



National Institutes  
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# Genetics of Parkinson Disease

**PFNCA Symposium**

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**National Institutes of Health**

**National Institute of Neurological Disorders and Stroke**

# Disclosures

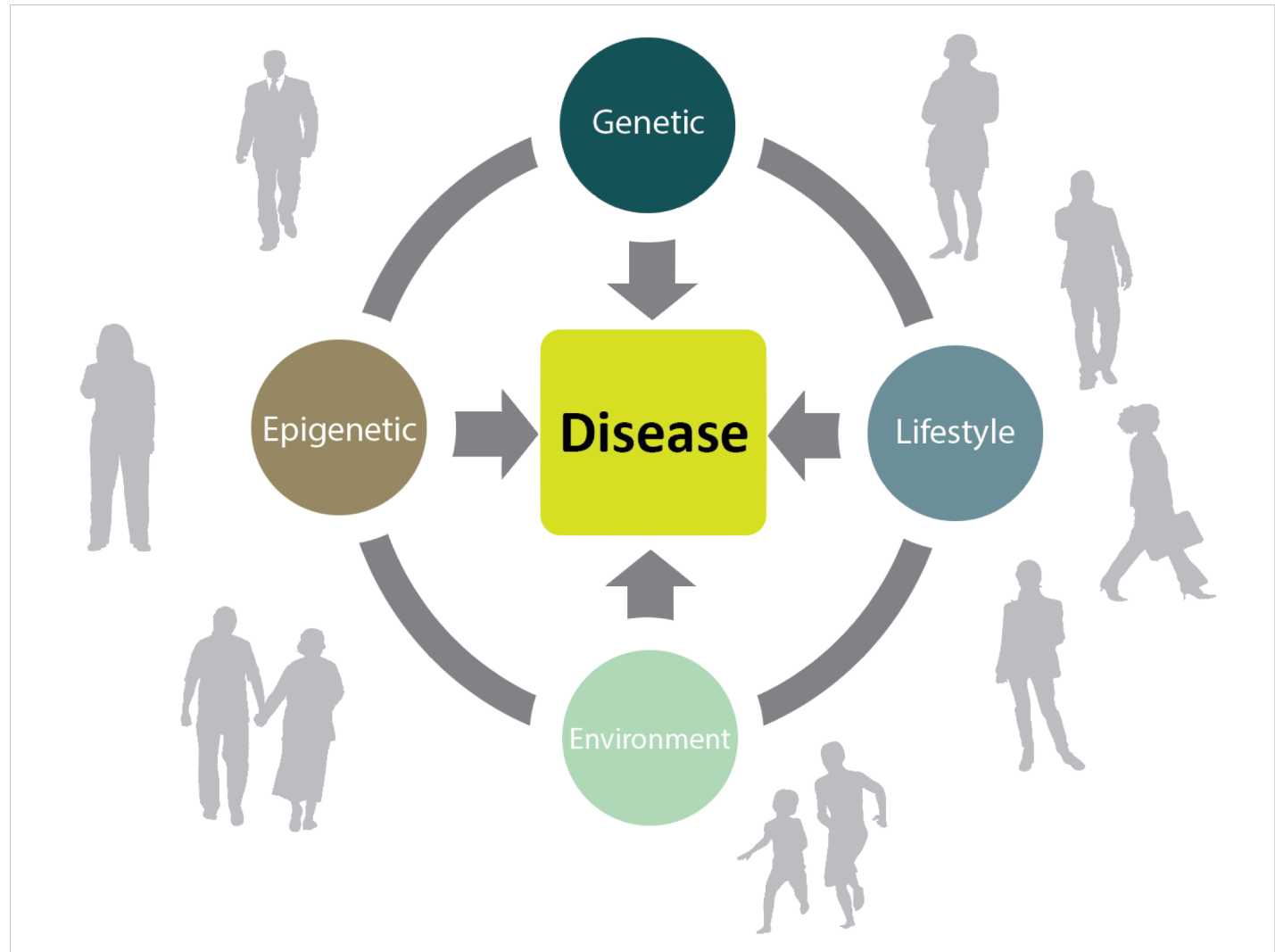
- Research supported by the intramural research program of the NIH, NINDS
- Dr. Ehrlich receives grants for research in Parkinson's Disease from Medtronic, Inc

