



Parkinson's disease -

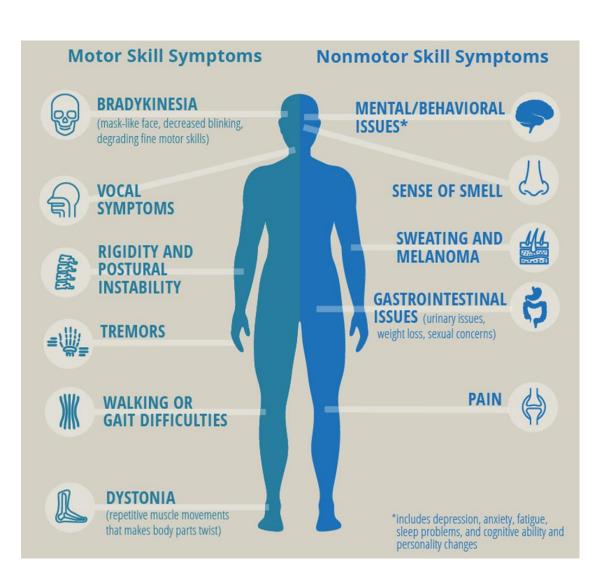
focus on proteotoxicity

Parkinson's Disease (PD)

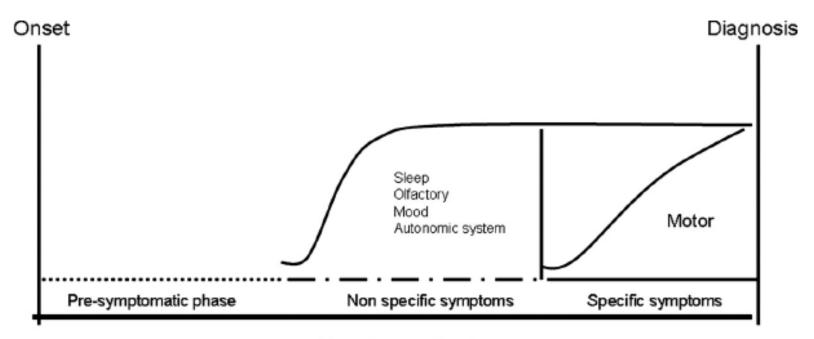
Chronic, degenerative neurological disorder affecting 1-2% people over age 60



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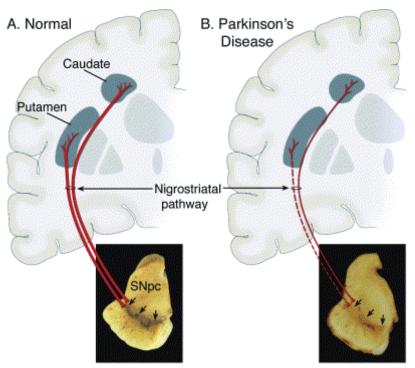


