Table of contents

Acknowledgements

Scientific Committee

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Programme Overview

Friday June 6th

17:00 **Welcome to Participants**
Dott. L. Bresciani *(Assessore Sanità Regione Lombardia)*
Prof. A. Stella *(Preside Facoltà Medicina e Chirurgia Università degli Studi Milano-Bicocca)*

17:30-17:45 **Introduction**
Dr. Eric Souêtre *(Labco Diagnostics),*
Prof. Andrea Biondi *(Università degli Studi di Milano-Bicocca, Italy)*

17:45-19:15 **Personalized Genomics: Myth or Reality?**
Prof. Fabio Macciardi *(Università degli Studi di Milano, Italy)*

Personalized Medicine: from Pharmacogenetic Investigations in Drug Research and Development to Applications in Medical Practice
Dr. Iris Grossman *(GlaxoSmithKline, United States)*

20:30 **Symposium Diner**

Saturday June 7th

09:00-10:45 **Contribution of Genomics in Disease Susceptibility**
Chair Prof. Alberto Piperno *(Università degli Studi di Milano-Bicocca, Italy)*
and Prof. Leda Dalprà *(Università degli Studi di Milano-Bicocca, Italy)*

Evolving Technologies in Genetics of Human complex Traits
Prof. Maurizio Ferrari *(Ospedale San Raffaele di Milano, Italy)*

Biomarkers in Parkinsons's Disease: Gene Expression in de novo Blood and post-mortem Brain
Dr. Jarlath Ffrench-Mullen *(GeneLogic, United States)*

Genomics and Predisposition to Pathologies: Cardiovascular Disorders
Prof. Daniele Cusi *(Università degli Studi di Milano, Italy)*

10:45-11:00 **Coffee Break**

11:00-13:00: **Cancer Mutations and Targeted Therapies**
Prof. Alberto Bardelli *(IFOM Milano and Università di Torino, Italy)*

Molecular Epidemiology for the Identification of Environmental and Occupational Risks
Prof. Pier Alberto Bertazzi *(Università degli Studi di Milano, Italy)*

Occupational Medicine can be Efficient: our Experience
Dr. Miquel Mira *(Transports Metropolitans de Barcelona, Spain)*

13:00-14:00: **Walking Lunch**

14:00-16:00 **New Trends for Risk Assesment**
Chair Dr. Bernard Gouget *(Fédération Hospitalière de France)*

Risk Estimation of Alzheimer Disease
Prof. Federico Licastro *(Università di Bologna, Italy)*

Perspectives from Pharmacogenomics
Dr. Frédéric Eberlé *(Roche Diagnostics, France)*

Myocardial Infarction: Biochips can save lives!
Dr. Martin Crockard *(Randox Laboratories, Ireland)*

Preeclampsia: Novel Aspects on Diagnosis and Management
Dr. Ralf Deschend *(University of Berlin-Charite, Germany)*

16:00-16:30 **Coffee break**

16:30-18:00 **Economical aspects of Preventive Medicine and the Expectations of General Practitioners**

Exploring the Economics of Prevention
Prof. Stefano Capri *(Università C. Cattaneo di Castellanza, Italy)*

Expectations of General Practitioners: the CON-FORM Project, an Italian Experience
Dr. Vincenzo Costigliola (*European Medical Association, Belgium)*

Closing of the Symposium

Organization

Symposium Venue

Università degli Studi di Milano-Bicocca
Via Cadore 48
20126 Monza, Milano. Italy

Registration

On-site registration fee: 150 €
Registration fee includes: entrance to lectures, symposium information package, certificate of attendance, coffee and tea during breaks, and Saturday lunch.
Participation to Friday dinner fee: 30 € per person.

Certificate of attendance

A certificate of attendance will be issued to participants properly registered, and will be available at registration desk.

Languages

Official language is English; all lectures will be simultaneously translated into Italian and French.

Symposium dinner

Saint Georges Premiere Restaurant
Via Vedano 7
20052 Monza Parco Reale

Accommodation

Hotel Cosmo
Via Torri Bianche 4
20059 Vimercate

Hotel de la Ville
Viale Regina Margherita di Savoia 15
20052 Monza

Transportation

Buses will pick up participants for transportation between hotels, University and restaurant.

