Unitat de Biologia Cel·lular
Dept de Biologia Cel·lular, de Fisiologia i d'Immunologia
Facultat de Biociències (Edifici C)
Univ. Autònoma de Barcelona
08193-BELLATERRA SPAIN
Tel. : +34 93 58 13 728
E-mail: joan.blanco@uab.cat

Jean-Michel DUPONT
Laboratoire de Cytogénétique
Hôpitaux Univ. Paris Centre
Hôpital Cochin -
Bât Jean DAUSSET 4e
27 rue du Fbg St Jacquesl
75014 PARIS
FRANCE
Tel.: +33 1 58 41 35 30
E-mail.:
jean-michel.dupont@ aphp.fr

José M. GARCIA-SAGREDO
Pabellón Docente, Med. Genetics
Univ. Hospital Ramon y Cajal
Carretera de Colmenar Km 9.100
28034 MADRID
SPAIN
Tel.: +34 91 33 68 550
E-mail:
jgarcias.hrc@salud.madrid.org

J.S. (Pat) HESLOP-HARRISON
Genetics and Genome Biology
University of Leicester
LEICESTER LE1 7RH
UK
Tel.: +44 116 252 5079
E-mail: phh4@le.ac.uk

Thierry LAVABRE-BERTRAND
Laboratoire de Biologie Cellulaire et Cytogenetique Moleculaire
Faculté de Médecine
Avenue Kennedy
30900 NÎMES
FRANCE
Tel.: +33 4 66 68 42 23
E-mail: tlavabre@univ-montp1.fr

Anna LINDSTRAND
Clinical Genetics and Genomics
L4:03
Karolinska University Hospital
17176 STOCKHOLM SWEDEN
Tel.: +46 705436593
E-mail: anna.lindstrand@ki.se

Kamlesh MADAN
Dept. of Clinical Genetics
Leiden Univ. Medical Center
P.O.Box 9600
2300 RC LEIDEN
THE NETHERLANDS
Tel.: +31 72 51 28 953
E-mail: k.madan@lumc.nl

Konstantin MILLER
Institut für Humangenetik
Medizinische Hochschule
30623 HANNOVER
GERMANY
Tel.: +49 511 532 6538
E-mail:
miller.konstantin@mh-hannover.de

Franck PELLESTOR
Unit of Chromosomal Genetics
Arnaud de Villeneuve Hospital
Montpellier CHU
34295 MONTPELLIER cedex 5
FRANCE
Tel.: +33 4 67 33 07 70
E-mail: fpellestor@yahoo.fr or
f-pellestor@chu-montpellier.fr

Maria Rosario PINTO LEITE
Cytogenetics Laboratory
Centro Hospitalar de Trás-os-Montes e Alto Douro
Av. da Noruega
5000-508 VILA REAL
PORTUGAL
Tel.: +35 1 25 93 00 500
E-mail:
mlleite@chtmad.min-saude.pt

Harald RIEDER
Institut fuer Humangenetik und Anthropologie
Universitaetsstraße 1
40225 DUESSELDORF
GERMANY
Tel.: +49 211 8110689,
E-mail:
harald.rieder@uni-duesseldorf.de

Mariano ROCCHI
Emeritus Professor
Dip. di Biologia
Campus Universitario
Via Orabona 4
70125 BARI
ITALY
Tel.: +39 080 544 3371
E-mail: mariano.rocchi@uniba.it

Elisabeth SYK LUNDBERG
Dept. of Clinical Genetics
Karolinska Hospital
17176 STOCKHOLM
SWEDEN
Tel.: +46 85 17 75 380
E-mail:
elisabeth.syk.lundberg@ki.se

Roberta VANNI
Dept. of Biomedical Sciences
Biochemistry, Biology and Genetics Unit
University of Cagliari
09142 MONSERRATO (CA)
ITALY
Tel.: +39 07 06 75 41 23
E-mail: vanni@unica.it

Meral YIRMIBES KARAOGUZ
Gazi University Medical Faculty
Department of Medical Genetics
Besevler
06500 ANKARA TURKEY
Tel.: +90 312 2024644
E-mail: karaoguz@gazi.edu.tr

