

有翅膀的小人類-

果蠅的醫學研究

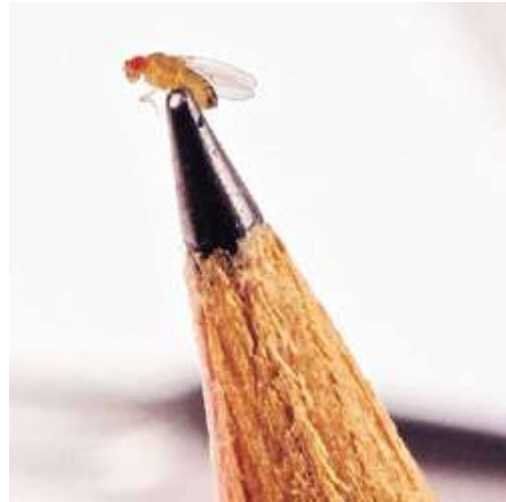
中正大學 生科系

黃敏郎

# Model organism (模式生物)

- Grow quickly
- Relatively simple
- Inexpensive
-

# *Drosophila melanogaster* (果蠅)



- Short life cycle
- Ease of culture and maintenance
- Small genome size
- Extremely low cost of maintenance, propagation, and screening and the rapidity of studies in the fly compared with traditional mammal-based models.

# Nobel prizes in physiology or medicine



T.H. Morgan



Chromosome



H.J. Muller



X-ray mutagenesis



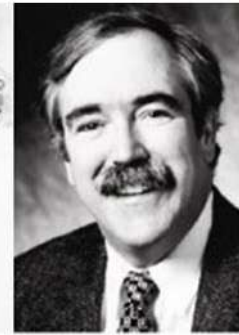
E.B. Lewis



Embryo development and Hox genes



C. Nüsslein-Volhard



E. Wieschaus



R. Axel



Olfactory system

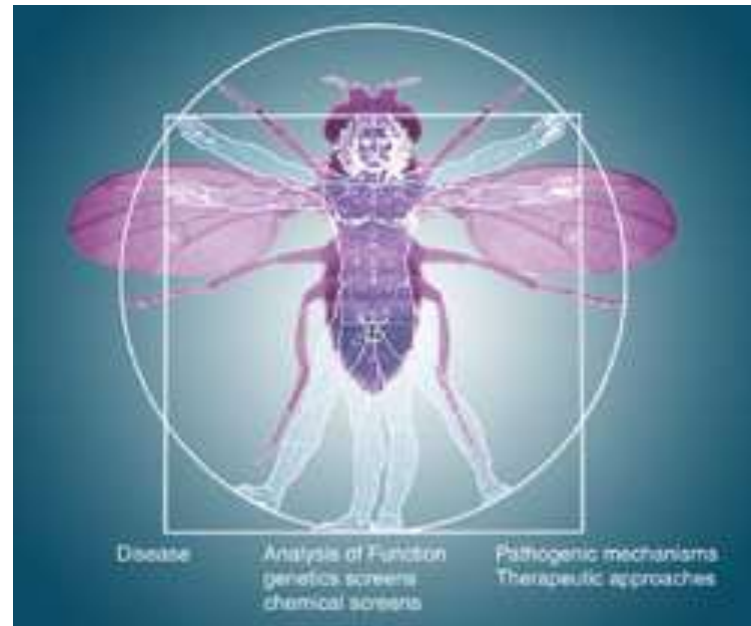
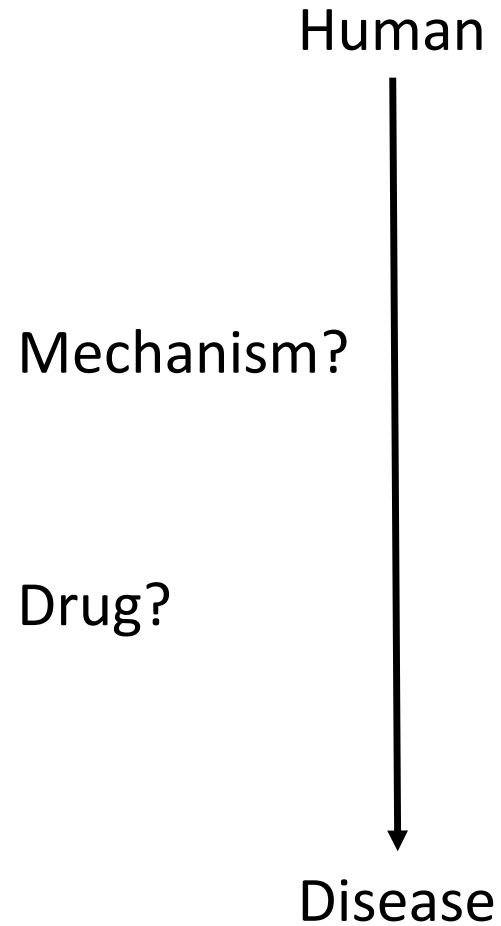


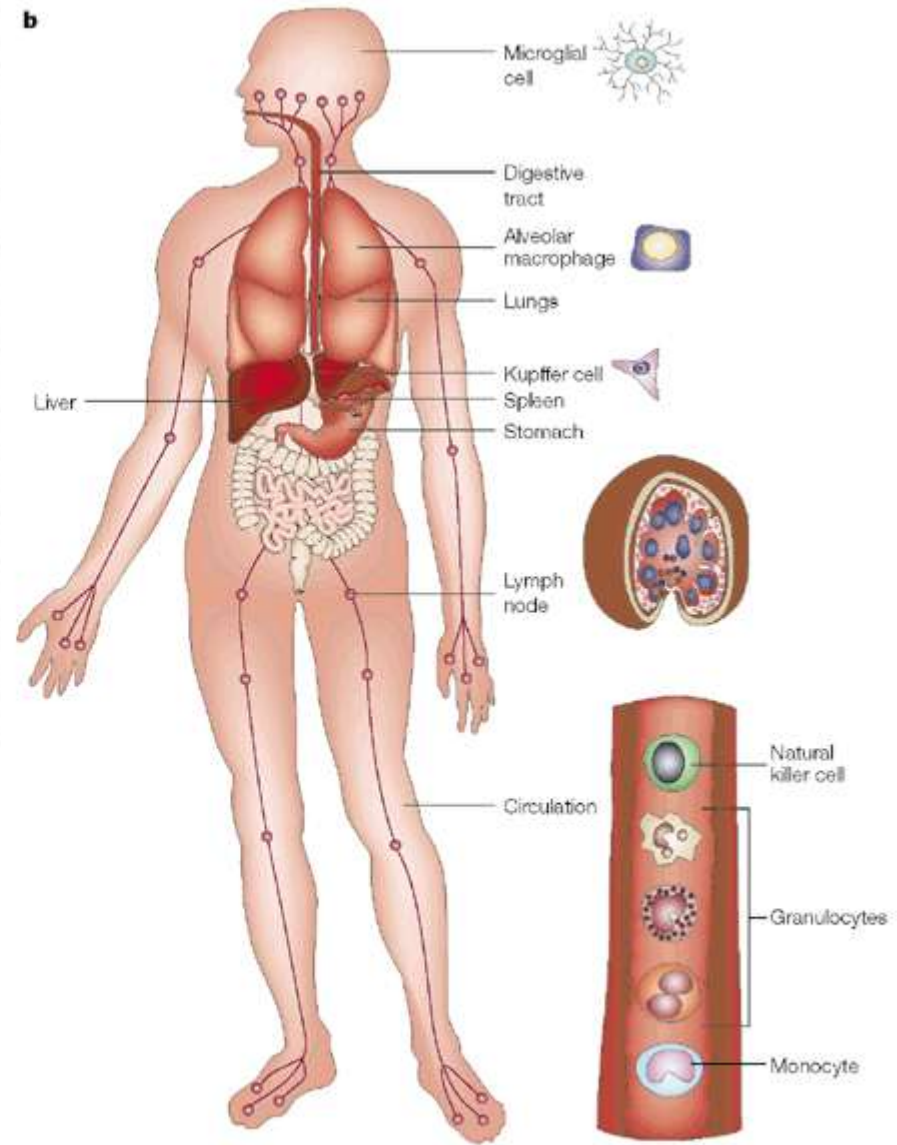
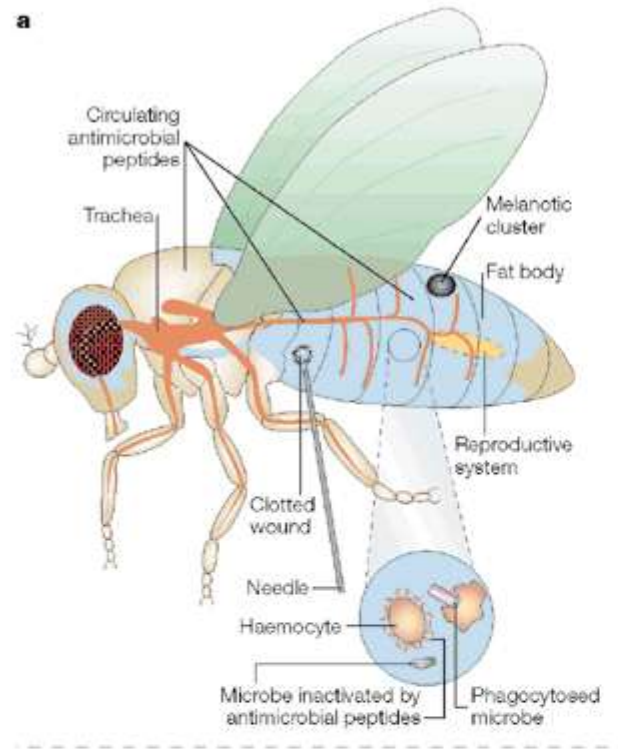
J.A. Hoffmann