ABSTRACT

PERSONALIZED GENOMICS: MITH OR REALITY?

FABIO MACCIARDI MD PHD (Dept. of Science and Biomedical Technologies (DSTeB), Laboratory of Genetics of Complex Traits, University of Milano, Italy)

As a consequence of the sequencing and mapping of the human genome, and the advancements of the new microarray technologies, our current knowledge on the genetic mechanisms underlying complex diseases and complex traits have greatly improved. This lead not only to discovering genes responsible for diseases like Diabetes, Obesity, Schizophrenia, Hypertension and many others, but also prompted the development of "personalized genomics", currently seen more as a marketing opportunity than a scientific approach. However, the scientific foundation of the new genomics approach is nonetheless creating a reality.

There is now strong evidence that existence of both genetic heterogeneity and genetic complexity are to be expected in complex traits, in addition to the already known clinical heterogeneity. Therefore, much attention has been placed on association /Linkage Disequilibrium (LD) methods, even across the entire human genome, since they can deal more appropriately with the issues of complexities. Technically, the recent improvement in the technology of high-throughput SNP genotyping and the availability of a large number of SNP databases make association studies and fine mapping of disease loci more convenient, using a Genome-wide Association Study (GWAS) framework.

Other critical issues relate to the definition of the phenotype and to the use of bioinformatics to build a predictive model based on the genetic profiling of complex traits. An ideal phenotype would allow both for a measurable effect of the trait and for the correlation with the clinical domains: for example, in the field of neurosciences, the more advanced and sophisticated fMRI techniques satisfy both requirements. A simple clinical phenotype, like schizophrenia, can be easily quantified with serial fMRI sessions under specific conditions while, at the same time, choosing the specific task performed within the fMRI as supposedly related to functional derangements affecting the disease, like short term memory impairment.

Once performed GWAS and completed the identification of genes that control for the trait, the next step is to develop an algorithm to detect the genotypic profiles that discriminate patients from controls with the minimal set of significant SNPs.

We present an example of this approach, with an algorithm that has the ability to predict outcomes when the relationships between the variables are multidimensional and nonlinear as found in complex medical applications.

ABSTRACT

"PERSONALIZED MEDICINE: FROM PHARMACOGENETIC INVESTIGATIONS IN DRUG RESEARCH AND DEVELOPMENTS TO APPLICATIONS IN MEDICAL PRACTICE"

IRIS GROSSMAN (GlaxoSmithKline, Stati Uniti)

The increasing cost of drug discovery, development and marketing, coupled by observations relating differential degrees of efficacy and safety risks to subgroups within any given target population, are leading pharmaceutical companies to develop market differentiation strategies and personalize new pharmaceutical entities according to unmet medical needs. The increasing ease and reliability with which genetic and genomic markers across entire genomes can be typed and analyzed, allow investigation and development of genetic diagnostics at various points along the development process, to the point of companion launch.

Proof-of-concept demonstrating the medical benefit, clinical utility and cost-effectiveness of targeting therapies to patient subsets in a tailored fashion was first shown in oncology, and is gradually disseminating into other therapeutic areas. Via the first prospective genotype-guided clinical trial GSK has been able to increase the safety profile of an HIV marketed drug (abacavir) and gain the trust of both physicians and patients by effectively counter indicating treatment to *HLA-B*5701* carriers. Similarly, the incorporation of *APOE* genetic testing prospectively as a recruitment criterion in an ongoing phase III Alzheimer's disease clinical trial, serves as a pioneering case-study for efficacy genetic markers in small molecule drug development.

In this talk experiences gathered through the utilization of genetic diagnostics in clinical trials, both in-development and post-marketing, will be shared. Business models depicting Rx:Dx collaborations will be discussed, along with discussion of market, logistics and regulatory barriers. Emphasis will be given to the attributes of the expected Dx application along risk:benefit ratios and its impact on the co-development path.

