## Programa Cooperación Farma-Biotech Neurociencias

#### **New Genetic Biomarkers**

Ensuring the efficacy and safety of new drugs in Phase III trials



Barcelona, 15 de febrero 2011







## Programa Cooperación Farma-Biotech Neurociencias

# **Content**

# 1. The Company

## 2. The Service

- a) Therapeutic focus
- b) Innovative proposal
- c) Differential features facing the market
- d) Current status of development
- e) IPR protection

# 3. Availability for cooperation





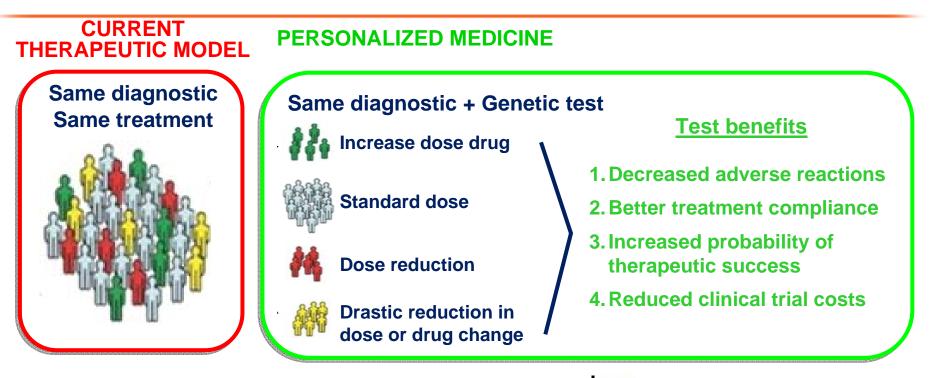




## 1. The Company



#### a) Therapeutic focus



• Since 2006 FDA publishes an official list of drugs for which the genetic analysis of patients is required prior to drug prescription.

• Nowadays 10% of FDA labeled products contain pharmacogenetic information, and this percentage will increase in the future.

Table of Valid Genomic Biomarkers in the Context of Approved Drug Labels



CONCEPT PAPER ON THE DEVELOPMENT OF A GUIDELINE ON E USE OF PHARMACOGENOMIC METHODOLOGIES IN THE PHARMACOKINETIC EVALUATION OF MEDICINAL PRODUCTS

Food and Drug Administration - <u>http://www.fda.gov/Drugs/ScienceResearch/Re</u>

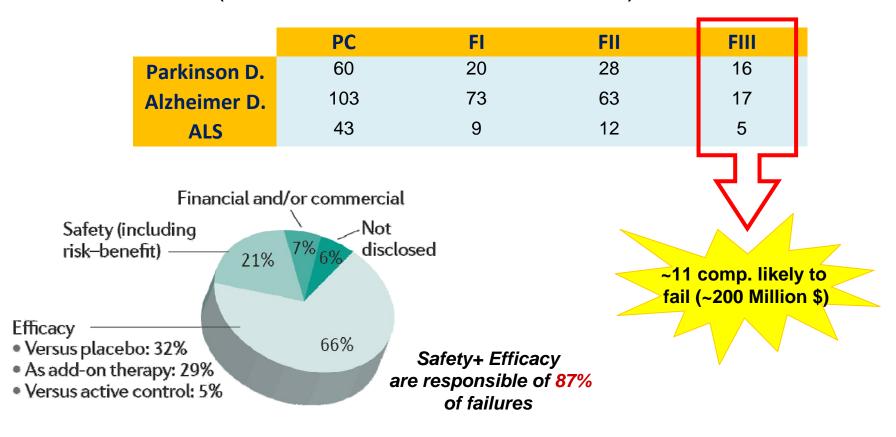








World's Pipeline in Neurological Degenerative Diseases (Alzheimer, Parkinson & ALS):



(1) Arrowsmith J. *Phase III and submission failures 2007-2010*, Nature Reviews Drug Discovery 2011, vol. 10: pp.1
(2) Medtrack Business Intelligence 2011.

