

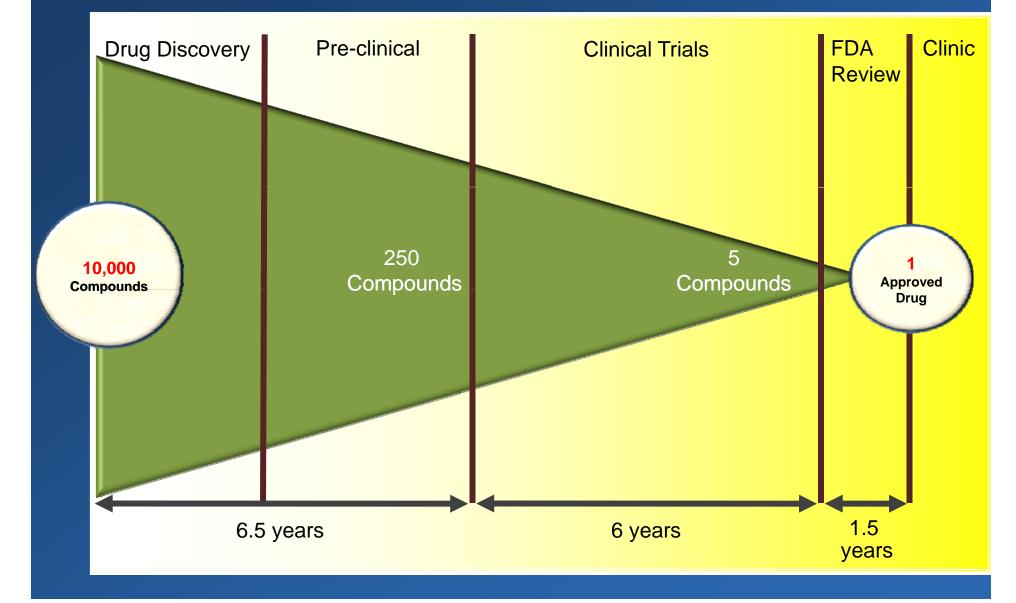


Target Selection and Validation: A More Strategic and Collaborative Approach

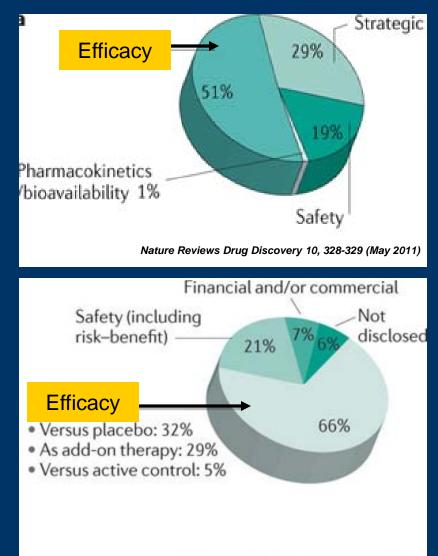
Amy P. Patterson, M.D. Associate Director for Science Policy National Institutes of Health

December 8-9, 2011 Advisory Committee to the Director

Development of New Therapeutics

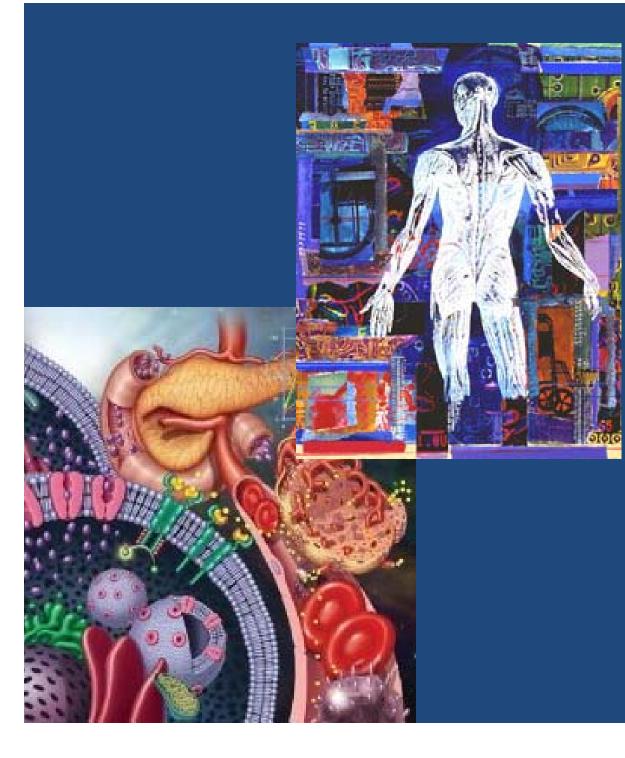


High attrition rate of late-stage drug development points to the need for better target validation