ABSTRACT

"CONTRIBUTION OF GENOMICS IN DISEASE SUSCEPTIBILITY"

PROF. ALBERTO PIPERNO (University of Milano-Bicocca)

In the last few years, large-scale, high density genome wide association studies has improved our understanding of the genetic basis of many common phenotypes of biomedical importance. For some diseases, such as prostate and breast cancer, type 1 and 2 diabetes, inflammatory bowel disease, there has been rapid expansion in the number of loci implicated in disease susceptibility. For other diseases, including asthma, coronary heart disease and atrial fibrillation, fewer loci have been identified, although results are evenly promising. Several polymorphisms influencing important continuous tracts, such as lipid levels, height and fat mass have also been discovered. Overall, these findings are providing relevant clues to the comprehension of the allelic structure of complex traits. In addition, many methodological and technical concerns that are relevant to the success of large-scale association studies have been now addressed. However, despite these indubitable advancements, there remain many challenges ahead.

First, the observation that the genetic variants identified to date, explain only a fraction of the observed familiar aggregation of complex disorders, limiting the potential for application to define the individual risk to diseases. The final and more ambitious objectives aiming to disclose the susceptibility architecture of major clinical traits and translate these findings into clinical practice are still distant. This session highlights the knowledge gained in some interesting biomedical fields and describes the uncertainties and the challenges that should be resolved in the future.

ABSTRACT

"EVOLVING TECHNOLOGIES IN GENETICS OF HUMAN COMPLEX TRAITS"

FERRARI M. (Università Vita-Salute San Raffaele, - Genomic Unit for the Diagnosis of Human Pathologies, San Raffaele Scientific Institute, Milan, Italy and Diagnostica e Ricerca S. Raffaele SpA, Milan, Italy)

The completion of human genome project and the development of new technologies for DNA testing started the revolution of the diagnostic laboratory. For the diagnosis of genetic diseases, DNA-based diagnostics provide a sensitive alternative to protein-based diagnostics. Mutation detection is one of the most important areas of molecular diagnostics today and can be divided into two categories:, a diagnostic mode, where specific tests are designed to detect known mutations and a scanning mode, where a strecht of DNA is searched for unknown mutations.

Advances in DNA analysis to develop methods, which are increasingly specific, sensitive, fast, simple, autamatable, and cost-effective, are considered paramount. These demands are currently driving the rapid evolution of a diverse range of newer technologies (sequencing, DHPLC, OLA, FRET etc.).

This growth in knowledge fuels, in turn, the expansion of DNA testing both for diagnosis and prediction of disease susceptibility. Moreover in the post genomic era, the screening of many different genetic polymorphisms in large populations represents a major goal that will facilitate the understanding of individual genetic variability in the development of multifactorial diseases and drug response and toxicities.

For the future of genomics is demanding the rapid evolution of miniaturization and high-throughput genotyping technologies toward increased speed and reduced cost.

Through miniaturization of the test platform, microchip-based nucleic acid technologies allow rapid analysis of genetic information in large sample populations thus reducing time and manual work.

ABSTRACT

"NEUROLOGICAL DISORDERS"

J.M.H. FFRENCH-MULLEN[1], L. BRIGHNA[2, 3], M. KUZIORA[1], C. FERRARESE[2] AND D.M. MASH[4] ([1]GeneLogic Inc, MD, USA; [2]Laboratory of Neurobiology, Department of Neuroscience and Biomedical Technologies, University of Milano-Bicocca, Monza, Italy, [3]Department of Neurology, San Gerardo Hospital, Monza, Italy and [4]Dept. of Neurology, University of Miami, Miami, FL., USA).

Our research program is focused on validation of biomarkers for Parkinson disease. To identify candidate markers, we conducted gene expression profiling (Affymetrix U133 Plus 2 gene chip) on: (A). 21 postmortem brain (PM) regions [e.g. substantia nigra (SN)] from end-stage Parkinson's disease (PD) patients (n=21) and matched aged control (CTRL) patients (n=23) with no history or pathological diagnosis of neurologic or psychiatric disease; (B), a second independent PM cohort of PD patients (n=6) and controls (n=6) patients and (C), peripheral blood from staged and de novo diagnosis PD patients(n=11). Gene expression was validated with qRT-PCR.