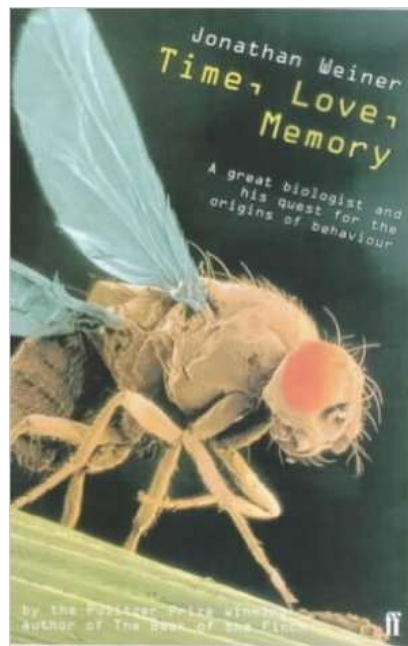
Innate immunity

# *Drosophila* research on human disease





Nature Reviews | Genetics



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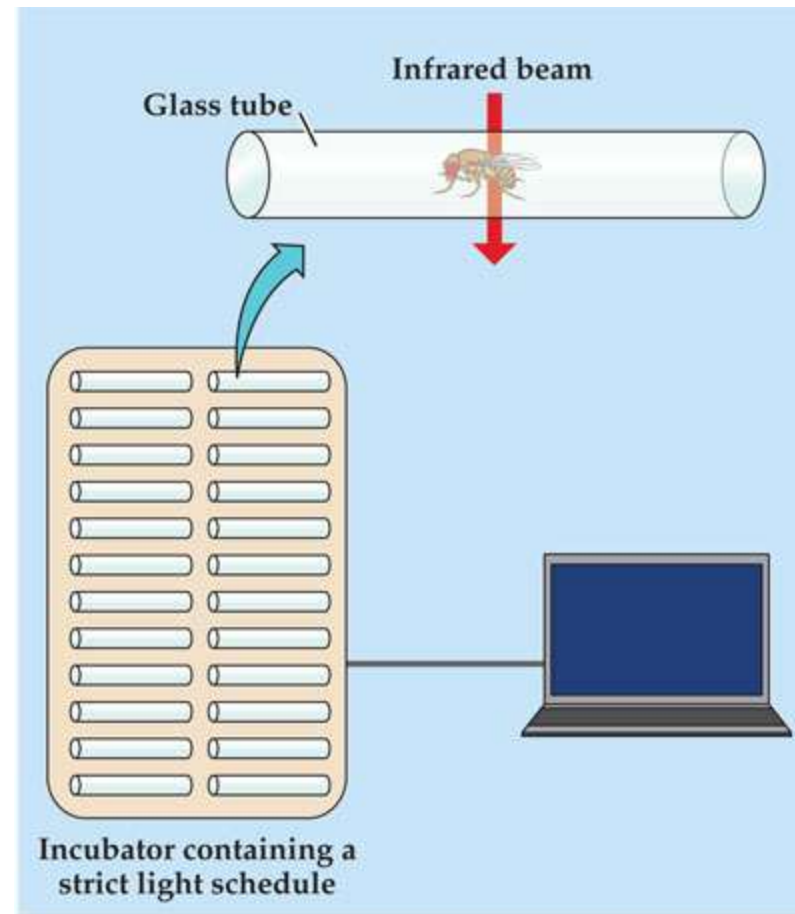
Seymour Benzer

[http://img.pcstore.com.tw/~prod/M15725320\\_big.jpg?pimg=static&P=1428467225](http://img.pcstore.com.tw/~prod/M15725320_big.jpg?pimg=static&P=1428467225)

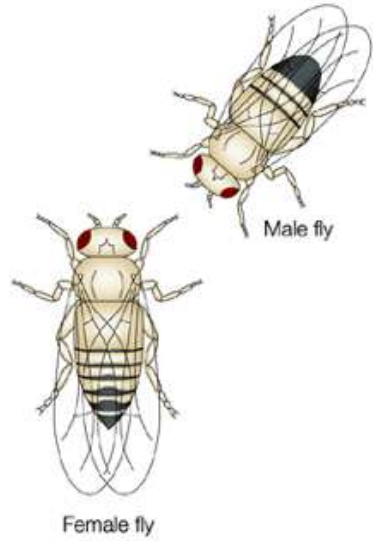
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<https://images-na.ssl-images-amazon.com/images/I/41XSEFN7L.jpg>

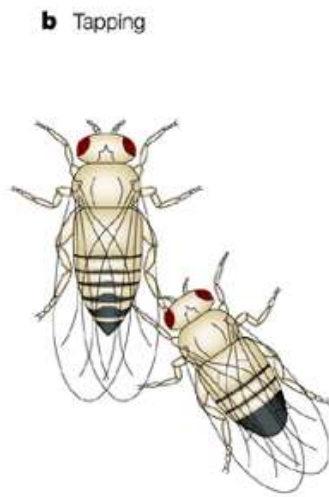




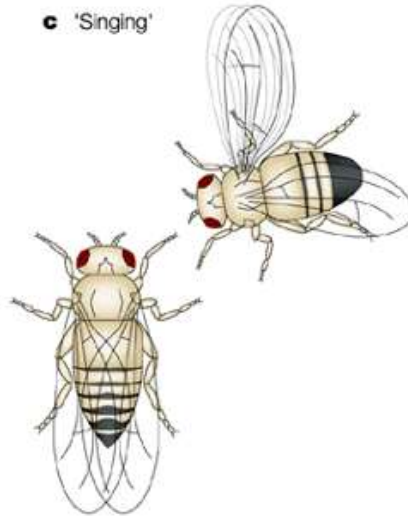
**a** Orienting



**b** Tapping



**c** 'Singing'

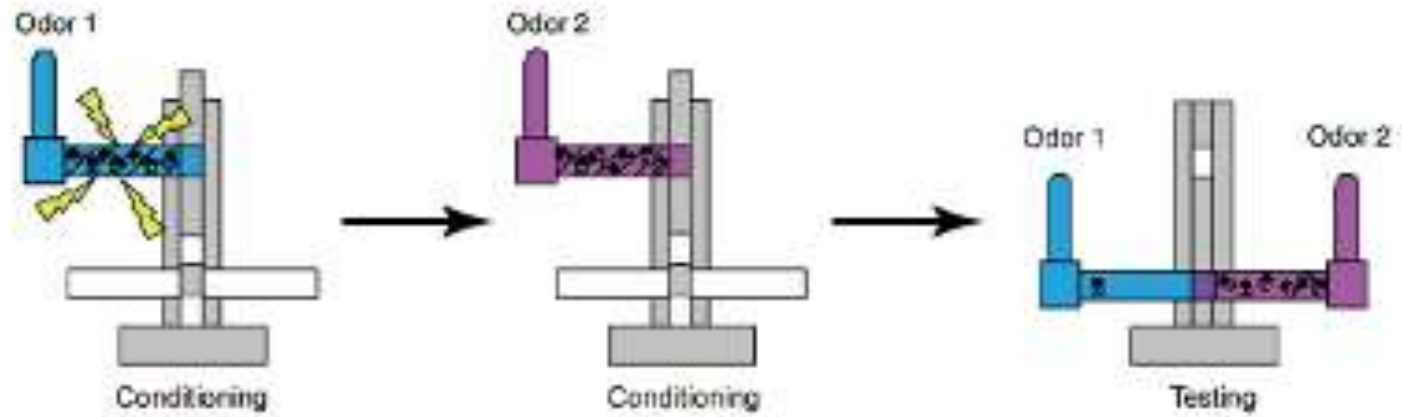


Mating (micro CT)