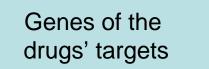




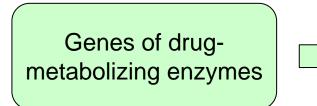




## Effects of gene polymorphisms on drugs



May affect the drug-to-target interaction (*e.g* drug binding or target expression), thus lowering **efficacy** 



Effect on the pharmacokinetics of the drug or its metabolites, resulting in:

- Lower efficacy
- Increased adverse events

Genes of transporter proteins

Effect on the pharmacokinetics of the drug or its metabolites, resulting in:

- Lower efficacy
- Increased adverse events

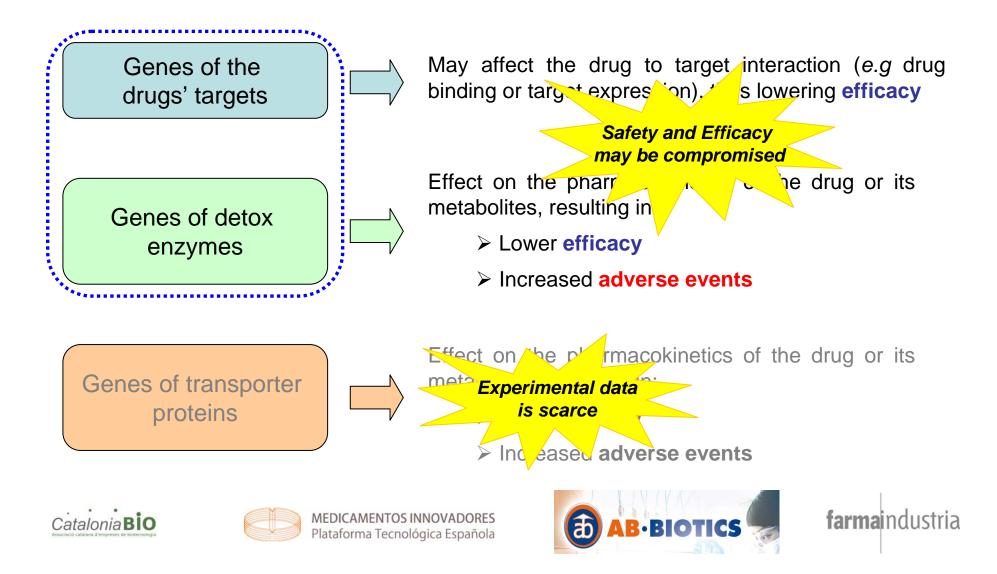






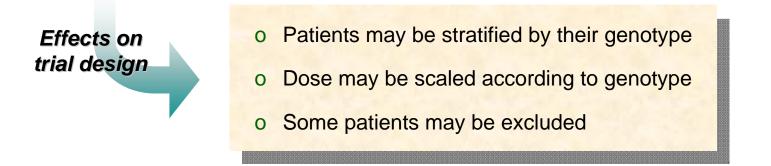


#### Effects of gene polymorphisms on drugs



#### EMA opinion on pharmacogenetic analyses...

- 1. They are **required** when preclinical data shows that polymorphic enzymes are involved in the metabolism of the drug.
- 2. They are **recommended** whenever large interindividual pharmacokinetic variability is observed or safety concerns are observed.
- 3. Prospective sampling of DNA for genotype analysis *a posteriori* is always recommended



(1) European Medicines Agency, Guideline on the use of pharmacogenetic methodologies in the pharmacokinetic evaluation of medicinal products – Draft, EMA/CHMP/37646/2009









- ✓ Genetic differences in genes encoding a drug's molecular target are a primary cause of personalized treatments.
- ✓ Moreover, around 40% of drugs are affected by polymorphic metabolizing enzymes (*detox*), such as CYP2A6, CYP2C9, CYP2C19 o CYP2D6, UGT1A, NAT1/2<sup>1</sup>.
- ✓ Around 20-25 % of the efficacy of all drug treatment is significantly affected by genetic differences in drug metabolizing enzymes<sup>1</sup>.
- ✓ Metabolizing enzymes are the leading cause of pharmacogenetic labeling (~70% of labels)<sup>1</sup>, followed by drug targets.

Both target and metabolizing enzymes should be included in pharmacogenetic analyses

(1) European Medicines Agency, Guideline on the use of pharmacogenetic methodologies in the pharmacokinetic evaluation of medicinal products – Draft, EMA/CHMP/37646/2009

