



Luis J. Lombardía

## Unit Head

Luis Lombardía, born in Nimes (France) in 1967, obtained his degree in 1991 in Biological Sciences at the *Université des Sciences et Techniques du Languedoc*, Montpellier (France).

After working within the agro-chemical industry for three years he moved to Spain in 1998 to complete his PhD studies at the *Universidade Da Coruña* in La Coruña. Funded by the EUROFAN EU project, he worked on transcription analysis of orphan ORFs *Saccharomyces cerevisiae* and then collaborated in the second phase of this project using DNA-microarray technology to pioneer yeast transcriptome studies in Europe.

He then completed his postdoctoral studies at the *Commissariat à l'Énergie Atomique* in Paris. For two years he participated in the BIOCHIP-CEA project collaborating in the first ever studies to compare the transcriptome versus the 2D-gel proteome in yeast.

In 2001 he joined the CNIO Genomics Unit as Staff Scientist, responsible for the implementation, development and support of large-scale gene expression studies in partnership with other CNIO Research Groups.

Since June 2007 he has organised and managed the Molecular Diagnostics Core Unit and coordinated the Molecular Diagnostic Service.

## Summary

The Molecular Diagnostics Core Unit provides specific and high quality molecular diagnostic assays not ordinarily available in hospitals of the Spanish National Health System. The Unit provides a wide range of highly sensitive molecular tests to determine changes in the sequence and/or expression levels of key genes involved in cancer.

Our Unit adopts a multidisciplinary and integrated panel of specialists and techniques to constantly improve early diagnosis, detection of Minimal Residual Disease in patients in clinical remission, monitoring response to therapy and therapeutic decision-making amongst different treatment options.

We also form part of international and national groups dedicated to standardising and improving molecular diagnostic tests in cancer. In addition we have promoted training and education by welcoming students, technicians and medical residents to our laboratory to share our techniques and methods.

## Main Objectives

- Strengthen, update and expand currently available assays, including tutoring and training in the field of molecular diagnostics
- Provide the CNIO Clinical Research Programme at the *Hospital Universitario de Fuenlabrada* with state-of-the-art facilities and technical expertise
- Further expand our end users portfolio and strengthen relationships with the pharmaceutical industry through partnerships



Technician: Diana Romero.

## Highlights

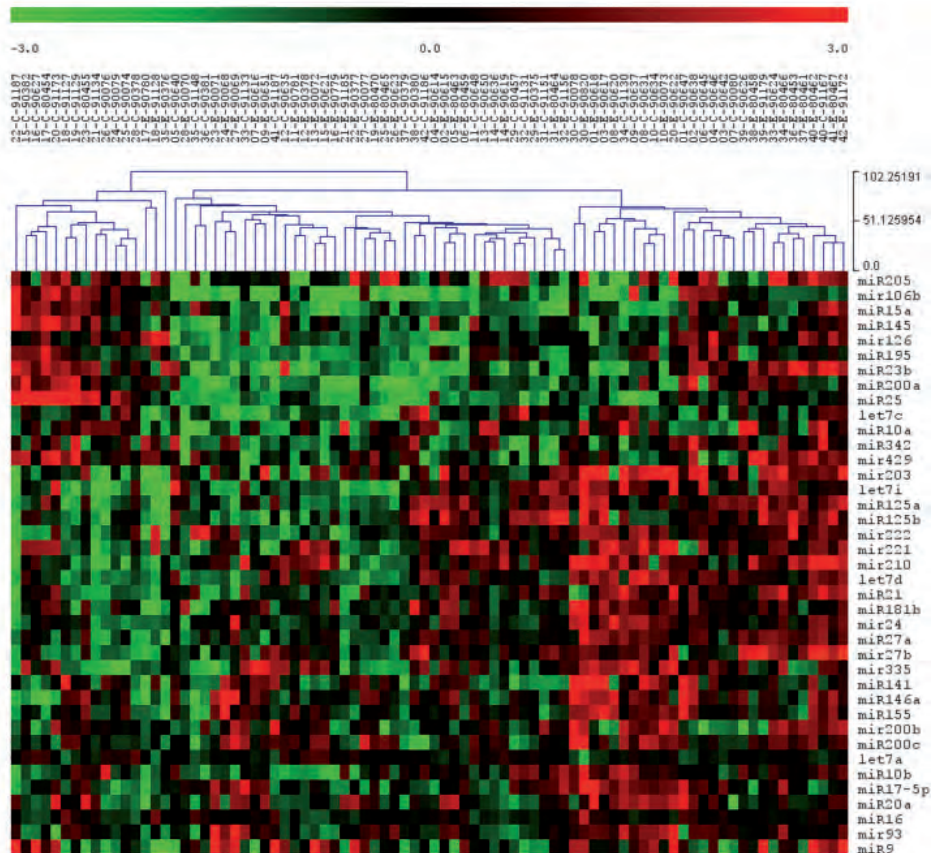
Despite the difficult global economic situation, the volume of diagnostic tests ordered by hospitals in 2010 has remained the same compared to the previous year. We have increased the range of services by adding two novel molecular diagnostic tests in our catalogue.

The first one allows the identification of activating somatic mutations in exon 4 of the *AKT1* gene (v-akt murine thymoma viral oncogene homologue 1), which are associated with a better clinical outcome in patients with colorectal, breast, ovarian and prostate cancers among others. The second assay allows for full detection of somatic mutations in the nine exons of tumour suppressor gene *PTEN* (Phosphatase and Tensin homolog), which are found in multiple sporadic tumours (e.g. endometrium, glioblastoma, prostate, thyroid and lymphoid malignancies) promoting tumourigenesis.

Finally, we have initiated a collaborative partnership with *Novartis Farmacéutica, S.A.* to discover biomarkers as potential predictors of complete molecular response in Chronic Myeloid Leukaemia patients.

We have also made considerable progress in the development and implementation of two new molecular diagnostic platforms. Firstly, we have completed the first phase of a project aimed at developing a low-density array for quantifying expression of a panel of microRNAs in biopsies obtained from breast cancer patients. Class prediction analyses have revealed 8 miRNAs as potential predictors for metastasis in breast cancer (Figure). At the same time, we are at the preliminary stages of implementing new technology (High Resolution Melting) to detect mutations more efficiently in genes (*EGFR*, *BRAF*, *KRAS*, etc.) involved in predicting the response to cancer therapy.

**Figure:** Classical hierarchical clustering based on the expression of microRNAs selected from prior literature screening, discriminating breast cancer patients who have developed metastasis from others without recurrence for at least seven years. A subsequent prediction analysis showed that some of these miRNAs can be used as specific and sensitive tools to predict relapse and metastasis in breast cancer patients.



## Publications

Rhiner C, López-Gay J, Soldini D, Casas-Tinto S, Martín F, Lombardía L, Moreno E (2010). Flower forms an extracellular code that reveals the fitness of a cell to its neighbors in *Drosophila*. *Dev Cell* 18, 985-998.

Ferreiro I, Joaquin M, Islam A, Gomez-Lopez G, Barragan M, Lombardía L, Domínguez O, Pisano DG, Lopez-Bigas N, Nebreda AR, Posas F (2010). Whole genome analysis of p38 SAPK-mediated gene expression upon stress. *BMC Genomics* 11, 1-17.