Bollettino d'Ateneo

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Medicina

PARTNER SEARCH HEALTH-EU-SMCP-9

01 dicembre 2017

Oggetto: PARTNER SEARCH HEALTH-EU-SMCP-9

Richiesta di un istituto di ricerca tedesco alla ricerca di partner italiani da includere in un loro progetto nella tematica Health nei topic Health-2007-2.4.2-4 Congenital pathologies affecting the heart.

Di seguito, una breve descrizione del progetto e le caratteristiche del partner richiesto.

Per informazioni sul progetto contattare tegas@apre.it facendo riferimento al codice PARTNER SEARCH HEALTH-EU-SMCP-9

------- PARTNER SEARCH HEALTH-EU-SMCP-9 --------

<Reference n.: HEALTH-EU-SMCP-9>
<Deadline: 18/09/2007>
<Programme: COOPERATION>
<Project Title: Cardiac malformations in CHD. >
<Financial Scheme: >

<Description: Cardiac malformations in CHD remain a major public health problem despite the dramatic advances that have been made in surgical repair, and they account for a large proportion of the infant mortality rate. Nonetheless, the molecular causes are unknown. Since 2001, I serve as principal investigator to a project in pursuit of molecular mechanisms leading to cardiac malformations. We are interested in broader investigations in the interplay between cardiac transcription components, mutations, somatic hypermutability and environmental factors in CHD.

We have investigated in the past a panel of cardiac-specific transcription factor genes in a rare collection of hearts from patients with complex malformations, including 31 hearts with HLHS.
Most of these patients died at birth or early infancy. Sequence analysis revealed mutations in diseased tissues, which were absent in matched normal heart samples. Common occurring mutations were identified, especially in the binding domains of transcription factors, which could affect DNA-protein or protein-protein interactions leading to CHD. While certain transcription factor genes (NKX2-5, GATA4) exhibited a high rate of mutations, others were not affected (HEY2, MEF2C). Results of these studies enabled us to put forward a hypothesis of somatic mutations as a novel molecular cause of CHD.
Through a collaborative study that utililized a yeast-based system to address human transcription factors, we established that many of the individual mutations altered transcription from specific human target sequences. Although the pattern of mutations is unusual, we propose environmental exposures to industrial chemicals as likely culprits, to result in hypermutability of cardiac transcription factor genes.
I have also been involved in heart-related studies pertaining to cardiac function and physiology, and have 25 PUBMED cited publications credited to my name in this area of research. Notably, among these studies were those published in the Lancet, the FASEB Journal, Circulation Research, and Molecular Pharmacology.
Furthermore, a key member in my department, Dr. Stella Marie Reamon-Buettner, leads a group of technicians and students in the lab in pursuit of understanding the molecular causes of CHD.
Equipment: Aside from those technology platform pertaining to genomics and proteomics studies described above, we are well-equipped to undertake genetic and/or epigenetic analysis including cell-based notably yeast-based assays to determine effects of sequence alterations on transcriptional activities, DNA-protein and protein-protein interactions. Detection or confirmation of genetic alterations can be carried out through Affymetrix microarray systems (e.g. GeneChip® Mapping 100K Set), denaturing high-performance liquid chromatography (dHPLC, Transgenomic), Applied Biosystems 3100 capillary genetic analyzer, Taq Man assays (Applied Biosystems 7500), fluorescence resonance energy transfer (FRET, Light Cycler), and PCR-RFLP assays. Furthermore, comparative sequencing analysis can be undertaken by the following softwares: Lasergene 7.0, Vector NTI 10, and SeqScape 2.0.

TOPIC: Health-2007-2.4.2-4 Congenital pathologies affecting the heart

<Organisation Type: Centro di Ricerca>
<Partner Sought: Keywords specifying your expertise: molecular mechanisms in cardiac malformations, yeast-based functional assays, molecular markers, DNA diagnostic assays.

Expected Commitment:
-research

Country /region: Germany, Italy, UK, Belgium