# Outline

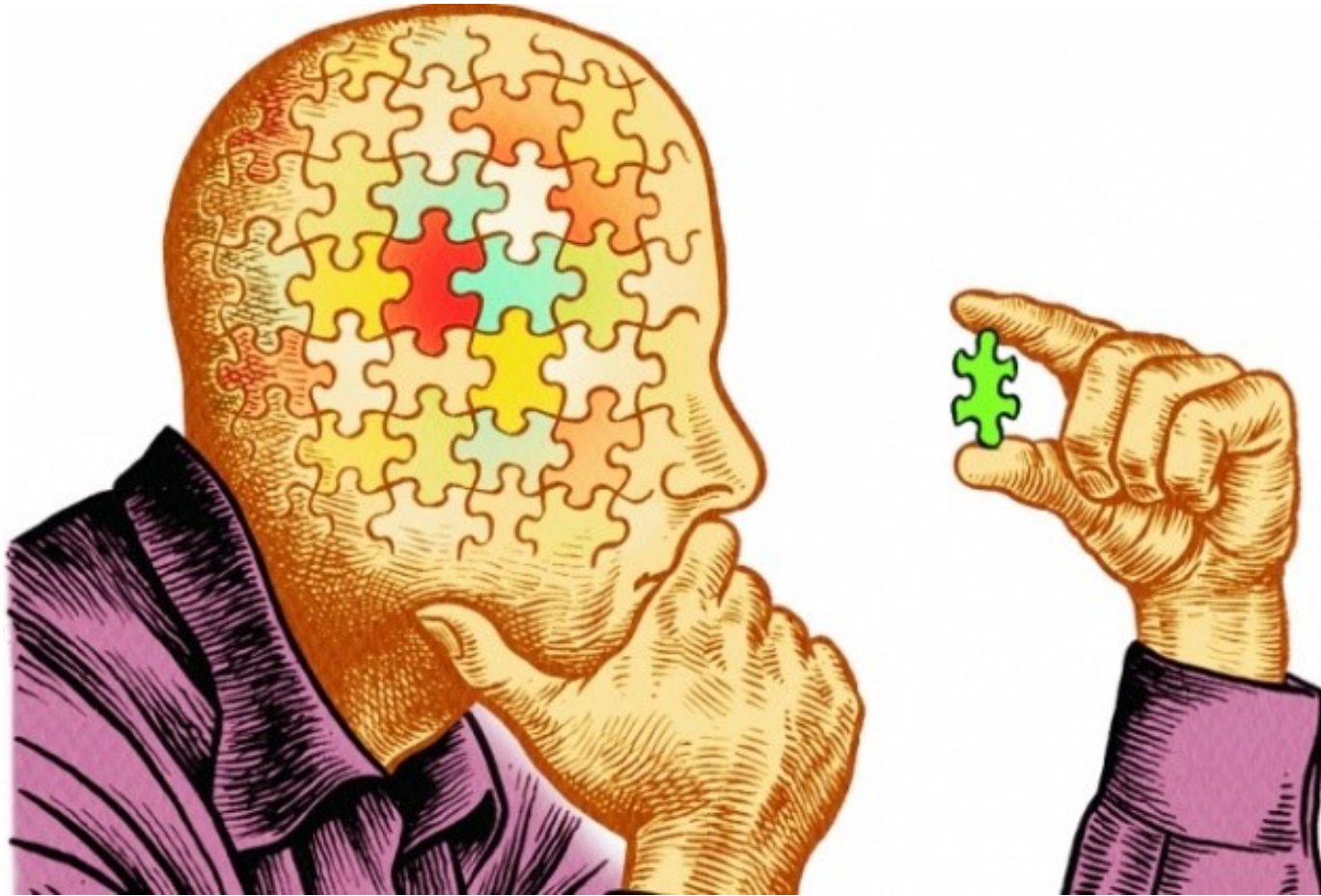
- Introduction
- Review basic genetics
- Genetics of PD
- Future uses of genetics in PD
- Is genetic testing right for you?