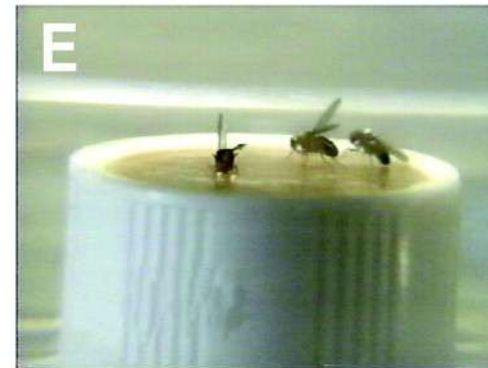
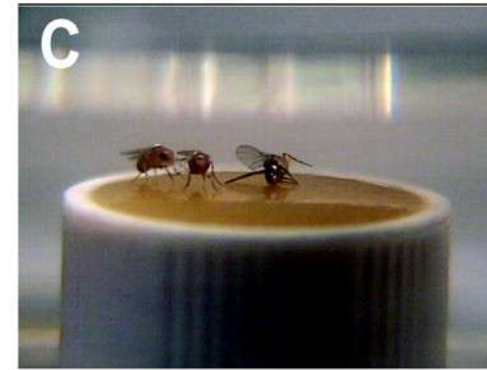
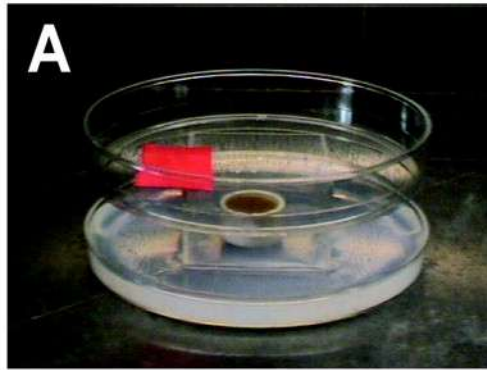
<http://3.bp.blogspot.com/-H3bzQrNCyY0/UuZl8tagZvI/AAAAAAAAACc8/AFuoEUmC-GU/s1600/5-courtship.gif>

<http://news.cornell.edu/stories/2015/06/3-d-scans-mating-fruit-flies-uncover-female-biology>

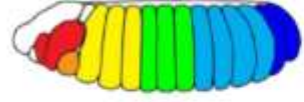
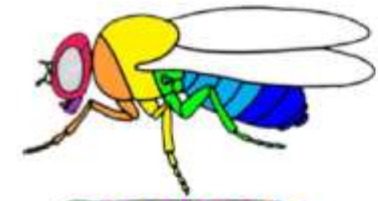
## Olfactory aversive conditioning and testing



## Experimental chamber and components of fruit fly fighting.



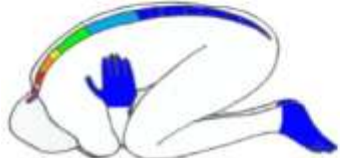
Selby Chen et al. PNAS 2002;99:5664-5668



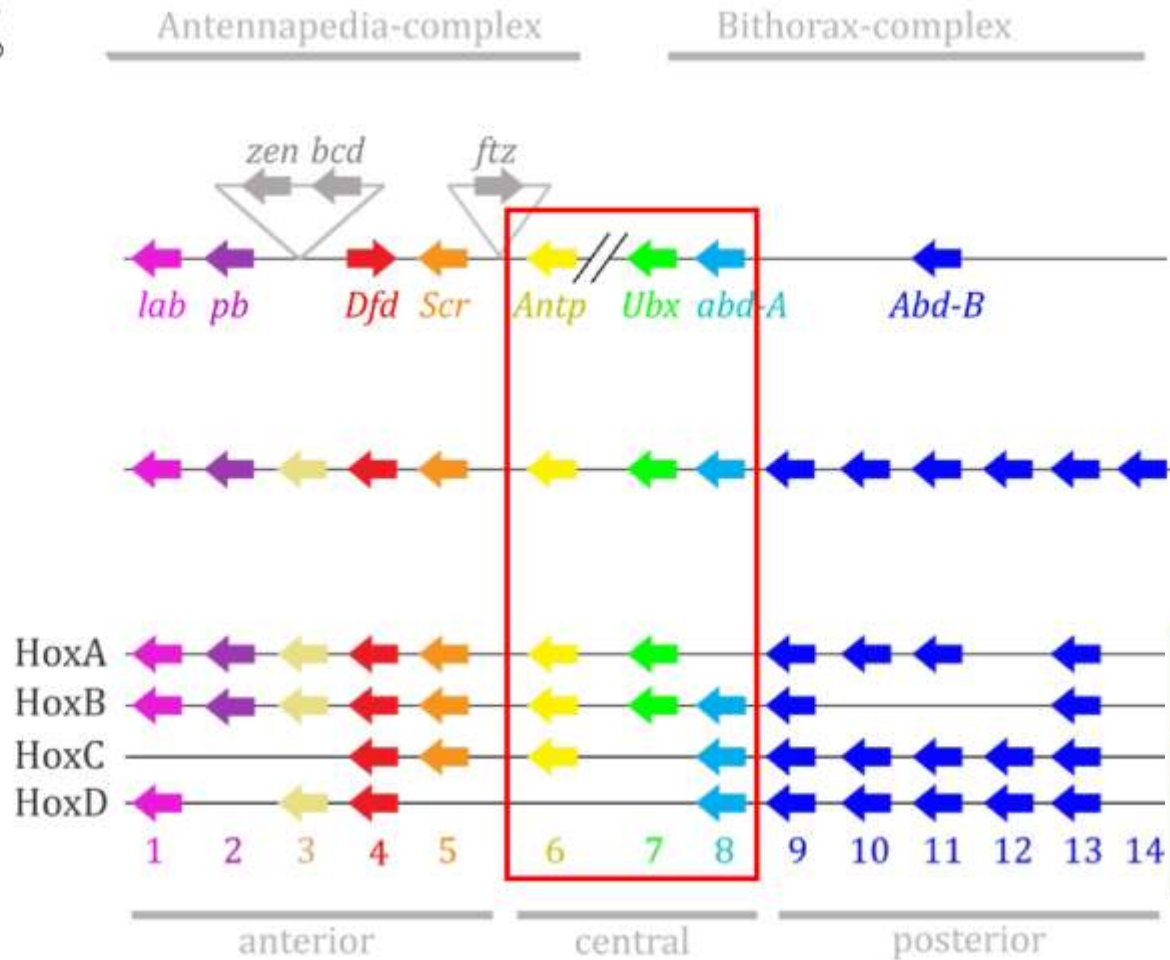
*Drosophila melanogaster*



*Branchiostoma lanceolatum*



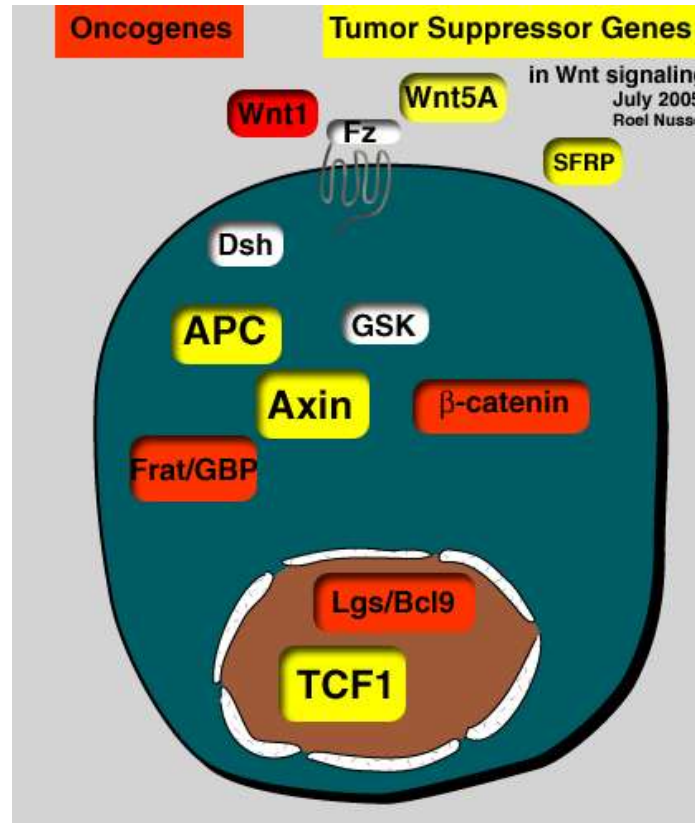
*Homo sapiens*



Synpolydactyly phenotype with mutation in HOXD13 (+10 Ala expansion) in heterozygous (left) and homozygous (hand and foot) individuals.