The first PD cohort identified 5 top disregulated candidate genes in 20/21 brain regions with a final list of 18 disregulated genes in 18/21 brain regions (Fold change (FC) ≥ ±1.3 and P<0.001). The top two up-regulated genes were the mitochondria ribosomal protein S6 (MRPS6) and the solute carrier family 5 (inositol transporter), (SLC5A3). MRPS6 is a building block of the human mitoribosome of the oxidative phosphorylation system (OXPHOS) and SLC5A3 is in an intron of MRSP6. OXPHOS impairments has been linked to the pathogenesis of PD.

The top 5 genes, including MRPS6 and SLC5A3, were also identically disregulated in the second PD cohort. The expression levels of MRSP6 and SLC5A3 were confirmed by qRT-PCR analyses in several regions. In mid-stage PD blood (n=6), both MRPS6 and SLCA3 were similarly up-regulated with almost identical FC and P values. Preliminary gene expression analysis of blood samples of the de novo PD patients suggests a similar pattern.

ABSTRACT

"CARDIOVASCULAR DISORDERS"

PROF. D. CUSI (University of Milano, Italy)

Over the last few years, substantial progress has been made in defining the molecular basis of several genetically transmitted non-atherosclerotic CVD such as hypertrophic and dilated cardiomyopathies, long-QT syndrome and essential hypertension. This review represents a summary of the current knowledge about the major gene polymorphisms found to be associated with these CVDs. Moreover, we will discuss how the discovery of disease-associated genes will greatly enhance the ability to formulate advanced diagnoses, to define prophylactic therapeutic strategies to prevent or reduce the progression of the disease and, finally, to proceed to the development of new drugs tailored for the specific cellular or molecular functions altered as consequence of the predisposing genes.

Cardiovascular disease (CVD) is a series of disorders that result from the interaction between genetic predisposing mechanisms and environmental factors. They represent a large public health threat due to their high prevalence, morbidity and mortality. Due to increases in life expectancy, diseases such as hypertension, coronary artery disease, heart failure, stroke and peripheral vascular diseases have become
pandemic in both developed and developing countries.

Whereas positional cloning has allowed great achievement into the genetic basis of various familial (but rare) diseases, such as hypertrophic cardiomyopathy, long-QT syndrome, Marfan syndrome and various congenital heart diseases, little progress has been done with common complex diseases as hypertension or atherosclerosis.

The availability of huge amount of data from the phase 2 of the human genome project as the HapMap project, as well as the tremendous technological advancement that allow the fine mapping of the entire human genome with up to 1 million SNPs at acceptable time and cost make the reach of the genetic disentangling of most common complex diseases accessible.

Provided that success will be obtained (but as a matter of example it has not yet been the case for hypertension), such success will have many implications in clinical practice, as:

1) the reassessment of clinical traits based on genotype, which will lead to the discovery of new, more sensitive and specific diagnostic criteria.
2) the identification of susceptibility genes or modifier genes which influence the prognosis of these diseases.
3) the development of pharmacogenetic tools that will allow to identify a priory which subjects will respond better to specific drugs at the minimum dosage.

ABSTRACT

"CANCER MUTATIONS AND TARGETED THERAPIES"

ALBERTO BARDELLI (Laboratory of Molecular Genetics, Institute for Cancer Research and Treatment, University of Torino-Medical School, Candiolo (TO) and FIRC Institute of Molecular Oncology, Milan, Italy)

It is now clear that cancer has a genetic basis and that mutations affecting the sequences of specific genes are the hallmark of this disease.

This knowledge has already had a dramatic impact in the clinical arena. First, many studies have demonstrated that tumours can be diagnosed and classified on the basis of their genetic profiles. Second, the pattern of genetic alterations present in individual cancers can, at least in part, be used to predict their clinical outcome. Third, the success of cancer drugs designed to target the molecular alterations underlying tumorigenesis has proven that genetic alterations are legitimate targets for therapy.

We have exploited cancer mutations using two complementary and interconnected approaches. On one side we coupled genetic alterations in genes involved in kinase-mediated signaling with the clinical response to molecularly targeted therapies. On the other we have generated tumor progression models closely recapitulating the genetic alterations present in human cancer using an innovative technology that allows targeted homologous recombination in human cells.