COMMITTEE

ECC SCIENTIFIC PROGRAMME COMMITTEE

E.C.A. News

- The 2024 General Assembly of the E.C.A. with Board elections will take place on Thursday, 22 August 2024, at 6:30 pm at Goldrain Castle, Schlossstraße 33, 39021 Goldrain / South Tyrol, Italy.
- Renewal of the Board in 2024: the following members are due for replacement or re-election in 2024 at the General Assembly: J-M. Dupont (France), J. Garcia-Sagredo (Spain), M. Rocchi (Italy), E. Syk Lundberg (Sweden), R. Vanni (Italy).
- Only one list has been received by the President, with the following candidates: J-M. Dupont (France), J. Garcia-Sagredo (Spain), M. Rocchi (Italy), E. Syk Lundberg (Sweden), R. Vanni (Italy).

E.C.A. Fellowships

- The **E.C.A.** offers two **Fellowships** for the following course:
  European Diploma in Classical and Molecular Cytogenetics
  to be held in Nîmes (France) 24-30 March 2025 (see page 18)

- The fellowships **include the course fees and the accommodation** during the lectures in Nîmes but **do not include travel expenses** for the course or for accommodation during the practical training. Applications with CV, list of publications and a letter of support should be addressed to the course organizer. The Educational Advisory Council of the E.C.A. will select the successful candidates.

Kind reminder

Dear E.C.A. member, please renew your membership: http://www.e-c-a.eu/

E.C.A. PERMANENT WORKING GROUPS (PWG)

PWG: ANIMAL, PLANT, AND COMPARATIVE CYTOGENOMICS.

Co-ordinators:

J.S. (Pat) HESLOP-HARRISON
Department of Genetics and Genome Biology
University of Leicester
LEICESTER LE1 7RH, UK
Tel.: +44 116 252 5079 Fax.: +44 116 252 2791
E-mail: phh4@le.ac.uk

Valérie FILLON
Laboratoire de Génétique Cellulaire
Institut National de la Recherche Agronomique de Toulouse
31326 CASTANET TOLOSAN, FRANCE
Tel: +33 0561285347
E-mail: valerie.fillon@inra.fr

A year after the exceptional presentations of Montpellier, our Working Group report includes pointers to some of the work discussed at the meeting which has now been published.
Pat Heslop-Harrison et al. show two key aspects of chromosome evolution in the grasses: relatively uniform expansion of grass genome between distant species with contrasting genome sizes, spreading the genes over all the chromosomes; and chromosomal rearrangements, including insertions of one chromosome into another and translocations. Liu Q, Ye L, Li M, Wang Z, Xiong G, Ye Y, Tu T, Schwarzacher T, Heslop-Harrison JS. Genome-wide expansion & reorganization during grass evolution: from 30 Mb chromosomes in rice and Brachypodium to 550 Mb in Avena Oats. BMC Plant Biology 23: 626. https://doi.org/10.1186/s12870-023-04644-7

PWG: MARKER CHROMOSOMES

Thomas LIEHR
Jena University Hospital, Friedrich Schiller University, Institute of Human Genetics
Postfach
07740 JENA, GERMANY
Tel: + 49 3641 93 96 850, Fax: +49 3641 93 96 852
E-mail: Thomas.Liehr@med.uni-jena.de

Isabel MARQUES CARREIRA
Cytogenetics and Genomics Laboratory,
Faculty of Medicine, University of Coimbra
Rua Larga
3004-504 COIMBRA, PORTUGAL
Tel/Fax . +351 23983886
E-mail: i_marques@hotmail.com

New achievements on sSMC research have been published and summarized and are freely available on http://cs-tl.de/DB/CA/sSMC/0-Start.html.

Here are some recent publications which could be of interest for those dealing with small supernumerary marker chromosomes (sSMCs) in diagnostics.