# Conserved signal pathways

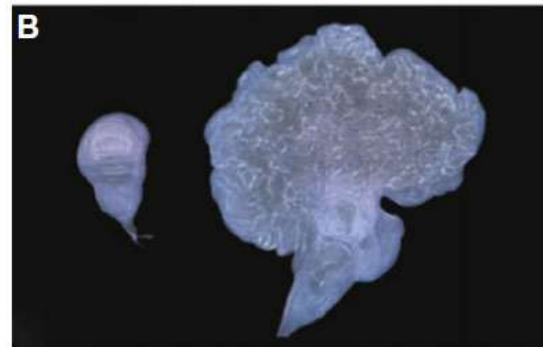
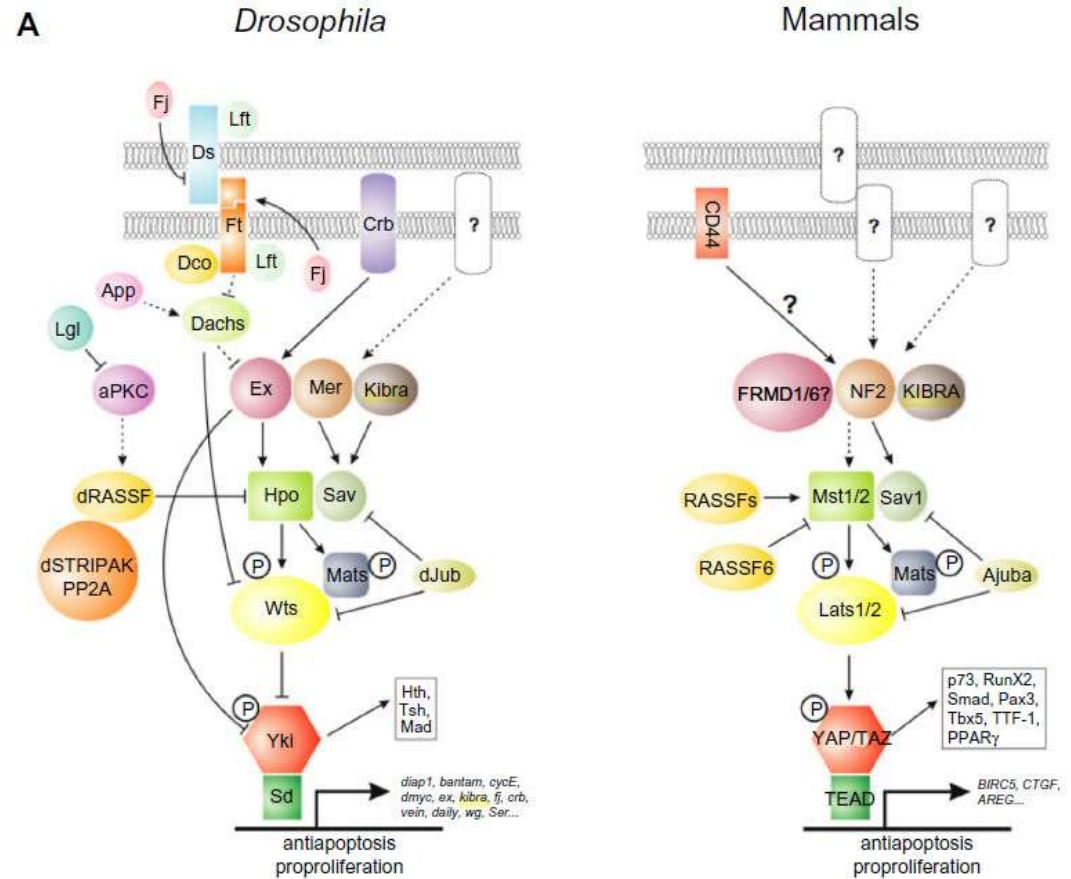
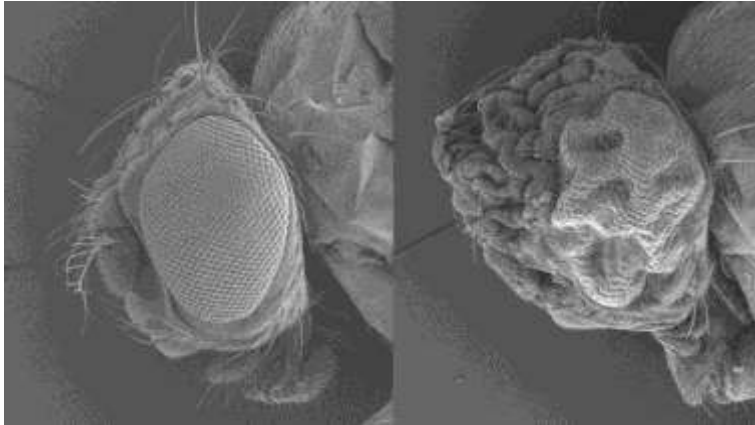
- EGFR (Ras)
- Wingless/Wnt
- Notch



**Table 1. Pathways associated with human congenital disorders**

Pathway <sup>1</sup>	Disease	Phenotype MIM no. <sup>2</sup>	Human causal gene	<i>Drosophila</i> ortholog <sup>3</sup>
Notch	Alagille syndrome	610205	<i>NOTCH2</i> <i>JAG1</i>	<i>N</i> <i>Ser</i>
	Congenital heart disease Tetralogy of Fallot	600001 187500	<i>JAG1</i> <i>JAG1</i>	<i>Ser</i> <i>Ser</i>
	Adams-Oliver syndrome 5	616028	<i>NOTCH1</i>	<i>N</i>
	Hajdu-Cheney syndrome	102500	<i>NOTCH2</i>	<i>N</i>
	Myofibromatosis, infantile 2	615293	<i>NOTCH3</i>	<i>N</i>
	Lateral meningocele syndrome	130720	<i>NOTCH3</i>	<i>N</i>
	Spondylocostal dysostosis 1	277300	<i>DLL3</i>	<i>dl</i>
	Wnt/PCP	Van Maldergem syndrome	615546	<i>DCHS1</i> <i>FAT4</i>
Exudative vitreoretinopathy 1		133780	<i>LRP5</i> <i>FZD4</i> <i>NDP</i>	<i>arr</i> <i>fzd</i> Unknown
Hennekam lymphangiectasia-lymphedema syndrome 2		616006	<i>FAT4</i>	<i>ft</i>
Robinow syndrome, autosomal dominant 2		616331	<i>DVL1</i>	<i>dsh</i>
Mental retardation, autosomal dominant 19		615075	<i>CTNNB1</i>	<i>arm</i>
Tetra-amelia syndrome		273395	<i>WNT3</i>	<i>wg</i>
Mullerian aplasia and hyperandrogenism		158330	<i>WNT4</i>	<i>wg</i>
SERKAL syndrome		611812	<i>WNT4</i>	<i>wg</i>
Fuhrmann syndrome		228930	<i>WNT7A</i>	<i>wg</i>
Odontoonychodermal dysplasia		257980	<i>WNT10A</i>	<i>wg</i>
Split-hand/foot malformation 6		225300	<i>WNT10B</i>	<i>wg</i>
Caudal duplication anomaly		607864	<i>AXIN1</i>	<i>axn</i>
Tooth agenesis, selective, 4		150400	<i>AXIN2</i>	<i>axn</i>

- Hippo pathway
- Size control
- Tumor suppression





# Advantage

- 13000 genes, including the counterparts of 65% human disease-causing genes
- Shares many similar features and pathways with humans
- Lack of genetic redundancy
- Bypass some of the ethical issues of biomedical research involving human subjects
- Powerful genetic tools

# Powerful genetic tools

- Mutants
- GAL4/UAS
- Mosaic analysis
- Time and tissue specific inducible promoters are available
- UAS-RNAi
- EP lines