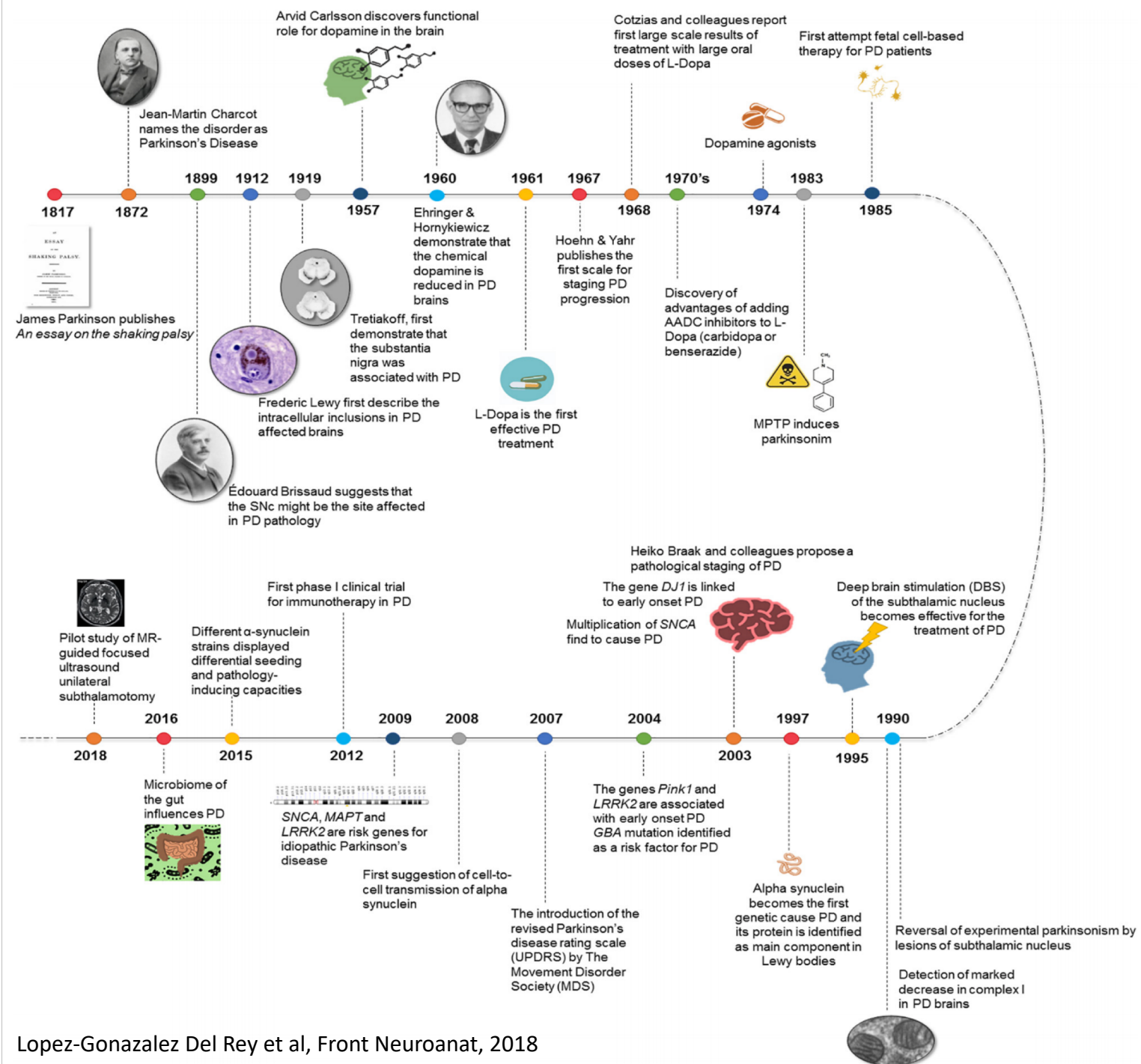
# Complex Disease



Genetics is only a piece of the puzzle



# Historic Breakthroughs in Parkinson's Disease



# Genes

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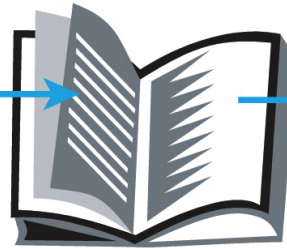


- Units of genetic information that come in pairs
- Located on chromosomes
- 1 chromosome inherited from mother and 1 inherited from father
- 25,000 genes per human genome
- Contain instructions for the production of proteins, which make up the structure of cells and direct their activities

## Types of Gene Mutations



**Chromosomes** are like encyclopedias;  
one set is from the mother, one is from the father.



**Genes** are like  
pages of descriptions.

RED  
↓  
RDD

**Mutations** are like misspelled words  
or the disruption of a sentence.

THE CAR WAS RED  
↓  
THE WAS RED

### **MISSENSE MUTATIONS** change one word or letter

THE CAR WAS RED → THE CAR WAS HAT  
→ THE CAR WAS RDD

### **NONSENSE MUTATIONS** end the instructions too soon

THE CAR WAS RED → THE CAR

### **INSERTION MUTATIONS** add one word or letter

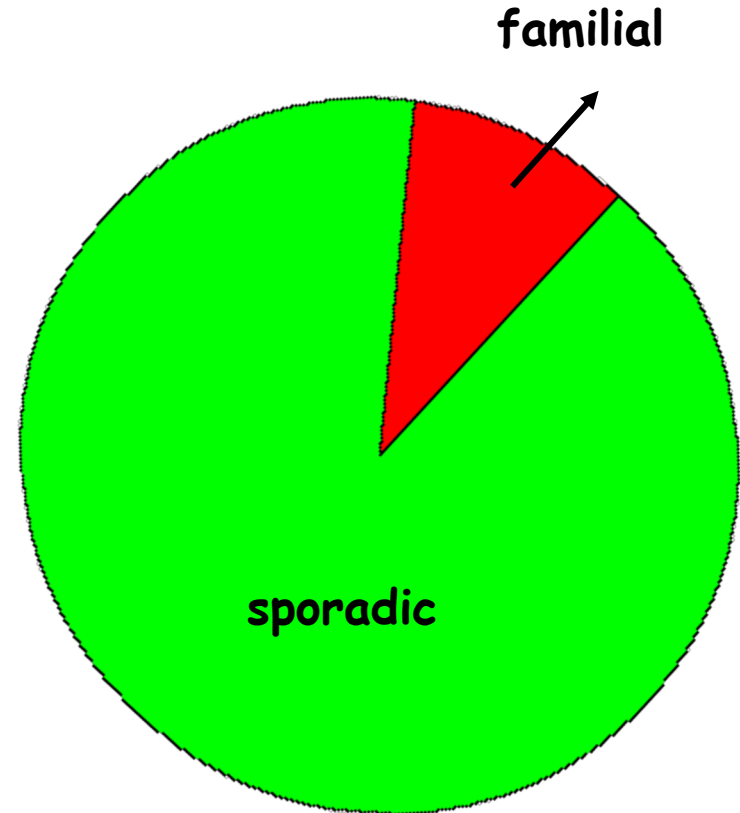
THE CAR WAS RED → THE CAR HAT WAS RED  
→ THE CAR ESW ASR ED

### **DELETION MUTATIONS**

THE CAR WAS RED → THE WAS RED  
→ THE RWA SRE D

# Sporadic vs Familial PD

- Idiopathic/Sporadic PD
  - Cause unknown
  - Majority of PD cases
  - Usually no family history
- Familial PD
  - Positive family history
  - Linked to a genetic cause
  - ~10% people with PD