Overall this approach is providing new insights into the pathogenesis of cancer and has led to results relevant for therapeutic intervention.

ABSTRACT

"MOLECULAR EPIDEMIOLOGY FOR THE IDENTIFICATION OF ENVIRONMENTAL AND OCCUPATIONAL RISKS"

PIER ALBERTO BERTAZZI (EPOCA Research Center for Occupational, Clinical and Environmental Epidemiology, University of Milan, and Department of Preventive Medicine, Ospedale Maggiore, Policlinico, Mangiagalli, Regina Elena. "Clinica del Lavoro L. Devoto", Milan, Italy)

Randox Laboratories Ltd. has developed Biochip Array Technology platforms and multi-marker assays to provide comprehensive clinical information relating to particular patient conditions. A clinical trial using one of these biochip arrays, the Cardiac Array, is described in greater detail. This array simultaneously and quantitatively measures six markers implicated in cardiac stress, using only 60µl of serum per multiplex assay. The markers are Troponin I (TnI), Myoglobin (MYO), Creatine Kinase – MB (CK-MB), Carbolic anhydrase III (CAIII), Glycogen phosphorylase BB (GPBB) and heart Fatty Acid Binding Protein (hFABP).

Troponin I is the current Gold standard marker for myocardial infarction (MI), but its levels only rise 4-6 hours after an event, peaking at 18-24 hours. This lag in elevation presents a Troponin-blind period, at the most critical diagnostic window. The earlier MI is detected and treated, the better the patient's prognosis. The Randox Cardiac Array contains early markers that fill this blind-spot with valuable diagnostic information relating to damage to the heart, indicating MI early and also identifying at-risk patients with Acute Coronary Syndrome (ACS). Results have indicated a 20% increase in sensitivity over the standard single-assay Troponin test. The results of a 3-year clinical trial, carried out at an inner-city Dublin hospital are presented and provide compelling evidence for a multi-marker approach to cardiac testing in the clinical setting.

ABSTRACT

"OCCUPATIONAL MEDICINE CAN BE EFFICIENT: OUR EXPERIENCE".

M. MIRA M.D. (Transports Metropolitans de Barcelona, Spain)

The occupational medicine is a medical speciality for the prevention of the damages caused by accidents at work and occupational diseases, as well as the promotion of the health of the workers. The alertness of the health is one of the activities of the occupational medicine which aim is the precocious detection of the alterations of the health, principally, or mainly related to the work, by means of procedures of withdrawal systematic and analysis of information.

The tests of laboratory and the determination of analytical parameters are habitually used in alertness of the health for the detection of the diseases in his subclinical phase. In our experience, this alertness is efficient in social and economic terms for the improvement of the labour climate and for the reduction of the labour absenteeism.

ABSTRACT

"RISK ESTIMATION OF ALZHEIMER'S DISEASE".

FEDERICO LICASTRO (Department of Experimental Pathology, School of Medicine, University of Bologna, Via S. Giacomo 14, 40126 Bologna, Italy)

Senile dementia is a frequent pathological condition affecting the elderly. Alzheimer's disease (AD) is the most frequent cause of cognitive deterioration among old people. AD is a complex multi-factorial disease and it is unlikely that a single biomarker may carry enough information to be used to reach this goal. Therefore, the use of several informative markers, either genetic or phenotypic may result of great help.

Few attempts to concomitantly evaluate allele association of different genes with AD and its clinical progression has been systematically performed. A comprehensive assessment of several inherited variations of immune related genes upon AD risk, and their relative importance compared to *APOE* allele will be presented. A multi-gene risk profile has emerged, where gene polymorphism association with AD has been tested. This multi-gene profile substantially increased the risk of developing age associated cognitive decline and dementia and may be use to predict individual propensity to this type of pathology. Individual genetic risk profile is a new tool for predictive medicine and can be used to set up preventive protocols for personalized early intervention and prevention of chronic degenerative diseases.