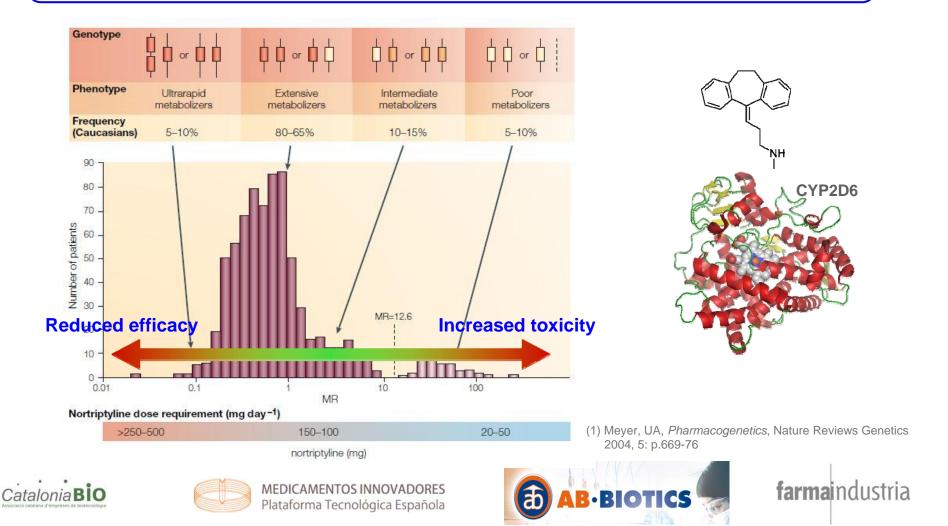








Example: *Nortriptilin* and similar antidepressants display increased toxicity in subjects with low CYP2D6 activity, and reduced efficacy in subjects with increased CYP2D6 activity.

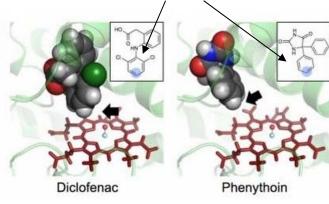


#### How do we select SNP's?

- ✓ The role of typical polymorphic metabolizing enzymes<sup>1</sup> is assessed *in vitro* during preclinical development to decide whether to include their SNPs or not.
- ✓ However, there are more than 200 known genes that can participate in ADME processes.
- ✓ In vitro assays for many of them are not available, and evaluating all their SNPs in a phase-III trial can be very expensive.

 Candidate enzymes can be selected by means of *in silico* analyses

#### Similarity between CYP2C9 substrates



(1) CYP1A, CYP2B6, CYP2C8, CYP2C9, CYP2C19, CYP2D6 y CYP3A4; UGT1A1,



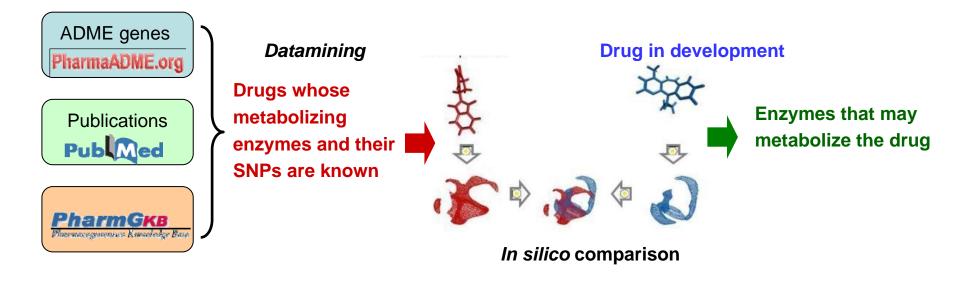






## How do we select SNP's?

- ✓ Data on phase-I and II metabolism is available for many compounds.
- $\checkmark\,$  The new drug may display global or local similarities to these drugs
- ✓ Therefore, we can compile a list of enzymes which are likely to metabolize the new drug, based on small molecule comparison and enzyme docking.











Genes	Our proposal	Marketed ADME pharmacogenetic analyses	
Target	SNPs included	SNPs not included	
Common polymorphic metabolizing enzymes	Those with <i>in silico</i> or experimental evidences are included	All are included, even if experimental data shows that many do not affect the drug	
Other metabolizing enzymes	Those with <i>in silico</i> or experimental evidences are included	Either not included or all included	
throu	One out of 5 drugs is me ugh CYP2D6. Evaluating its ~2 drugs would be wasting mone	25 SNPs <sup>1</sup>	

(1) <u>www.pharmgkb.org</u>, info retrieved on Feb 10<sup>th</sup> 2011









Genes	Our proposal	Marketed ADME pharmacogenetic analyses	
Target	SNPs included	SNPs not included	
Common polymorphic metabolizing enzymes	Those with <i>in silico</i> or experimental evidences are included	All are included, even if experimental data shows that many do not affect the drug	
Other metabolizing enzymes	Those with <i>in silico</i> or experimental evidences are included	Either not included or all included	
	rovides more information per S educes global cost.	SNP analyzed	

(1) <u>www.pharmgkb.org</u>, info retrieved on Feb 10<sup>th</sup> 2011









#### Example: CI1041 o *Besonprodil*<sup>®</sup> (Pfizer Inc.)

NMDA receptor antagonist (N-methyl-D-aspartic), selective for NR1-NR2B dimers.