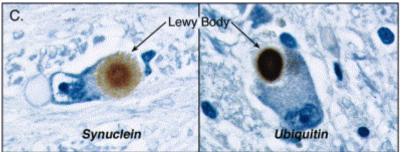
Years from disease onset to diagnosis



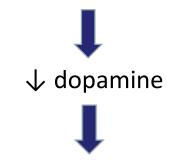
Pre-diagnostic phase

PD hallmarks





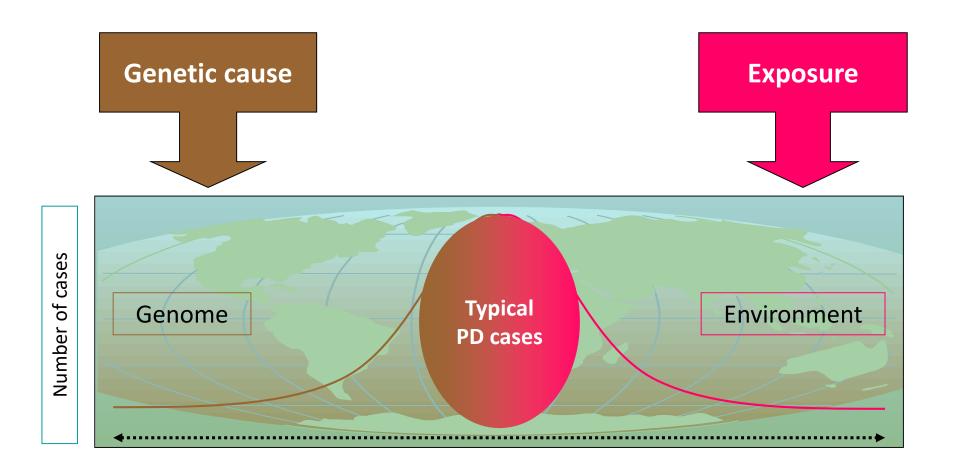
 Loss of dopamine-producing neurons in the substantia nigra pars compacta (SNpc)



PD is a movement disorder

 Alpha-synuclein-enriched inclusions known as Lewy bodies

Causes of PD



- 5-10% of PD patients have a monogenic form of PD with Mendelian inheritance
- ~15% of PD patients have family history

Genetics of PD: monogenic variants associated with PD

Table 1 Selected genetic loci associated with familial Parkinsonism

Locus	Locus map	Inheritance pattern	Gene	Clinical features	Reference
PARK1/4	4q22.1	AD	SNCA	Early onset, rigidity, cognitive impairment	Polymeropoulos et al. 1997
PARK2	6q26	AR	PRKN	Juvenile onset, dystonia	Kitada et al. 1998
PARK6	1p36.12	AR	PINK1	Early onset, dystonia	Valente et al. 2002
PARK7	1p36.23	AR	PARK7	Early onset, dystonia	Abou-Sleiman et al. 2003
PARK8	12q12	AD	LRRK2	Classic PD	Funayama et al. 2002
PARK9	1p36.13	AR	ATP13A2	Early onset, cognitive impairment	Di Fonzo et al. 2007
PARK14	22q13.1	AR	PLA2G6	Early onset, cognitive impairment, dystonia	Paisán-Ruíz et al. 2009
PARK15	22q12.3	AR	FBXO7	Early onset	Di Fonzo et al. 2009
PARK17	16q11.2	Unknown	VPS35	Adult onset, cognitive impairment, dystonia	Zimprich et al. 2011
PARK19a/b	1p31.3	AR	DNAJC6	Early onset, cognitive impairment	Edvardson et al. 2012
PARK20	21q22.11	AR	SYNJ1	Early onset, seizures	Krebs et al. 2013
PARK21	3q22	AD	DNAJC13	Classic PD	Vilariño-Güell et al. 2014
PARK23	15q22.2	AR	VPS13C	Early onset, rapid progression, cognitive impairment	Lesage et al. 2016

The inheritance pattern, gene, clinical features, and relevant reference for each locus are provided. Classic PD refers to symptoms that resemble sporadic PD. Abbreviations: AD, autosomal dominant; AR, autosomal recessive; PD, Parkinson's disease.