Multi variable approach to investigate factors associated with age-associated cognitive decline and dementia has been recently performed using a data base from an Italian population longitudinal study. 35 different variables have been tested using an innovative statistical and mathematical algorithm. This method, called the Auto Contractive Map (AutoCM), is based on an artificial adaptive system, and is able to define the strength of associations of each variable with all the others. Data recorded during the five years follow up of participants to the Conselice's population study were elaborated in relation with the three different clinical endpoints: no cognitive decline, cognitive decline without dementia and dementia. Three majors biological hubs connecting variables with the three different cognitive conditions were identified. This map shows new link among biological variables and suggest new investigations in the pathogenetic history leading to cognitive decline and dementia in old age.

Two questions:
Are genetic factors associated with sporadic non familial Alzheimer's disease?
Can genetic risk profile be used as a tool for predictive medicine?

ABSTRACT

"PERSPECTIVES FROM PHARMACOGENOMICS"

FRÉDÉRIC EBERLÉ (Roche Diagnostics, Francia)

The very large majority of assays of medical biology are contributors to screening and diagnosis of diseases as well as to the monitoring of treatments. Progress in genetics, availability of targeted molecules and an innovation-based industrial politics now allow the emergence of a new generation of tests to analyse genomic biomarkers specific of drugs. They then take place into the general trends of patient stratification and personalized medicine.

Based on the FDA's Table of Valid Genomic Biomarkers in the Context of Approved Drug Labels, we will show that biomarkers can served two different purposes, either being predictive of (in)efficacy (HER2, EGFR), or being predicitve of toxicity (pharmacogenetics). Because innovative and costly capital drugs, in particular in oncology,infectiology, transplantation, an psychiatry, may be only suitable to specific patients or alternatively should not be prescribed to others, modern state of the art should be to recommend some of the companion biomarkers in routine clinical application, as do already pharma companies in the very early process of drug development.

ABSTRACT

"MYOCARDIAL INFARCTION; BIOCHIPS CAN SAVE LIVES"

MARTIN CROCKARD (Randox Laboratories Ltd)

The incorporation of molecular and cellular markers, in addition to other biological and environmental measurements, in occupational health epidemiology was deemed capable of producing dramatic advancements in four core areas: providing evidence that specific environmental agents pose human hazards (hazard identification); establishing their causal role (mechanistic insight, e.g., D-R relation and inter-individual variability); identifying subsets of the population who are at special risk (exposure assessment, i.e. type, level and mode of exposure; genetically determined or acquired individual susceptibility); using the information to suggest or to develop new and more effective strategies to reduce risk (exposure monitoring, health surveillance and risk characterization to establish health based limits).

Indeed, research is accumulating knowledge in these fields at an exponential rate, but the actual relevance to health protection and disease prevention results still needs rigorous validation. There is consensus about the need to incorporate a mode of action into compound evaluation and standard settings, but not on how to apply it: the ongoing debate on a standard setting for genotoxic and non-genotoxic carcinogens is an example in point.

Genetic susceptibility testing at the workplace raises serious concerns about a significant threat to workers' privacy, autonomy and dignity. This is particularly true for pre-employment screening. Instead, testing done later in health surveillance programs is considered more acceptable since it appears to aim directly at protecting the worker exposed in particular circumstances.

To sum up, the passage from the study of molecular targets to applying the results in public health still seems lengthy and difficult, but there are strong reasons and sufficient data that urge traveling that path.

ABSTRACT

"RISK ESTIMATION ASSOCIATED WITH PREGNANCY"

RALF DESCHEND (Università di Medicina Charité di Berlino, Germania)

Preeclampsia is a major complication of pregnancy characterized by hypertension and proteinuria developing in the second half of the pregnancy. Preeclampsia affects at least 3-4% of all pregnancies, representing a major threat to maternal and fetal health, and responsible for approximately 50.000 maternal deaths annually. The etiology of preeclampsia remains unknown, but circulating factor(s) produced by a relatively hypoxic placenta is proposed to cause endothelial dysfunction, thereby inducing the main maternal clinical features of preeclampsia, including hypertension and proteinuria. A shallow placentation, possibly associated with immunological mechanisms involving maternal uterine natural killer cells, includes abnormal invasion of fetally derived cytotrophoblasts and incomplete remodeling o placenta-supplying maternal uterine spiral arteries. This results in a relative hypoxic uteroplacental circulation and augmented placental oxidative stress, hypothesized to induce the augmented placental release of endothelial deranging factors to the maternal circulation in preeclampsia.