- Book: T Liehr. Small supernumerary marker chromosomes, Basics. Epubli, 2023, ISBN 978-3758451935 – also available in German: ISBN 978-3758451669, Portuguese: ISBN 978-3758454387, Russian: ISBN 978-3758463709, and French: ISBN 978-3758458576
- Book: T Liehr. All you need to know about uniparental disomy, UPD and imprinting. Epubli, 2024, ISBN 978-3758465581 – also available in German: ISBN 978-3758465574
- Special issue in Frontiers in Genetics: Co-occurrence of numerical and structural aberration—small supernumerary marker chromosomes and B-chromosomes.
- Article: G Jedraszak et al. Cat eye syndrome: Clinical, cytogenetic and familial findings in a large cohort of 43 patients highlighting the importance of congenital heart disease and inherited cases. Am J Med Genet A 2024, 194:e63476.
- Article: VR Rajpal et al. Comprehending the dynamism of B chromosomes in their journey towards becoming unselfish. Front Cell Dev Bio 2023, 10:1072716.
- Article: H Cernohorska et al. Supernumerary marker chromosome identified in Asian elephant (Elephas maximus). Animals (Basel) 2023, 13:701.

Finally, we just want to remind everyone that we - the coordinators - are happy to receive ideas for projects and for cooperation.

MINUTES OF THE E.C.A. BOARD MEETING MARCH 2024

A meeting of the E.C.A. Board of Directors was held on Saturday 23 March 2024 in Hotel Vatel, Nîmes, France

The following 9 board members were present in person: Jean-Michel Dupont (General Secretary), Jose-Miguel Garcia-Sagredo,Thierry Lavabre-Bertrand (Treasurer), Anna Lindstrand, Kamlesh Madan (First Vice-President), Konstantin Miller, Harald Rieder, Mariano Rocchi (President), Roberta Vanni.
Present on-line were: Joan Blanco Rodríguez, Pat Heslop-Harrison (Second Vice-President) Maria Rosario Pinto Leite, Franck Pellestor, Meral Yirmbies Karaoguz. Apologies were received from: Elisabeth Syk Lundberg

The meeting opened at 17.05.
Board members were welcomed, attending both in person and remotely.
The Minutes of the E.C.A. Board meeting held on 24 March 2023 Hotel Vatel, Nîmes, France and the General Assembly 3 July 2023 in Le Corum, Montpellier, France, published in Newsletter 53, were approved.

Report from General Secretary
The General Secretary reviewed the state of the Membership with 1308 members in the database including ordinary members, honorary members, associate members and technologists.
The list of 48 new members in 2023 was approved. New members are welcomed immediately after first approval by the General Secretary, and their membership is activated upon payment of the fee. The membership is formally approved at the subsequent board meeting.

Report from the Treasurer
The Treasurer and former Treasurer reported that the two bank accounts were operating generally satisfactorily.
While the overall financial position and balance of the Society was good, result of the 14th European Cytogenomics Conference, Montpellier, was less satisfactory.
The accounts were approved unanimously by the Board.

Montpellier Conference Report
The Scientific Programme, reported in Newsletter 53 January 2024, was successful.
Overall, the number of attendees was lower than anticipated (in common with several other conferences); the usual companies sponsored the meeting.
The registrants were 75% from Europe and 25% from the rest of the world. There were equal number of paid-ECA members and non-members.
To ensure a better financial outcome in the future, it was decided to look for conference venues with a lower rental fee, which appears to be the main factor

Leuven conference 15th ECC 2025
Photographs of the Venue were shown and general organizion was considered. The Membership of the Scientific Programme Committee was discussed. Options for PWG sessions, and the potential for practical courses associated with the conference were considered. Company involvement might be encouraged. There was a discussion on the various ways in which the E.C,A members and the Board could attract partcipants to the conferences, including publisizing and disseminating information on Social Media

Education and Courses
The Nîmes course was ongoing at the time of the Board Meeting with good registration numbers. The complementarity and division of content between Goldrain and Nîmes courses is important. The courses are important for the Cytogenomic community and are well appreciated by Students.
The President noted that some students who attend one course go on to attend the other one, thus confirming the complementarity of the Nîmes and Goldrain courses.