# 樂於合作與分享的果蠅社群

- FlyBase
- Stock centers
- FlyCore (臺灣果蠅遺傳資源中心)

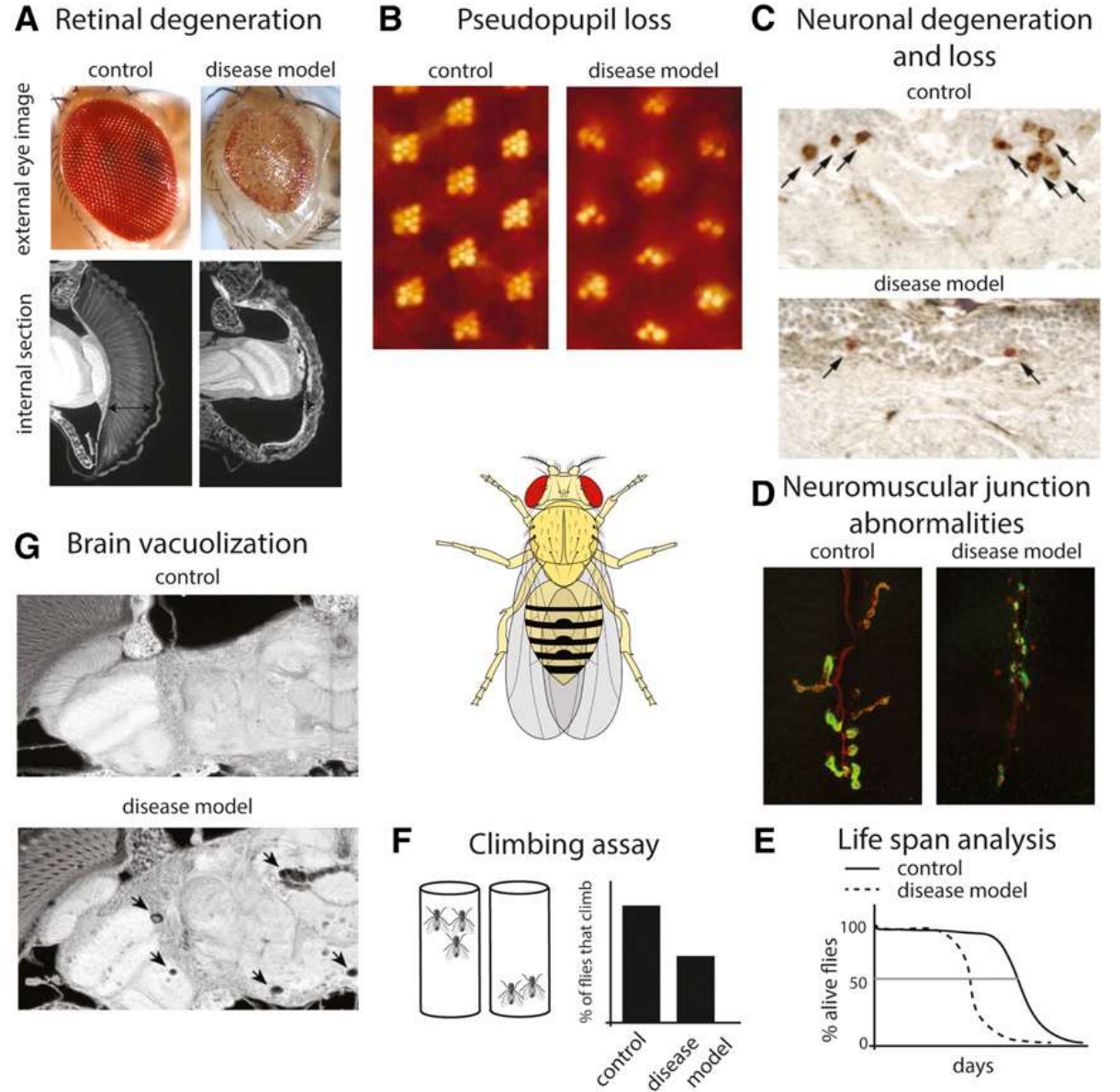
# 台灣的果蠅實驗室 > 50

- 中研院 13
- 台大 10
- 師大 1
- 國防醫 2
- 陽明 2
- 長庚 4
- 中央 1
- 清大 5
- 交大 1
- 國衛院 2
- 東海 2
- 中國醫 2
- 暨南 1
- 中正 1
- 成大 4
- 慈濟 1

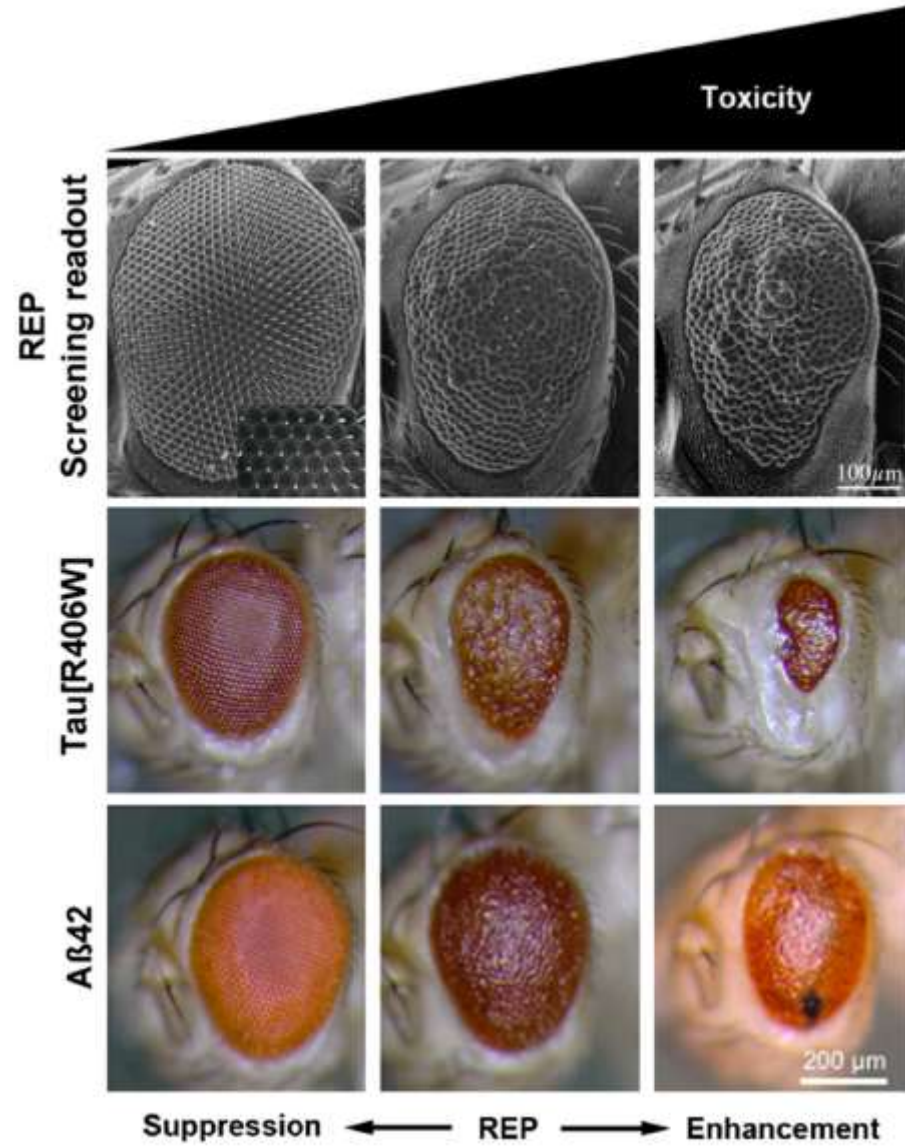
# Limitation

- No model organisms is expected to faithfully replicate the human disease phenotype
- Vertebrate- or human-specific factors, cells, tissues, or systems

- Overexpression of disease gene  
→ Disease model



- Modifier screen



- Alzheimer's disease ( $A\beta$ )
- Polyglutamine expansion disorders
  - Huntington's disease (Htt)
  - Spinocerebellar ataxias 3 (小腦萎縮症) (Ataxin-3)
  - Amyotrophic lateral sclerosis (肌萎縮性側索硬化; 漸凍人)

→ Modifiers include chaperone and ubiquitin-proteasome pathway



Nat Genet. 1999 Dec;23(4):425-8.

## **Suppression of polyglutamine-mediated neurodegeneration in *Drosophila* by the molecular chaperone HSP70.**

Warrick JM<sup>1</sup>, Chan HY, Gray-Board GL, Chai Y, Paulson HL, Bonini NM.