 Phase II failures (2008-2010):
> 51% due to lack of efficacy

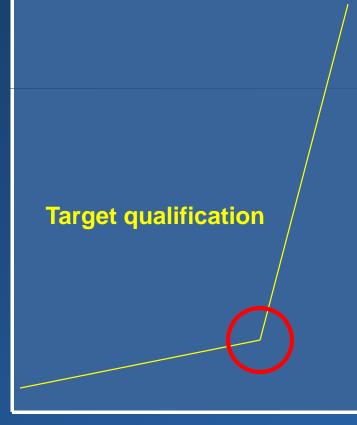
 Phase III and submission failures (2007-2010):
> 66% due to lack of efficacy



Needed: • • Full understanding of the target's role in normal physiology and disease pathogenesis

Taking Another Look at Criteria for Target "Qualification"

Investment of Resources



 Industry is taking a much closer look at the criteria for qualifying a potential target prior to investment of critical resources in drug development

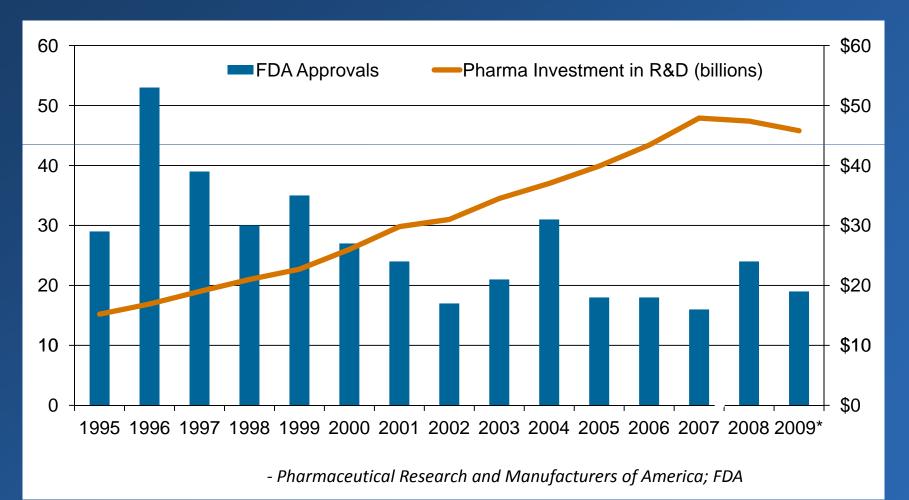
Time

An Abundance of Potential Targets



- Generating a significant inventory of potential targets for new diagnostics and therapeutics:
- Human genome sequence studies
- Large genome wide association studies coupled with meticulous clinical phenotyping
- Microbial genome sequence studies

Despite Greater Investments in R&D by Pharma, Number of New Drug Approvals Has Declined