- The ~15 SNPs of the genes coding for NR1 and NR2B subunits (grin1 and grin2B) would be analyzed.
- SNPs of any metabolizing enzyme with positive results during preclinical development would be analyzed.
- Additionally, only SNPs of other metabolizing enzymes and transporter proteins with *in silico* evidences would be analyzed.

SNPs in genes encoding the molecular target Besonprodil:

- grin1: C112T, C113T, G716A, A750G, G1001C, A290G, G301A, G308A, A1970G, G2108A, G6435A
- > grin2B: G366C, C2664T, C3538T, T4197C, T5988C









- ✓ Lower risk of adverse events due to drug overexposition (*poor metabolizers*) or metabolite overexposition (*ultrarapid metabolizers*).
- ✓ Higher chances of relating adverse events to genetic markers → better chances of product approval
- $\checkmark$  Description of new biomarkers  $\rightarrow$  IP
- ✓ Exposure variability is reduced → sample size and costs are reduced (10% lower variability allows for a sample 20% smaller):

	Trial N = 1000	Trial N = 800
Cost of ~4000€/subject	4.0 Mill €	3.2 Mill €
Genotyping 500€/subject	-	0.4 Mill €
Total Cost	4.0 Mill €	3.6 Mill €

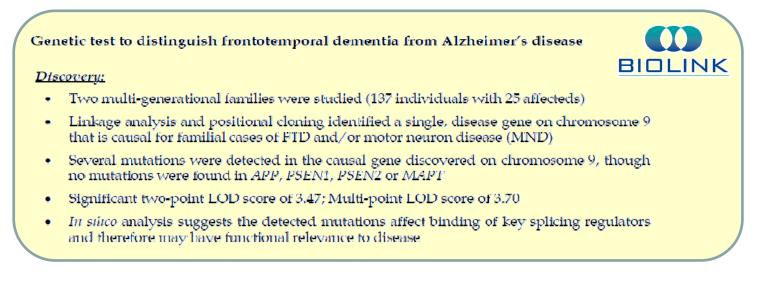








- ✓ New Biomarkers are protectable by IP.
- ✓ The protection can cover:
  - > Methods for genetic testing based upon proprietary genetic biomarkers.
  - Diagnostic kits.
  - Improved therapeutic protocols for the treatment of the target disease.
- $\checkmark$  This protection allows to sell both the drug and the genetic test.











In order to deliver the right planning and execution in each project, AB-BIOTICS offers the following assets to the Pharma industry:

- A team of widely-experienced PhD. geneticists in the area of Personalized Medicine and the discovery of new Biomarkers
- ✓ Full accredited laboratory to genetically test any kind of human samples
- Genetic analysis platforms to test both expression and mutation.
- CRO services are also available, head count, hospitals and physicians.



Generalitat de Catalunya www.gencat.cat











## 3. Availability for cooperation

Preclinical	Phase-I Phase-II	Phase-III
<ul> <li>Search of SNPs in target gene(s)</li> <li><i>In vitro</i> study of polymorphic enzymes</li> <li>In <i>silico</i> selection of additional metabolizing enzymes</li> <li>Phase-I and II designs may be influenced by available data</li> </ul>	<ul> <li>Evaluation of common SNPs</li> <li>Design of phase-III depending on results obtained</li> </ul>	<ul> <li>Validation of the effect of common SNPs</li> <li>Study of the effect of uncommon SNPs</li> <li>Reduced variability in efficacy data allowing for smaller trials</li> </ul>
<ul> <li>Consultancy:</li> <li>Technical proposal</li> <li>In silico analysis</li> <li>Advisory on phase-I and II clinical trial design</li> <li>Biomarkers' patent search</li> </ul>	<ul> <li>SNP's Analysis:</li> <li>&gt;Up to 100 SNP's per patient (logistics included)</li> <li>&gt;Data analysis</li> <li>Consultancy:</li> <li>&gt;Advisory on phase III clinical trial design</li> <li>&gt;Biomarkers: Freedom to Operate</li> </ul>	<ul> <li>SNP's Analysis:</li> <li>&gt;Up to 100 SNP's per patient (logistics included)</li> <li>&gt;Data analysis</li> <li>Consultancy:</li> <li>Patent protection</li> </ul>
	Cost: ~500€ per patient	Cost: ~500€ per patient

Catalonia **BIO** 





# **Thank You!**