### **⊖ Author information**

<sup>1</sup>Department of Biology, University of Pennsylvania, Philadelphia, Pennsylvania, USA.

### **Abstract**

At least eight inherited human neurodegenerative diseases are caused by expansion of a polyglutamine domain within the respective proteins. This confers dominant toxicity on the proteins, leading to dysfunction and loss of neurons. Expanded polyglutamine proteins form aggregates, including nuclear inclusions (NI), within neurons, possibly due to misfolding of the proteins. NI are ubiquitinated and sequester molecular chaperone proteins and proteasome components, suggesting that disease pathogenesis includes activation of cellular stress pathways to help refold, disaggregate or degrade the mutant disease proteins. Overexpression of specific chaperone proteins reduces polyglutamine aggregation in transfected cells, but whether this alters toxicity is unknown. Using a *Drosophila melanogaster* model of polyglutamine disease, we show that directed expression of the molecular chaperone HSP70 suppresses polyglutamine-induced neurodegeneration *in vivo*. Suppression by HSP70 occurred without a visible effect on NI formation, indicating that polyglutamine toxicity can be dissociated from formation of large aggregates. Our studies indicate that HSP70 or related molecular chaperones may provide a means of treating these and other neurodegenerative diseases associated with abnormal protein conformation and toxicity.

# SCIENTIFIC REPORTS



**OPEN** *Drosophila* screen connects nuclear transport genes to DPR pathology in c9ALS/FTD

Received: 07 August 2015

Accepted: 11 January 2016

Published: 12 February 2016

Steven Boeynaems<sup>1,2,\*</sup>, Elke Bogaert<sup>1,2,\*</sup>, Emiel Michiels<sup>1,2</sup>, Ilse Gijssels<sup>3,4</sup>, Anne Sieben<sup>3,4,5</sup>, Ana Jovičić<sup>6</sup>, Greet De Baets<sup>7,8</sup>, Wendy Scheveneels<sup>1,2</sup>, Jolien Steyaert<sup>1,2</sup>, Ivy Cuijt<sup>3,4</sup>, Kevin J. Verstrepen<sup>9,10</sup>, Patrick Callaerts<sup>11,12</sup>, Frederic Rousseau<sup>7,8</sup>, Joost Schymkowitz<sup>7,8</sup>, Marc Cruts<sup>3,4</sup>, Christine Van Broeckhoven<sup>3,4</sup>, Philip Van Damme<sup>1,2,13</sup>, Aaron D. Gitler<sup>6</sup>, Wim Robberecht<sup>1,2,13</sup> & Ludo Van Den Bosch<sup>1,2</sup>

Hexanucleotide repeat expansions in *C9orf72* are the most common cause of amyotrophic lateral sclerosis (ALS) and frontotemporal degeneration (FTD) (c9ALS/FTD). Unconventional translation of these repeats produces dipeptide repeat proteins (DPRs) that may cause neurodegeneration. We performed a modifier screen in *Drosophila* and discovered a critical role for importins and exportins, Ran-GTP cycle regulators, nuclear pore components, and arginine methylases in mediating DPR toxicity. These findings provide evidence for an important role for nucleocytoplasmic transport in the pathogenic mechanism of c9ALS/FTD.

**Amyotrophic lateral sclerosis (ALS) and frontotemporal degeneration (FTD)**

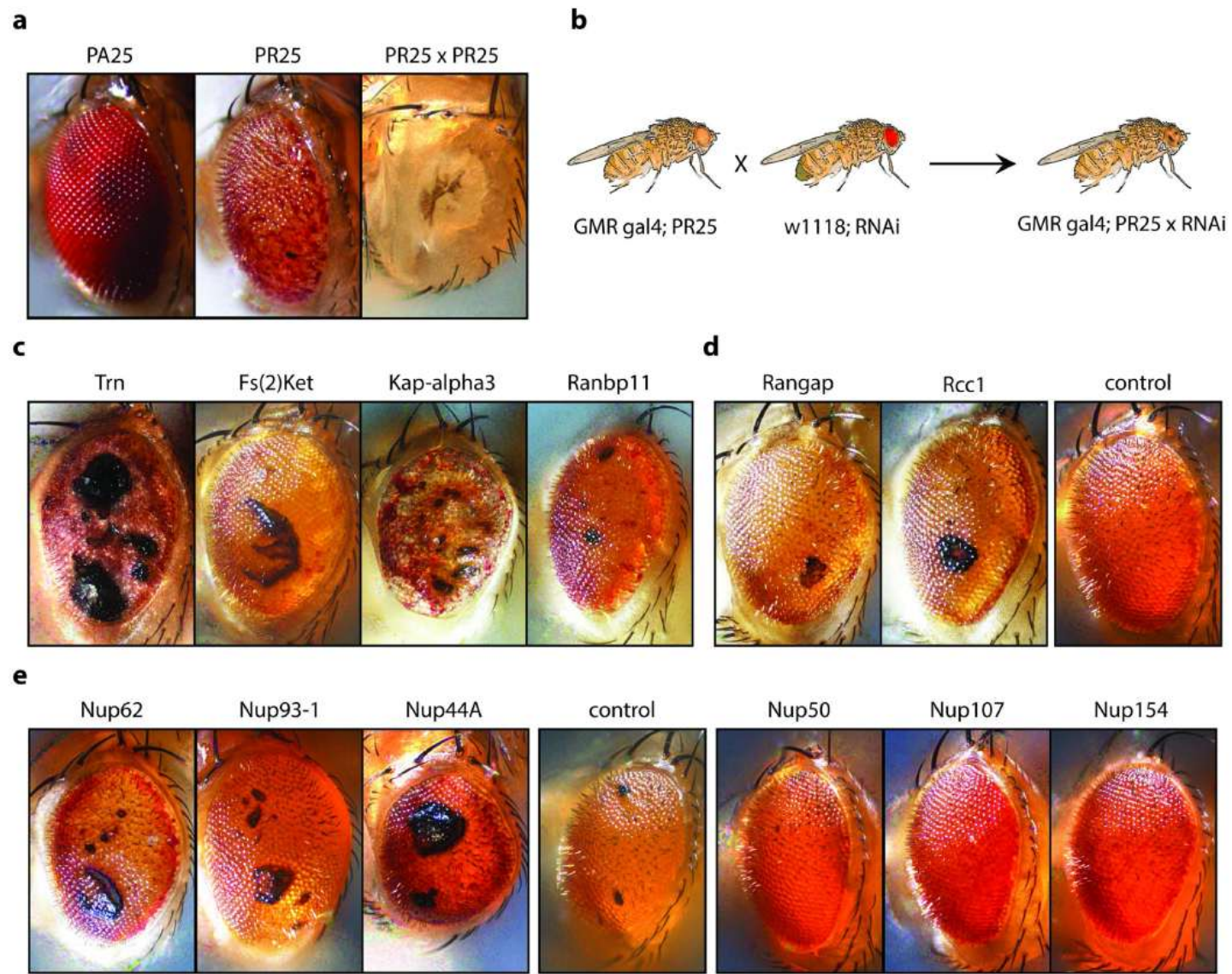
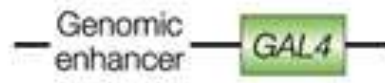
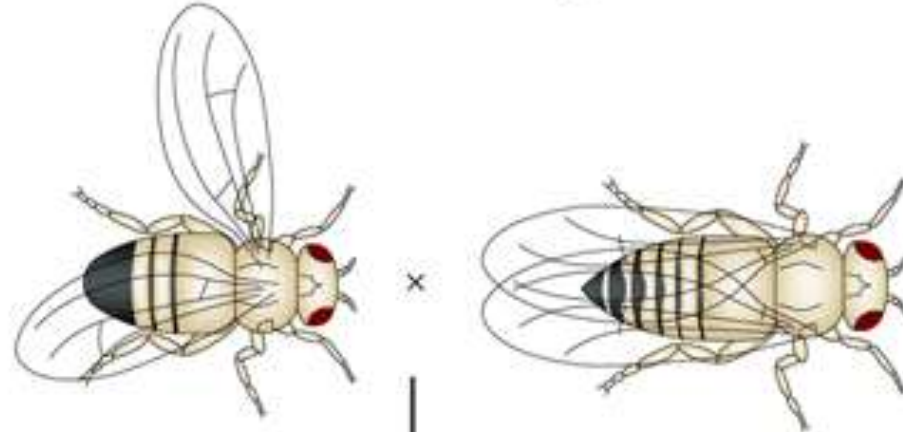


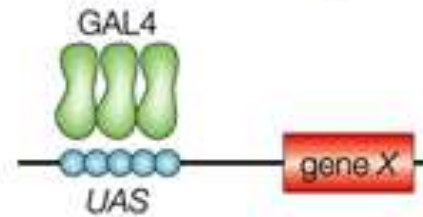
Figure 1. Genes implicated in nuclear transport are potent modifiers of PR toxicity in *Drosophila*.

