

Publishable executive summary

The retina is a highly complex biological system that accommodates both numerous tissue-specific and ubiquitously expressed developmental and pathologic pathways. The number of genes identified in Inherited Retinal Degenerations (IRD) has steadily increased. The commonest cause of blindness, (12.5 Million affected in Europe) Age-Related-Macular-Degeneration (ARMD), is likely to depend on both mostly unknown genetic and modifying factors. Preventing blindness from IRD and ARMD requires the understanding of the genetic and cellular interactions controlling retinal development, maintenance and function.

In EVI-GENORET, 24 academic and industrial partners form five interacting components (phenotyping, development, genetics, therapy and functional genomics) to establish working platforms, share tools and knowledge within and outside the academic community (dissemination through patient organisations and transfer to industrial partners).











The objectives of EVI-GENORET are to:

1. Obtain and integrate the information on gene function through numerous human, animal and in vitro models of retinal degeneration available as well as data from studies during development;
2. Standardize and analyse these informations (databases, bioinformatics, transcriptome, proteome and expression studies);
3. Validate the information (bioinformatics and functional assays);
4. Generate conceptual and biological models of genes, gene networks and pathways relevant to major functions involved and/or impaired in retinal health and disease;
5. Design novel cell-based and genomic-based therapies that would obviously potentially benefit patients but also validate the pathways and targets identified using the above-described approaches that might be modulated by rational drug, cell or gene therapies.















The consortium has already provided significant results towards these objectives:

- Harmonization of Standard Operating Procedure and development of the relational EVI-GENORET database ;
- Identification of candidate genes involved in retinal degeneration by DNA chips and proteomic analysis;
- Retinoid dehydrogenases/reductases (RDH) catalyze key oxidation-reduction reactions in the visual cycle that converts vitamin A to 11-*cis* retinal, the chromophore of the rod and cone photoreceptors. We have shown that mutations in *RDH12*, encoding a retinal dehydrogenase, result in severe and early-onset autosomal recessive retinal dystrophy (arRD)

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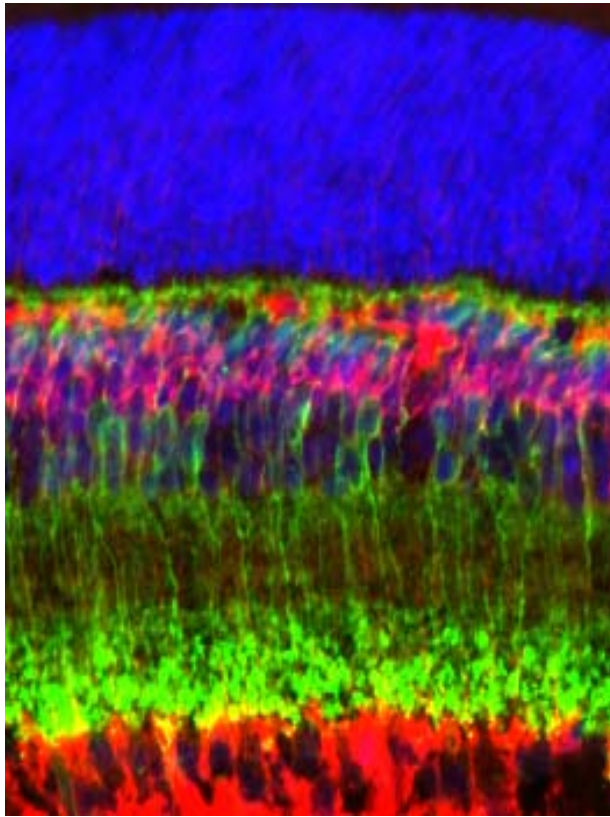
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