

**ECNP Targeted Expert Meetings (TEMs)
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**Report on the TEM Addiction
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Progress in understanding the genetic basis of addiction is derived from both preclinical studies in animals and human studies. In this TEM we discussed in a multidisciplinary group of researchers from 12 different countries a new translational approach for the integration of data sets that derive from forward genetics in animals and genetic association studies including genome wide association studies (GWAS) in humans.

The aim of forward genetics in animals and association studies in humans is to identify mutations (e.g. SNPs) that produce a certain phenotype, i.e. 'from phenotype to genotype'. The repertoire of forward genetics includes the generation of random mutations in an organism, either by radiation or by a chemical mutagen such as N-ethyl-N-nitrosourea (ENU), and then through a series of breeding of subsequent generations, isolating individuals with a phenotype relevant for addictive behaviour. Most powerful however, in terms of forward genetics, is combined QTL analysis and gene-expression profiling in recombinant inbred rodent lines or genetically selected animals for a specific phenotype, e.g. high versus low drug consumption. By Bayesian filtering genomic information from forward genetics in animals are then combined with data from a meta-analysis of GWAS on a similar addiction-relevant phenotype. This integrative approach generates a robust candidate gene list that has to be functionally validated by means of reverse genetics in animals, i.e. 'from genotype to phenotype'.

We conclude that studying addiction-relevant phenotypes and endophenotypes by this convergent functional genomics approach will allow us to pin down the genetic determinants of addictive behaviour. A state of the art review paper has now been submitted to the ECNP journal *European Neuropsychopharmacology* and a symposium on this topic will be presented at the 24th ECNP Congress in Paris, 3-7 September 2011. We are really grateful to ECNP for organising this high-calibre two-day TEM meeting. All 30 attendees benefitted enormously!