Enhancer-trap GAL4

UAS-gene X



Tissue-specific expression of GAL4



Transcriptional activation of gene X

Nature Reviews | **Genetics**

- Drugs can modify the phenotypes.

- 薑黃素

OPEN

## Curcumin modulates cell death and is protective in Huntington's disease model

Anjalika Chongtham & Namita Agrawal

Received: 31 July 2015

Accepted: 25 November 2015

Published: 05 January 2016

Huntington's disease (HD) is a progressive, dominantly inherited neurological disorder caused by an abnormal expansion of polyglutamine (polyQ) repeat within the Huntingtin (Htt) protein with no disease modifying treatments. In a *Drosophila* model of HD, expression of mutant Huntingtin (Htt) protein with expanded polyQ leads to formation of inclusion bodies (IBs), increase in cellular toxicity, progression of motor disabilities and reduced viability. Multiple cellular events such as oxidative stress, mitochondrial dysfunction, inflammation and transcriptional dysregulation are reported to contribute to pathology, however, till date there are no disease-modifying treatments with least side effects. Therefore, we investigated effect of the phytochemical curcumin on HD pathogenesis. Curcumin, a phytochemical and commonly used ingredient in Asian food has a wide spectrum of anti-oxidant, anti-inflammatory and anti-fibrillogenic properties. In this study, we provide evidence that curcumin significantly ameliorates disease symptoms in a *Drosophila* model of HD by suppressing cell death and can be a key to halting the progression of Huntington's disease with least side effects.

# Problem of drug screens

- For example, a recent screen of **184,880** novel compounds using a “filter retardation assay” of **Huntington's disease** (HD) aggregates led to the identification of multiple lead compounds, including a number of benzothiazoles that inhibited polyglutamine-mediated aggregation of toxic and misfolded proteins.
- Because riluzole, a closely related benzothiazole, had previously shown therapeutic benefit in patients with amyotrophic lateral sclerosis drugs from this structural class of molecules were tested for further development.
- In a cell culture model of aggregation, **all** primary hits were found to be **toxic to cells**, and in an **animal model** of HD, **none** of the compounds was of **therapeutic**.

- High-throughput screening
- Fully automated scoring of a visible phenotype, either live/dead, or a visible marker.

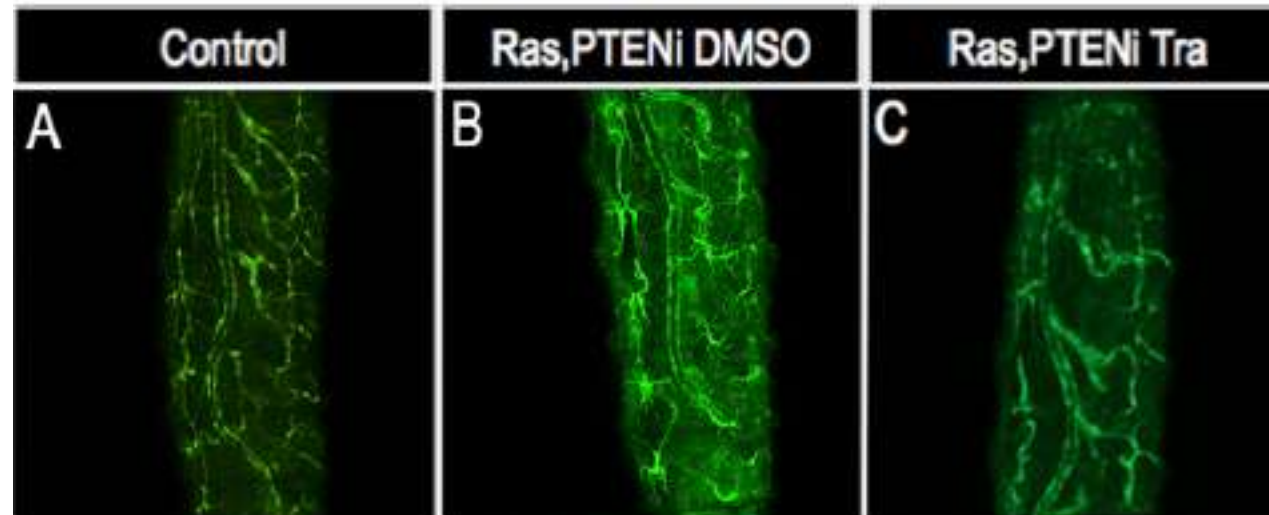
→ fly!



# *Drosophila* Lung Cancer Models Identify Trametinib plus Statin as Candidate Therapeutic

Benjamin D. Levine<sup>1</sup> and Ross L. Cagan<sup>1,\*</sup>

<sup>1</sup>Department of Developmental and Regenerative Biology and the Graduate School of Biomedical Sciences, Icahn School of Medicine at Mount Sinai, One Gustave Levy Place, New York, NY 10029-1020, USA



Screen  
1,192 FDA-approved drugs

Trametinib: cancer drug;  
MEK inhibitor

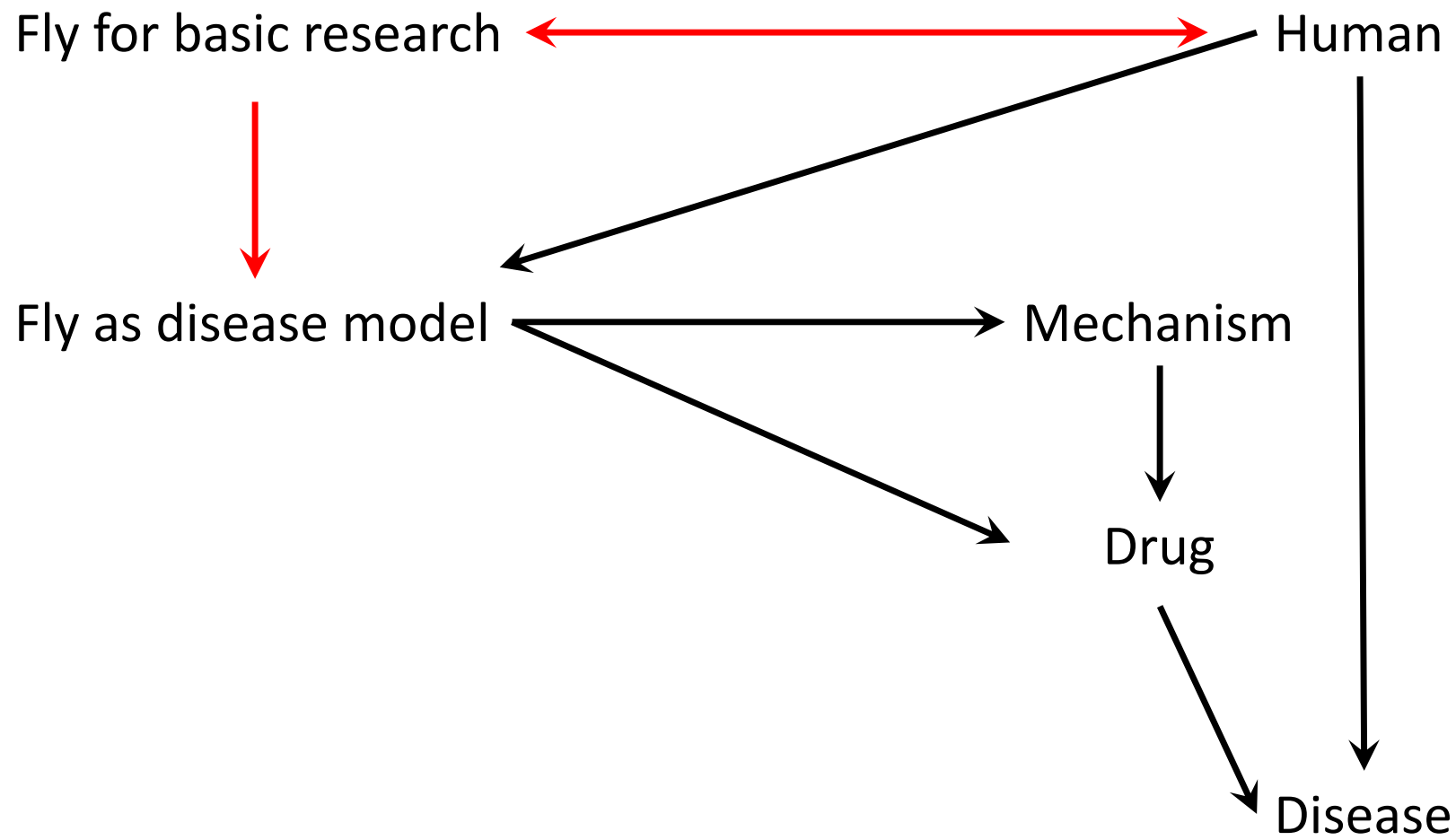
Statin: lipid-lowering; HMG-  
CoA reductase inhibitors