Affiliation with Molecular Cytogenetics
The continuation of the agreement with the Molecular Cytogenetics journal, Editor-in-Chief Emanuela Volpi, in the context of the history of the collaboration, was considered. The Board was not convinced of benefits for the ECA. It was decided not to renew or enter into any new affiliation agreement. The General Secretary will write to Emanuela Volpi to communicate this decision.

Date of next Meeting
The Annual General Assembly and Board Meeting will be held in August 2024.

Thanks for Montpellier Organization
The local member of the SPC for the 14th ECC, Frank Pellestor and the local organizer Thierry Lavabre-Bertrand were thanked for their input and arrangements for the conference.
The Board expressed their appreciation of the helpful and efficient organizational work from Dekon as congress management organization. The President will communicate this to the Company.

The President closed the Board Meeting at 20.00.

17th Goldrain Course in
Clinical Cytogenetics

August 20-26, 2024

(arrival 19, departure 27)

DIRECTORS

A. Schinzel (Zurich, Switzerland); **M. Rocchi** (Bari, Italy)

PROGRAMME COMMITTEE

A. Schinzel, M.Rocchi, J-M. Dupont, K. Miller, K. Madan, 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), E. Errichiello (Pavia, Italy), E. Klopocki (Würzburg, Germany), K. Madan (Leiden, The Netherlands), K. Miller (Hannover, Germany), R. Pfundt (Nijmegen, The Netherlands), M. Rocchi (Bari, Italy), G. van Buggenhout (Leuven, Belgium), M. Vismara (Rome, Italy), J. Wisser (Zurich, Switzerland), O. Zuffardi (Pavia, Italy)

LOCATION

Goldrain Castle, Goldrain, South Tyrol, Italy

Website of the course: **www.biologia.uniba.it/SEC/**

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.

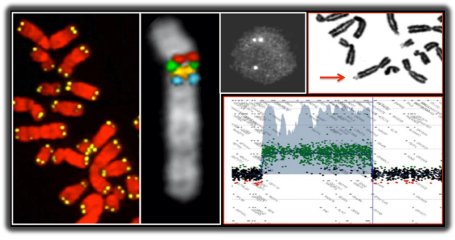
TOPICS

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 – Optical genome mapping – 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 to perform a test at the end of the course.

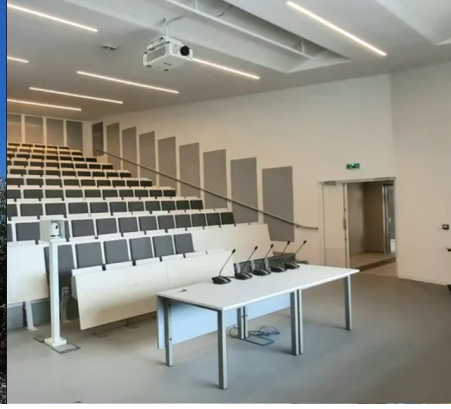
Scholarships, in the form of reduced fee, will be granted to students who make payments from their personal accounts (not through the institution).

For further questions:
schinzel@medgen.uzh.ch
or
mariano.rocchi@uniba.it



Full fee is Euro: 1.400-1750, depending on the accommodation and on the time of registration. It includes tuition, course material, free access to internet, accommodation for 8 nights, all meals, coffee breaks and a ½ day excursion.





Nîmes – France, March 24-30, 2025

EUROPEAN CYTOGENETICISTS ASSOCIATION (E.C.A.)

European Diploma
in Classical and Molecular Cytogenetics

Director: Professor Jean-Michel Dupont, Paris - France

http://www.biologia.uniba.it/SEC/

This course was started by Professor Jean Paul Bureau in 1997 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

(September 2024 – January 31st, 2025)

You can select either

- Basic diploma: only the lectures and a final online examination (no previous experience required)
- Advanced diploma: lectures + 2 months training in a cytogenetic laboratory (6 months experience in cytogenetics required), and onsite final examination (written and oral) 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).

Registration fee is the same for both: €1034 if paid by the participant, 2034€ if paid by an institution.