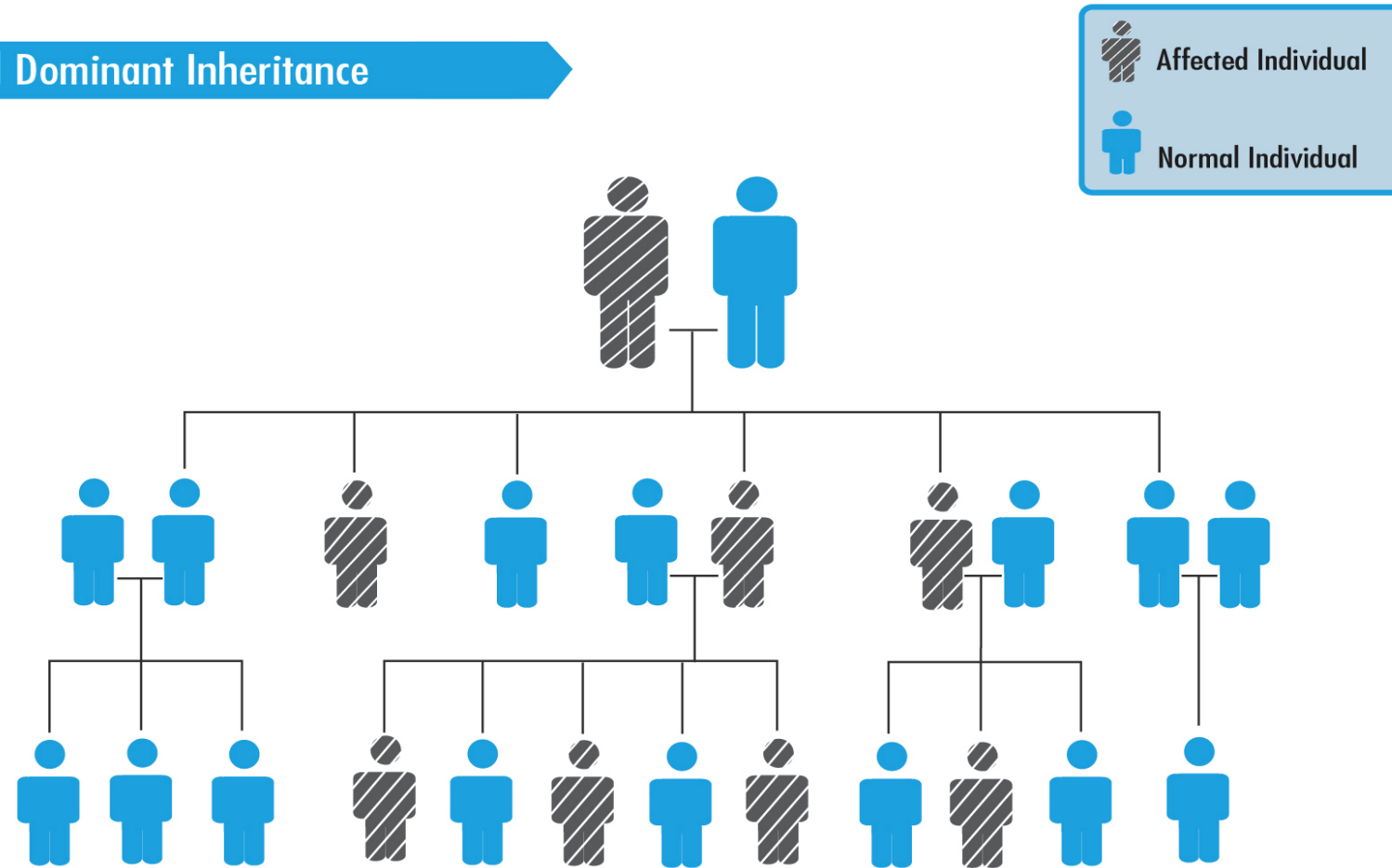


# Monogenic PD

- PD caused by a single gene mutation
- Only 1-5% of all PD cases
- Collectively account for about 30% of familial PD
- Modes of inheritance
  - dominant
  - recessive



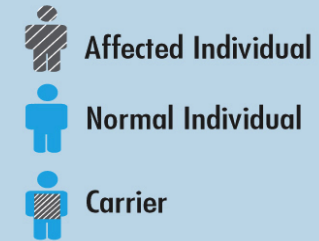
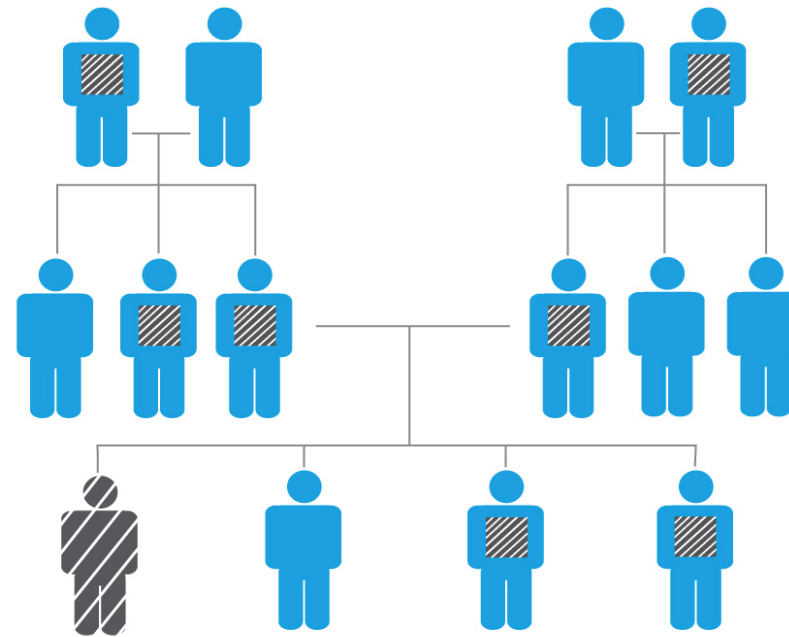
## Autosomal Dominant Inheritance