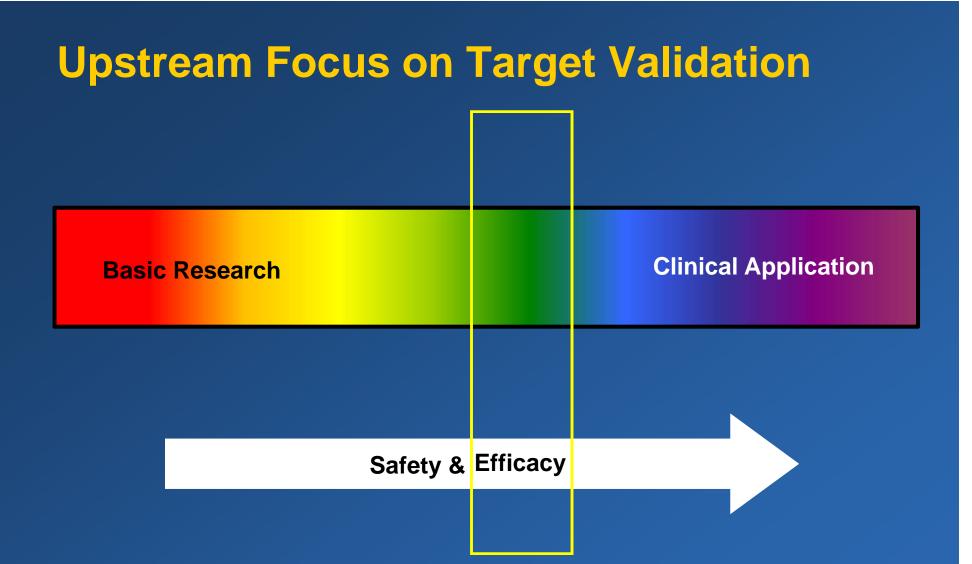


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Missing: Innovation

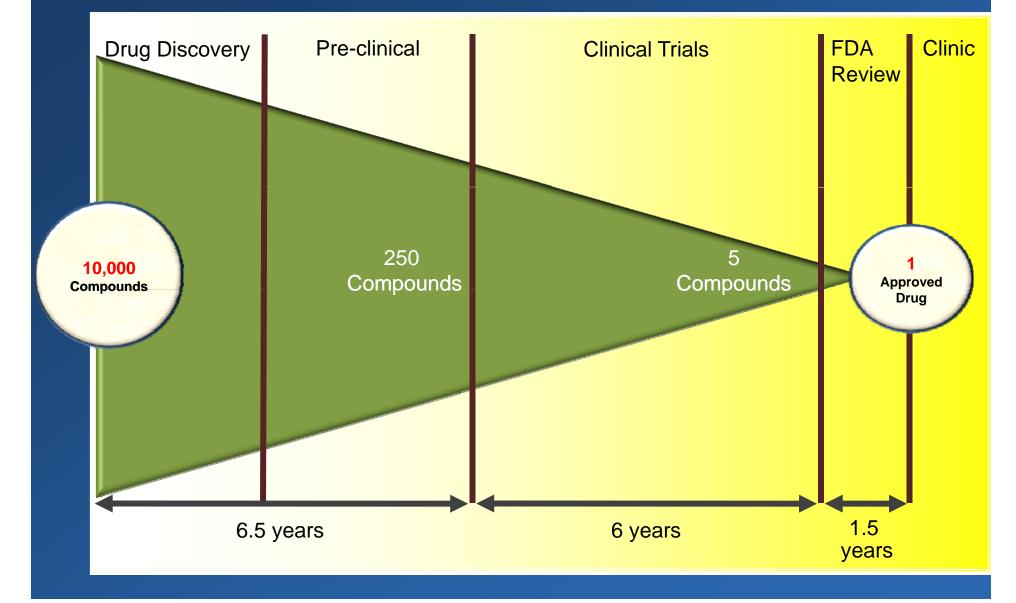


- Rate of innovation in novel target drugs has remained stable over the last 30 years
- Majority of new drugs approved between 1982-2010 target previously exploited structures encoded by the human genome

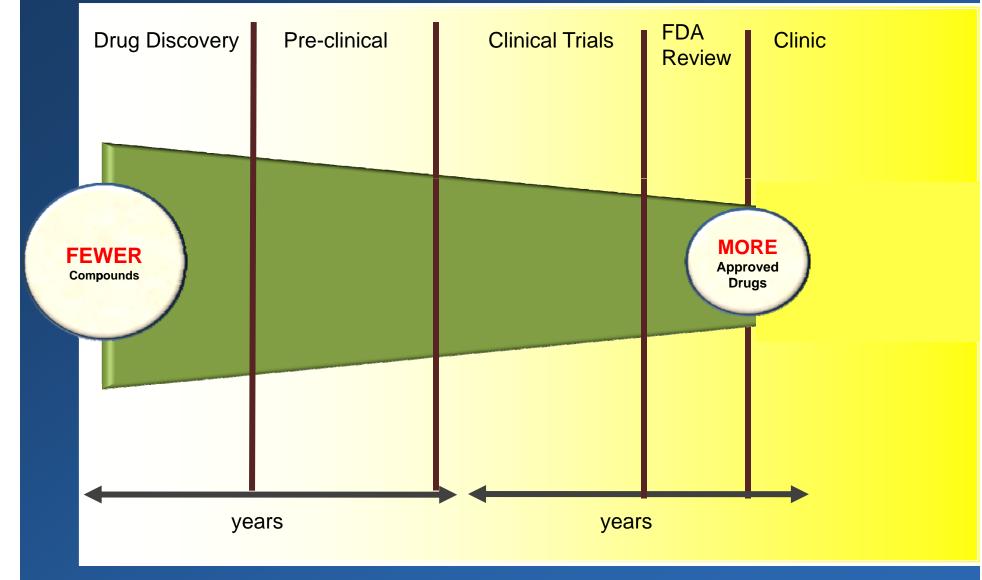


Need new methods, approaches, tools, and technologies to undertake validation in a more efficient and predictable fashion