Beware: the fee does not include accommodation during the lectures or the training

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.

Students whose registration is paid by a third party institution are not eligible for a scholarship

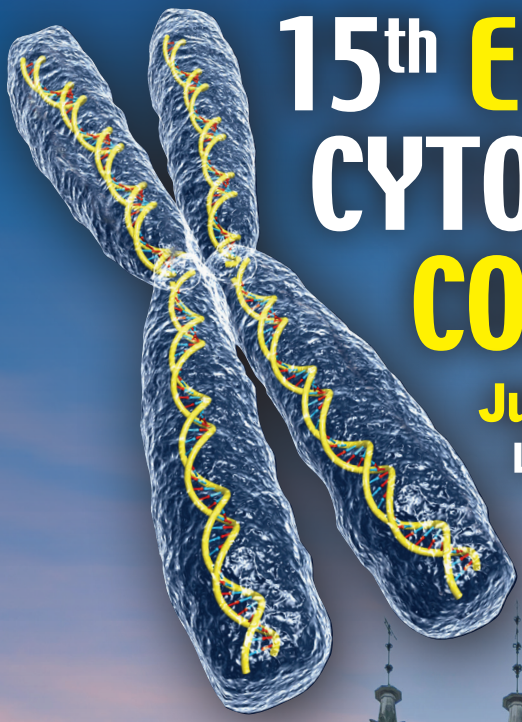
Topics

Technical Aspects: *Classical Cytogenetics:* Cell culture techniques; Chromosome staining methods (Q-, G-, C-, R-banding); *Molecular Cytogenetics:* Methods and principles of Fluorescence In Situ Hybridization (FISH); CGHarray and SNParray; Application of Massively Parallel Sequencing to Cytogenetics; Optical Genome Mapping ; Databases 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 2024; *Clinical:* Phenotype of common autosomal and sex chromosome 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 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 aberrations; Origin of aneuploidy; Evolution and plasticity of the human genome; Animal cytogenetics; Plant cytogenetics.

European Cytogeneticists Association



15th EUROPEAN CYTOGENOMICS CONFERENCE

June 29-July 1, 2025

LEUVEN, BELGIUM

www.eca2025.org

European Cytogeneticists Association

15th EUROPEAN CYTOGENOMICS CONFERENCE

June 29-July 1, 2025

LEUVEN, BELGIUM

www.eca2025.org

ECA 2025 - The 15th European Cytogenomics Conference will take place in **Leuven, Belgium** on **June 29 - July 1, 2025.** Please save the date!

Innovative Format

We are evolving the conference format to include a series of pre-conference workshops designed to provide hands-on experience and in-depth knowledge on specialized topics.

Program Highlights

Several eminent scientists have agreed to contribute their expertise in various fields of cytogenomics, complemented by presentations in developing areas.

The meeting covers all aspects of chromosome and genome biology as well as clinical cytogenomics. The scientific sessions cover **technological advances** in long and short read sequencing, in situ sequencing, methylation analysis, multi-omics, single cell omics, cfDNA analyses; **fundamental aspects of genome biology** including centromere organization and evolution; **telomeres and genome aging,** animal and plant cytogenomics, structural variation, chromatin structure, the origins and evolution of aneuploidy in cancers and chromosomal disease mechanisms; **microplastic genome toxicity; clinical progress** including constitutional and acquired cytogenetics; preimplantation and prenatal diagnosis; **AI in cytogenomics and medicine.**

Permanent Working Group workshops will include presentations on topical issues, large project outcomes, and introductions to cytogenomic websites and databases.

Participants are invited to present their findings as posters with some selected for presentation during the conference sessions and workshops. There will be many opportunities for early-career scientists to make presentations and be involved in discussions.

Registration

Registration details and early bird discounts will be available soon on our conference website. Be sure to secure your spot early to take advantage of these offers.

We look forward to welcoming you to the **15th European Cytogenomics Conference** in Leuven!

For more information, visit our conference website **www.eca2025.org**

For any inquiries, please contact the conference organizing secretariat at **eca2025@eca2025.org**