### Characteristics of Autosomal Dominant Inheritance

- Multiple generations affected
- Males and females are equally likely to be affected
- Male to male transmission occurs
- Each offspring of an affected parent has a 50% chance of being affected and a 50% chance of being unaffected

## Autosomal Recessive Inheritance



### Characteristics of Autosomal Recessive Inheritance


- Greatest recurrence risk is among siblings of affected individuals (horizontal pattern of disease in the family)
- Males and females are equally likely to be affected
- If parents are both carriers of mutations in the same recessive gene, each pregnancy has a 25% chance of inheriting both normal genes, a 50% chance of being a carrier, and a 25% chance of inheriting both gene mutations and being affected
- Ethnic background and consanguinity may influence the likelihood of a specific recessive disease

# Age of Onset Terminology

Juvenile onset  
(before age 20)



Early onset  
(before age 50)



Late onset  
(after age 50)

# Summary of genes associated with Parkinson's Disease

**TABLE 1** | Summary of genes associated with Parkinson's disease.

| Locus          | Gene           | Inheritance                 | Onset | Location   | Variants                                                                   | Function                                           |
|----------------|----------------|-----------------------------|-------|------------|----------------------------------------------------------------------------|----------------------------------------------------|
| <i>PARK1/4</i> | <i>SNCA</i>    | Dominant<br>Risk factor     | EO    | 4q21.3-q22 | 5 point mutations,<br>multiplications Rep1 risk<br>variant in the promoter | Synaptic vesicles trafficking                      |
| <i>PARK2</i>   | <i>PARKIN</i>  | Recessive                   | EO    | 6q25.2-q27 | >250 point mutation,<br>ins/de and exon<br>rearrangements                  | Mitophagy                                          |
| <i>PARK3</i>   | Unknown        | Dominant                    | LO    | 2p13       | ?                                                                          | ?                                                  |
| <i>PARK5</i>   | <i>UCHL1</i>   | Dominant                    | LO    | 4p13       | 1 missense variant in one<br>sibling pair                                  | Proteasome                                         |
| <i>PARK6</i>   | <i>PINK1</i>   | Recessive                   | EO    | 1p36.12    | >100 point mutations,<br>ins/del and exon<br>rearrangements                | Mitophagy                                          |
| <i>PARK7</i>   | <i>DJ-1</i>    | Recessive                   | EO    | 1p36.23    | >20 point mutations and<br>deletions                                       | Mitophagy                                          |
| <i>PARK8</i>   | <i>LRK2</i>    | Dominant<br>Risk factor     | LO    | 12q12      | 7 point mutations<br>Risk variants p.R1628P and<br>p.G2385R                | Autophagy?                                         |
| <i>PARK9</i>   | <i>ATP13A2</i> | Recessive                   | EO    | 1p36       | >20 point mutations                                                        | Lysosomes                                          |
| <i>PARK10</i>  | Unknown        | Risk factor                 | ?     | 1p32       | ?                                                                          | ?                                                  |
| <i>PARK11</i>  | <i>GIGYF2</i>  | Recessive                   | EO    | 2q36-7     | 7 missense variants                                                        | Insulin-like growth factors<br>(IGFs) signaling    |
| <i>PARK12</i>  | Unknown        | Risk factor                 | ?     | Xq21-q22   | ?                                                                          | ?                                                  |
| <i>PARK13</i>  | <i>HTRA2</i>   | Dominant                    | ?     | 2p13.1     | 1 missense variant                                                         | Mitophagy,                                         |
| <i>PARK14</i>  | <i>PLA2G6</i>  | Recessive                   | EO    | 22q13.1    | >18 missense variants                                                      | Lipids metabolism                                  |
| <i>PARK15</i>  | <i>FBXO7</i>   | Recessive                   | EO    | 22q12.3    | 4 point mutations                                                          | Mitophagy                                          |
| <i>PARK16</i>  | Unknown        | Risk factor                 | ?     | 1q32       | ?                                                                          | ?                                                  |
| <i>PARK17</i>  | <i>VPS35</i>   | Dominant                    | LO    | 16q12      | 2 point mutations                                                          | Endosomes                                          |
| <i>PARK18</i>  | <i>EIF4G1</i>  | Dominant                    | LO    | 3q27.1     | 1 missense variant                                                         | Protein translation                                |
| <i>PARK19</i>  | <i>DNAJC6</i>  | Recessive                   | EO    | 1p31.3     | 9 missense variants                                                        | Endosomes                                          |
| <i>PARK20</i>  | <i>SYNJ1</i>   | Recessive                   | EC    | 21q22.11   | 3 missense variants                                                        | Endosomes                                          |
| <i>PARK21</i>  | <i>DNAJC13</i> | Dominant                    | LO    | 3q22.1     | 1 missense variant                                                         | Endosomes                                          |
| <i>PARK22</i>  | <i>CHCHD2</i>  | Dominant                    | LO/EO | 7p11.2     | 1 missense variant, 1<br>truncation                                        | Mitochondria-mediated<br>apoptosis and metabolism? |
| <i>PARK23</i>  | <i>VPS13C</i>  | Recessive                   | EO    | 15q22.2    | 2 missense variants, 1<br>truncation                                       | Mitophagy                                          |
| –              | <i>GBA</i>     | AD, AR in GD<br>Risk factor | LO    | 1q22       | >10 missense variants                                                      | Lysosomes                                          |
| –              | <i>MAPT</i>    | Sporadic<br>Risk factor     |       | 17q21.31   | H1 haplotype increase PD<br>risk and disease severity                      | Microtubules                                       |

EO, early onset; LO, late onset.