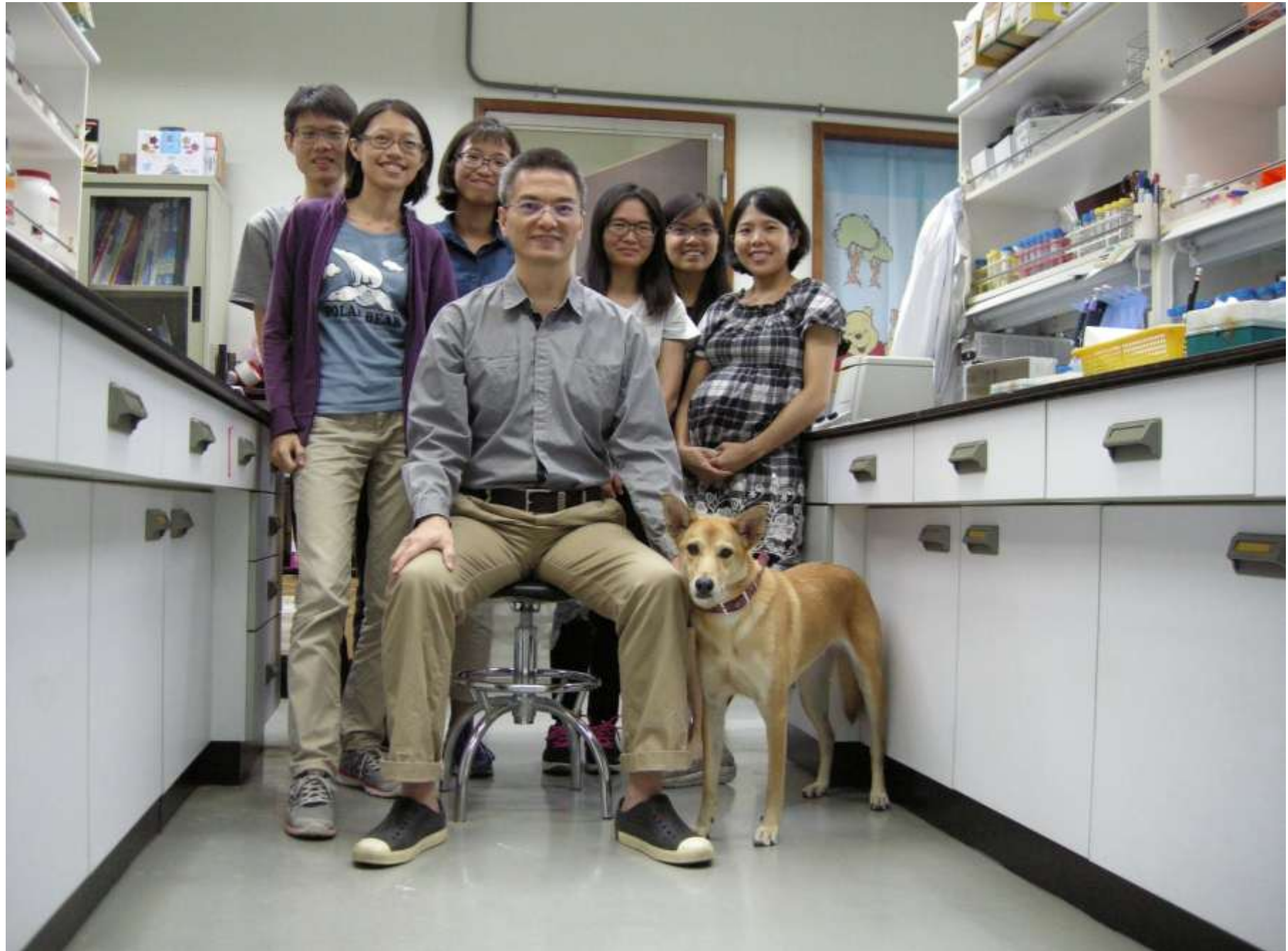
# From a human disease gene to the fly homolog

- Studying the fly's homolog of the disease gene *parkin* for Parkinson's disease

# From a fly gene to human disease

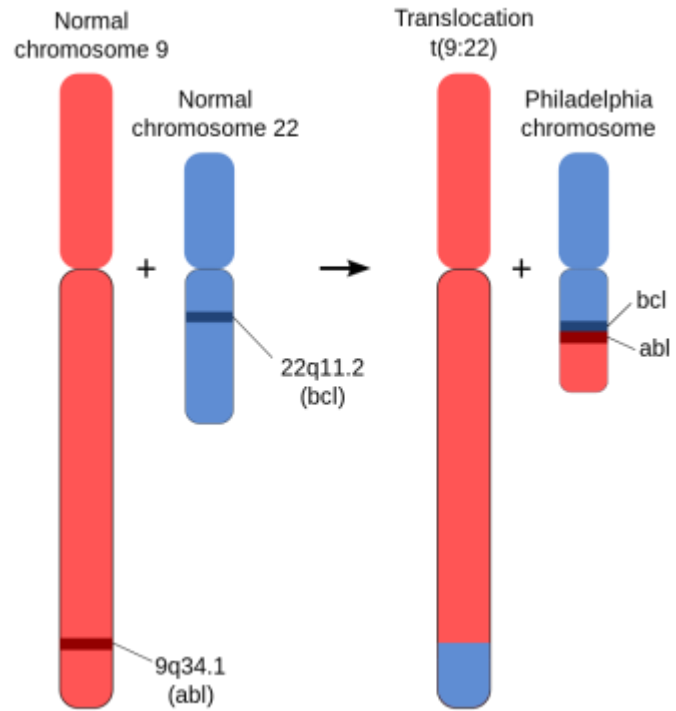
- study of a fly gene
  - → mutant phenotype
  - whether its human homolog is a disease gene?
  - the mutant can be the disease model



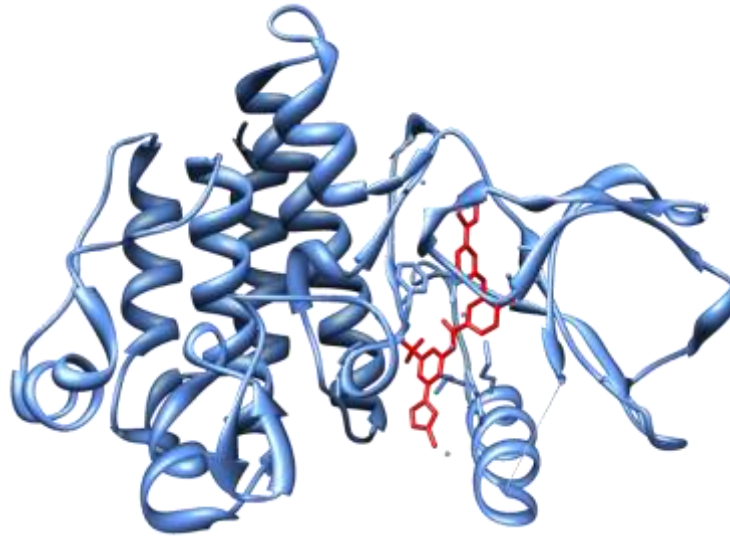


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- Lepesant J.-A. 2015. Comptes Rendus Biologies. The promises of neurodegenerative disease modeling.
- Pandey U. B. and Nichols C. D. 2011. Pharmacological Reviews. Human disease models in *Drosophila melanogaster* and the role of the fly in therapeutic drug discovery.



Philadelphia chromosome



Crystal structure of Abl kinase domain (blue) in complex with 2nd generation [tyrosine kinase inhibitor](#) (TKI) [nilotinib](#)(red)