Development of New Therapeutics



Vision: Development of New Therapeutics with Well Qualified Targets



Challenges

- Insufficient understanding of biologic networks
- Incomplete understanding of the biology of drug-target interaction
- Lack of efficient and accurate ways to determine clinical relevance
- Need to integrate of massive amounts of sequence and phenotype data from public and private sector sources

Select, Relevant NIH Programs

- Whole exome and whole genome sequencing
- The Cancer Genome Atlas (TCGA)
- Genotype-Tissue Expression Resource (GTEx) Pilot Program
- **ENCODE** and Epigenomics Programs
- RNAi Screening
- Library of Integrated Network-based Cellular Signatures (LINCS)
- iPSCs to model disease phenotypes
- Knockout Mouse Project (KOMP)
- The Brain Atlas
- The Biomarkers Consortium

NIH Sequencing Projects: Current Inventory

- Opportunity to strategically mine genome and exome sequencing projects for target validation
 - 192 projects in 16 Institutes and Centers
 - Involve ~68,000 subjects
 - 31% include some whole genome sequencing
 - 38% intramural from seven ICs (NCI, NEI, NHGRI, NIAID, NICHD, NIDCR, NINDS)
 - 30 projects (16%) have <u>></u> 10% samples of non-European ancestry; 55% of projects unspecified

JOINT NH-INDUSTRY TARGET VALIDATION WORKSHOP

NATIONAL INSTITUTES OF HEALTH BUILDING 31, C WING • CONFERENCE ROOM 10 NOVEMBER 3–4, 2011



Workshop Participants

• Leaders and experts from:

- Industry
- Academia
- Government







Workshop Focus

• Development of a collective understanding of the landscape of the target validation through review of:

Current industry target validation process > Illuminating case studies examining Biological relevance of the target to clinical condition >Mechanism of action of the target >Druggable attributes > Potential therapeutic agents Lessons learned >Successful examples illustrated importance of confirming mechanisms of action and biological relevance

Gene- and Phenotype-Directed Target Validation: Selected Examples

Target	Abbreviation (Gene)	Disease/ Condition	Initial Id	Characteristics	Development
Voltage Gated Sodium Channel 1.7	Na _v 1.7 (SCN9A)	Pain, Pain Disorders	Phenotype	Known - MOA, LoF/GoF	Preclinical Lead
Renal Outer Medullary K ⁺ Channel	ROMK (KCNJ1)	Hypertension, Congestive Heart Failure	Phenotype	Known – MOA, LoF/GoF, SNP	Preclinical Lead
lsocitrate Dehydrogenase 1	IDH1 (IDH1)	Secondary Glioblastoma Multiforme	Exome Sequencing	Known – LoF/GoF	Preclinical Lead
Proprotein Convertase Subtilisin Kexin Type 9	PCSK9 (PCSK9)	Hypercholesterolemia	Phenotype	Known – MOA, LoF/GoF	Preclinical Lead, Clinical Trials,
p38 Mitogen- Activated Protein Kinase	P38 MAPK (several isoforms)	Rheumatoid Arthritis, Crohn's Disease, Disorders involving CNS	Biochemical	Biochemical Evidence	Preclinical Lead, Clinical Trials

Workshop Focus (continued)

- Ways to optimize the target validation process
 - Brief overview of relevant resources including an inventory of NIH exome and genome sequencing projects
 - Breakout groups
 - Sequencing
 - Gene expression/epigenomics
 - Networks/perturbagens
 - Multi-cell systems

Moving Forward

- Develop more accurate processes and techniques to identify the most promising targets and to predict which targets are likely to be biologically relevant and tractable
 - Take advantage of advances in sequencing, perturbagens, humanized tissue models, epidemiology, and systems biology
- Capitalize more fully on large scale genome wide association studies and phenotyping efforts to verify clinical relevance of potential targets
- Develop analytic platforms to store, harmonize, and analyze data from multiple sources
- Create a precompetitive shared space or "biology knowledge commons"

Outcomes and Next Steps: Stand Up the Target Validation Consortium

- Launch four workstreams:
 - Genotype2Phenotype
 - Phenotype2Genotype
 - Information Commons for Biological Function
 - Workshop in Boston
 - Cancer Information Commons
 - NCI Workshop
- Further develop the consortium
 - Mission, shared values, value proposition for stakeholders
 - High level governance
 - Explicit goals and milestones
 - > Funding





"The odds of hitting your target go up dramatically when you aim at it." -- Anonymous