# PD Causative Genes

- Autosomal Dominant
  - SNCA
  - LRRK2

- Autosomal Recessive
  - Parkin
  - PINK1
  - DJ-1
  - ATP13A2

# SNCA mutations

- 1997, researchers at the NIH found mutations in the SNCA gene in several families with a high prevalence of PD (Polymeropoulos et al)
  - Missense mutation A53T in SNCA gene
  - Other pathogenic mutations
- SNCA gene encodes for  $\alpha$ -synuclein
  - Function of  $\alpha$ -synuclein is not known
  - Abnormal  $\alpha$ -synuclein leads to aggregated  $\alpha$ -synuclein in Lewy Bodies



# SNCA mutations

- Clinical symptoms and disease course vary depending on specific mutation

| P.Ala53Thr  | P.Ala30Pro       | P.glu46Lys | P.Gly51ASP and p.Ala53Glu |
|-------------|------------------|------------|---------------------------|
| Early-onset | Late-onset       | Late-onset | Early onset               |
| dementia    | Cerebellar signs | dementia   | dementia                  |
| Most common |                  |            | Autonomic dysfunction     |

# LRRK2 mutations

- Most common genetic cause of PD
  - Mutations found in 5% of all familial and 1-2% of sporadic PD
  - At least 7 pathogenic mutations
  - Variations at the LRRK2 locus also mildly increase the risk for sporadic PD



# LRRK2 mutations

- Clinical significance
  - Late-onset PD
  - Generally good response to dopaminergic therapy
  - Slower progression/less severe clinical symptoms
  - Not everyone who has the gene will develop PD
  - Clinical presentation can vary even within same family



# Selected PD causative genes

| SNCA                   | LRRK2              | PRKN                | PINK1               | DJ-1                |
|------------------------|--------------------|---------------------|---------------------|---------------------|
| Autosomal dominant     | Autosomal dominant | Autosomal recessive | Autosomal recessive | Autosomal recessive |
| Early onset-late onset | Late onset         | Early onset         | Early onset         | Early onset         |
| Rapid progression      | Slow progression   | Slow progression    | Slow progression    | Slow progression    |
| Autonomic dysfunction  |                    | dystonia            | dystonia            | dystonia            |
| dementia               |                    | Sleep benefit       | dementia            | dementia            |
|                        |                    | Preserved smell     |                     |                     |

# Population differences

- GBA, LRRK2 in Ashkenazi Jews
- LRRK2 in North African Arabs
- MAPT in Caucasians



# PD Risk genes

- GBA
- MAPT

# GBA Mutations

- Most common genetic risk factor for PD
- Link to Gaucher Disease (Sidransky et al, 2001)
  - GD patients have 2 copies of mutated GBA gene
  - Unaffected family members frequently exhibited parkinsonism
  - Family members unaffected by GD found to carry a single GBA mutation confer a significant risk for developing PD
  - GBA mutations found 5x as frequently in PD patients vs controls
- Clinical significance in PD
  - Earlier age of onset
  - Dementia