Placental sFlt1 (soluble fms-like tyrosine kinase 1), also named VEGF-R1 (vascular endothelial growth factor receptor-1), has been proposed as a possible circulating endothelial damaging factor in preeclampsia. sFlt1 mRNA is upregulated in preeclamptic placentas, possibly due to placental hypoxia. Recently, soluble Endoglin (sEng) was suggested to work in synergy with sFlt1 in the development of preeclampsia.

The only effective treatment for preeclampsia is delivery. Oftentimes, if gestation could be continued by only a few days, fetal development would improve to the point that a viable outcome is far more likely. Preeclampsia disappears rapidly after the pregnancy is terminated. At the moment current hypothesis favor a two-stage model. The disease starts with an abnormal placentation, leading to the production of a soluble factor in the placenta, leading to the maternal syndrome. However, the etiology of preeclampsia is unknown. At present, four hypotheses are the subject of intensive study

Questions:

1. Are sFlt1 measurements ready to be used in clinical practise ?
2. What are new therapeutic strategies ?

ABSTRACT

EXPLORING THE ECONOMICS OF PREVENTION

STEFANO CAPRI (Istituto di Economia, Università C. Cattaneo-LIUC, Castellanza)

Investing in prevention and improved control of noncommunicable diseases (NCD) would improve the quality of life and well-being of people and societies. Since in every healthcare programme, also in preventive medicine, there is a competition between scarce resource, the principles of the economics of prevention will be illustrated.

Prevention ranges from medical decisions such as vaccinations and clinical preventive services delivered during periodic health examinations to private health lifestyle decisions such as regular exercise and non-smoking. Health economics provides some conceptual and empirical arguments for policies to encourage prevention. However, the economic perspective often remains quite different from the perspective of many public health professionals who are strong advocates of prevention.

Demand of disease prevention and demand of disease treatment compete for shares of the healthcare expenditures on equal terms. The wrong question is: can prevention make money for the healthcare system? The right question is: does prevention promote health at a reasonable cost? Cost-effectiveness studies are the instrument to give the right answer.

In particular, some examples from laboratory testing involved in programme of screening will be illustrated (HIV testing, Human Papillomavirus DNA Testing for Cervical Cancer Screening, Prostate Specific Antigen (PSA) for cancer screening).

ABSTRACT

"EXPECTATIONS OF GENERAL PRACTINIONERS. THE CON-FORM PROJECT: AN ITALIAN EXPERIENCE"

VINCENZO COSTIGLIOLA MD - LUCA PUCCETTI MD
(EMA European Medical Association - Bruxelles)

The recent achievements in clinical biology, both diagnostic and predictive, though often limited by regulations and high costs of insurance, produced in the physician a series of expectations, but there is also the risk of inadequate use with inappropriate demands and waste of resources.

Physicians are at times unaware of available tests, their indications, of the laboratories, which can provide them, and of their limitations.

When the physician decides to utilise (1) clinical biology tests, should know exactly which test to request, what to expect from it and, especially, how to evaluate the results and to integrate them with one another, to obtain indications useful for diagnosis, prevention, prognosis and therapeutic follow up.

Information, formation, and counseling are the key points.

Information. Very often, since diagnostic products are sold solely to clinical biology laboratories, these are the only ones to perform specialized information, neglecting the physicians who, prescribing them to their patients are the final consumer (2).

Formation. This implies an effort by all health operators to keep informed and to follow the technological progress. It is important to have appropriate programs on the correct use and interpretation of the results provided by the most recent diagnostic, laboratory, and instrumental techniques.

Counseling. This implies an effort by the technician (3) to be willing to provide to the physician the support necessary to take full advantage on the available technical resources.

An example of the collaboration between physician and technician is the **CONFORM** PROJECT PROPOSED BY THE Promedgalileo group, based on the "learn by doing" method, in which a tutor functions as a distant coach, which counsels providing both COUNSELING and FORMATION.

CONFORM, a project that puts MMG in the center of the diagnostic-therapeutic system, has been applied in an hepatological field, but its format is also useful in the field of laboratory and instrumental diagnostics.

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