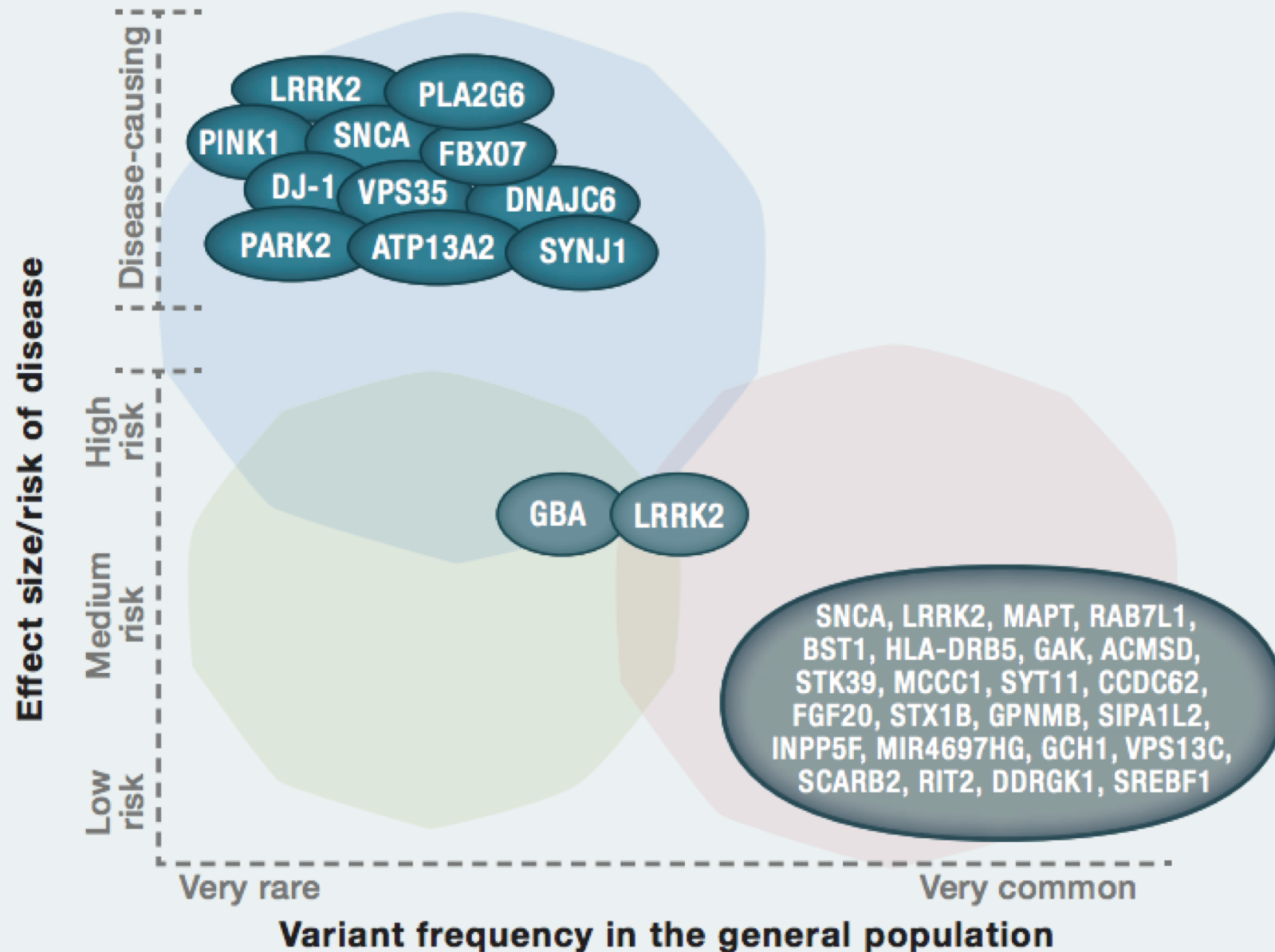


# Genetics in sporadic PD

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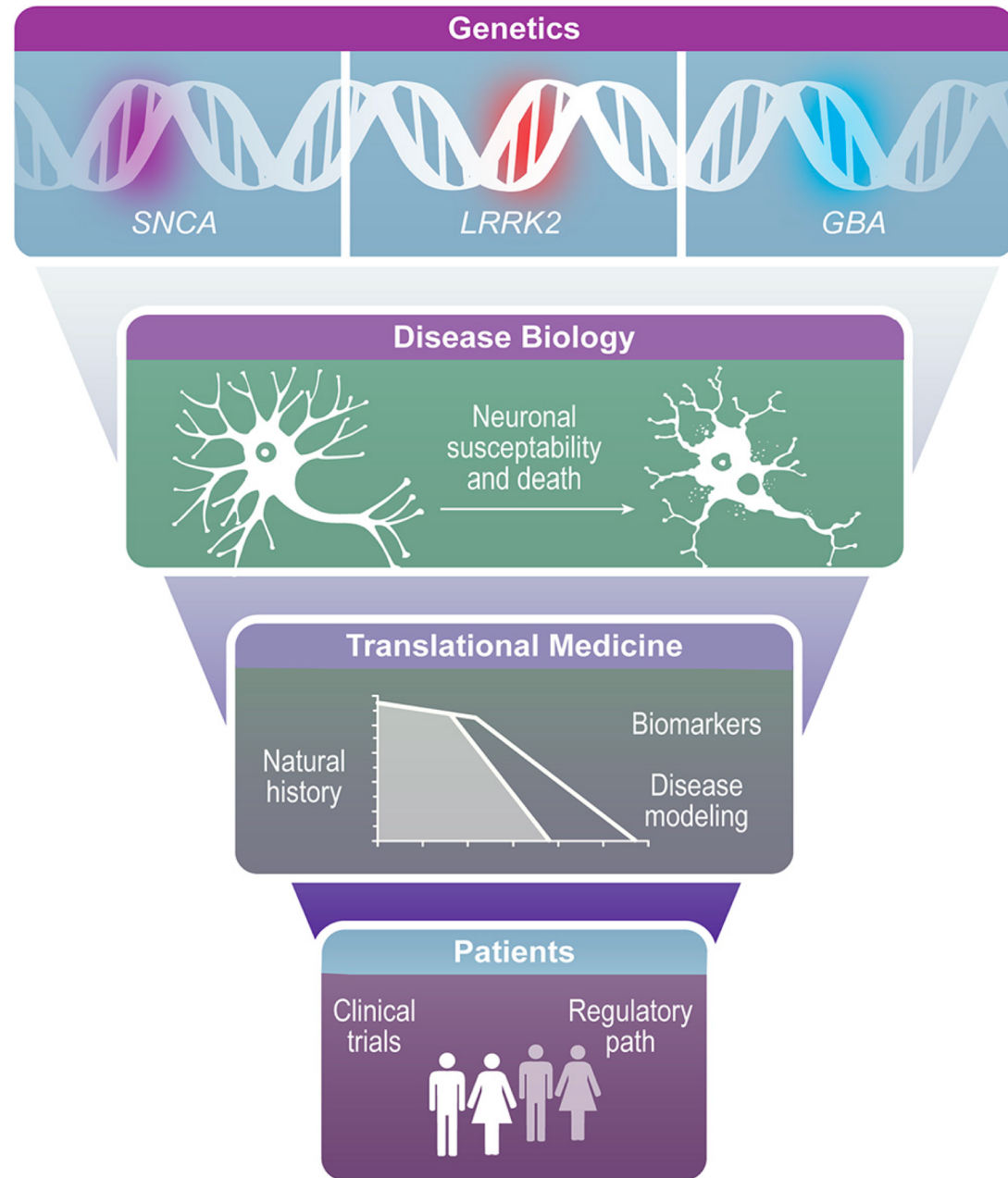
- No large pedigrees (genetic family trees) to search for a genetic contribution to disease
- Genome wide association studies
  - Compare millions of DNA variants (SNPs) between cases and controls
  - Enabled the identification of PD genetic risk loci
  - Most recent GWAS identified 90 PD risk loci

## Genetic landscape of Parkinson's Disease



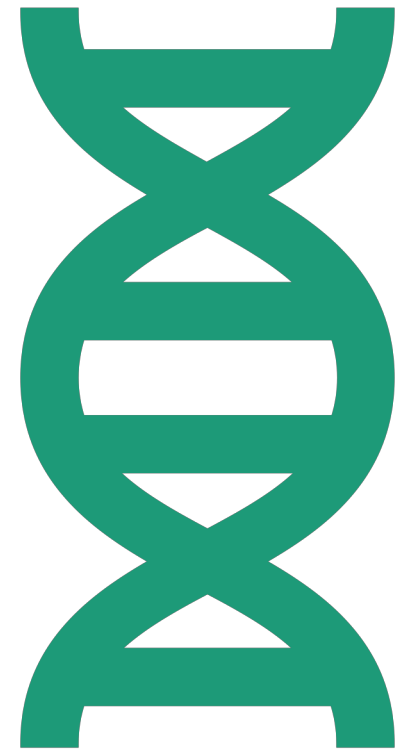
# Targeted therapies for PD: From genetics to the clinic

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# Genetically based therapeutics: Work in progress

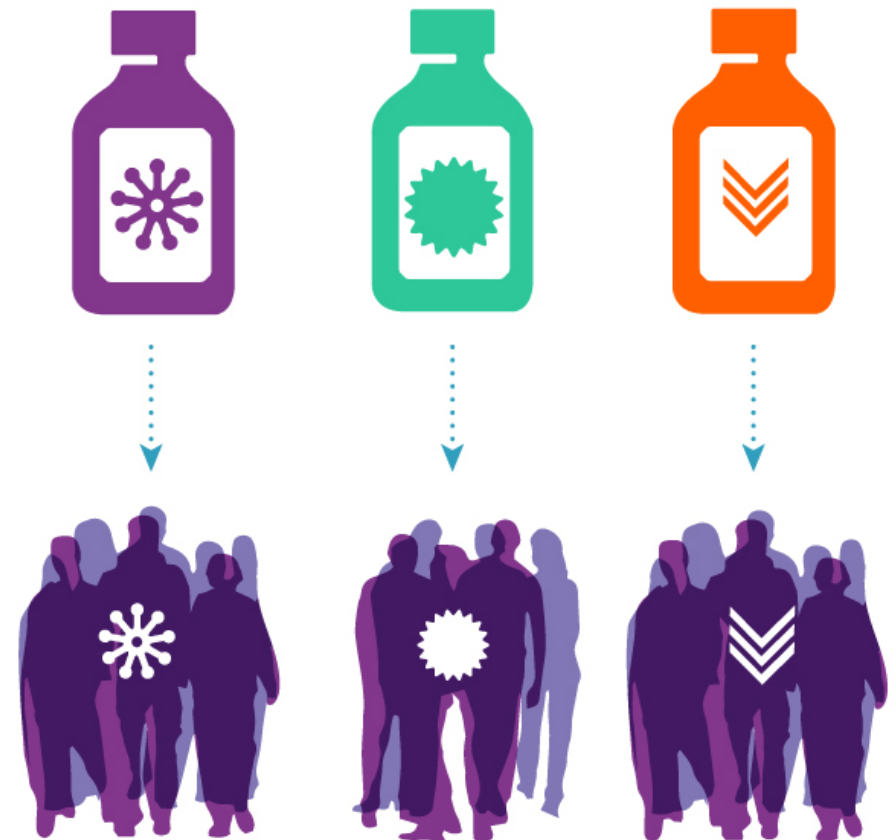
- Reduction of  $\alpha$ -synuclein
  - Antibodies
  - Vaccines
- Inhibition of LRRK2 activity
- Modulation of GBA related pathways



# Future Goals: Precision Medicine

## UNDERSTANDING PRECISION MEDICINE

In precision medicine, patients with tumors that share the same genetic change receive the drug that targets that change, no matter the type of cancer.



# Should I get genetic testing?

| Pros                                    | Cons                                    |
|-----------------------------------------|-----------------------------------------|
| Support clinical diagnosis              | Does not change treatment (yet!)        |
| Better understanding of cause/course    | Cost                                    |
| Family planning                         | Emotional burden                        |
| Involvement in specific clinical trials | Reveal information about family         |
| Help advance research                   | Secondary findings                      |
|                                         | Results may have uncertain significance |
|                                         | Testing of limited genetic variants     |

If I have a  
mutation, will  
I get the  
disease?

Not  
necessarily

Some people with SNCA or LRRK2  
mutations never develop symptoms

Risk genes indicate increased risk, but  
are not causal

Genetic  
counseling

Highly recommended if considering  
testing

Pre-test counseling: can help  
understand if testing is right for you

Post-test counseling: can help interpret  
significance of results



## Summary

- Genetic factors play a role in both familial and sporadic Parkinson's disease
- Some genetic variants are causative of the disease while others increase the risk
- Genetics gives us clues about impaired pathways and can identify targets for therapeutic interventions
- Genetics can help advance knowledge and treatment of Parkinson's disease, though it is only a piece of the puzzle

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