Genetics of PD: over 90 risk loci identified

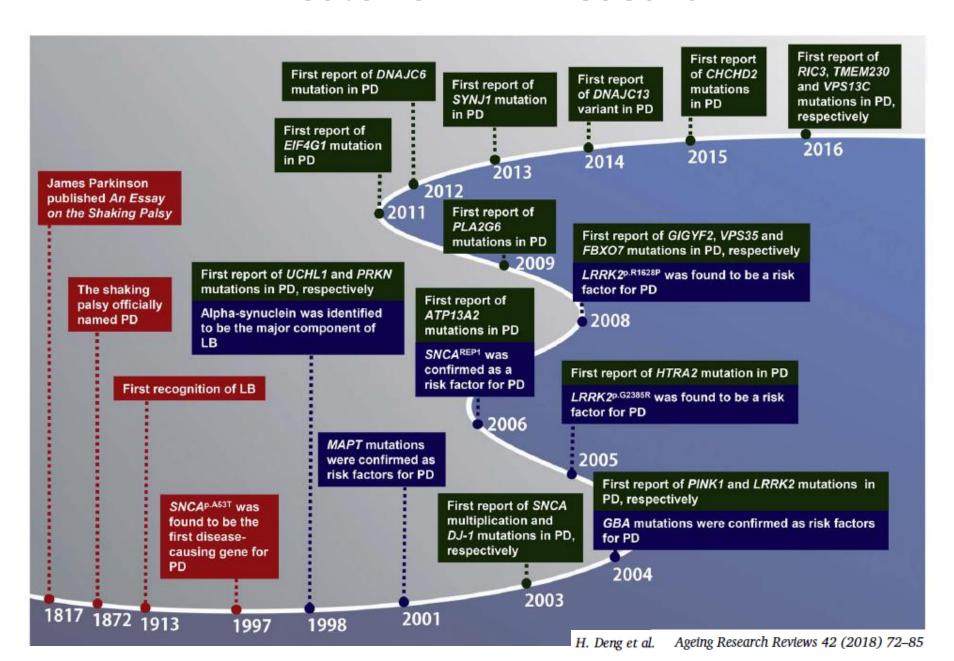
Table 4 Genes associated with single nucleotide polymorphisms that modulate Parkinson's disease risk

Category	Candidate genes		
Cytoskeleton	CAB39L, TUBG2, MAPT, DNAH17, ANK2, PDLIM2, SORBS3		
Endosomal and vesicular trafficking	VAMP4, SIPA1L2, SNCA, CHMP2B, LRRK2, BIN3, RIMS1, DDRGK1, SYT4, ATP6V0A1, GBF1, ARHGAP27, SH3GL2		
Immune system	FCGR2A, IL1R2, HLA-DRB6, HLA-DQA1, FYN, CD19, CD38, NOD2, TRIM40, FAM49B, IT1H3, IT1H4, TLR9, STAB1		
Ion channels, transporters, and neurotransmitter signaling	KCNS3, KCNIP3, TMEM163, SCN3A, CHRNB1, CLCN3, GCH1, NCKIPSD, CAMK2D		
Lipid metabolism and signaling	SPTSSB, ELOVL7, DGKQ		
Lysosome and autophagosome	GBA, CTSB, GALC, KAT8, TMEM175		
Mitochondria	SLC41A1, COQ7, VPS13C, BAG3, MCCC1, CRLS1, MICU3		
Nucleus and gene regulation	NUCKS1, CCNT2, SATB1, KPNA1, MED12L, LCORL, MBNL2, MEX3C, MIR4697, TOX3, UBTF, LSM7, BRIP1, ASXL3, RPS6KL1, PSMC3IP, SREBF1, RAI1, KANSL1, RNF141, RPS12, CDC71, PHF7, NUPL2, ZNF184		
Ubiquitin pathway	UBAP2, BAP1, KLHL7		
Miscellaneous	ITPKB, LINC00693, DYRK1A, OGFOD2, FAM171A2, ZNF646, FAM47E, FBRSL1, MIPOL1, SCAF11, PAM, TMEM229B, CRHR1, STH, SPPL2C, DLG2, C5orf24, C8orf58, GS1-124K5·11, ALAS1, NISCH, GPNMB, FAM200B, STK39		

All genes are organized into functional categories. The miscellaneous category is reserved for genes with unknown function or with functions that do not fit into the other categories.

Polygenic risk score (PRS) accounts for 16-36% of the genetic contribution to idiopathic non-monogenic PD

Milestone in PD research



Risk factors

age

heredity

sex (↑ risk in man > women)

head injury and pesticide exposure

smoking and caffeine consumption ↓ risk

Drugs and treatments

L-dopa

Dopamine agonists

MAO-B inhibitors

COMT inhibitors

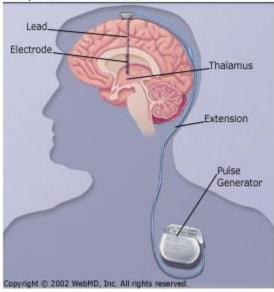
tDCS



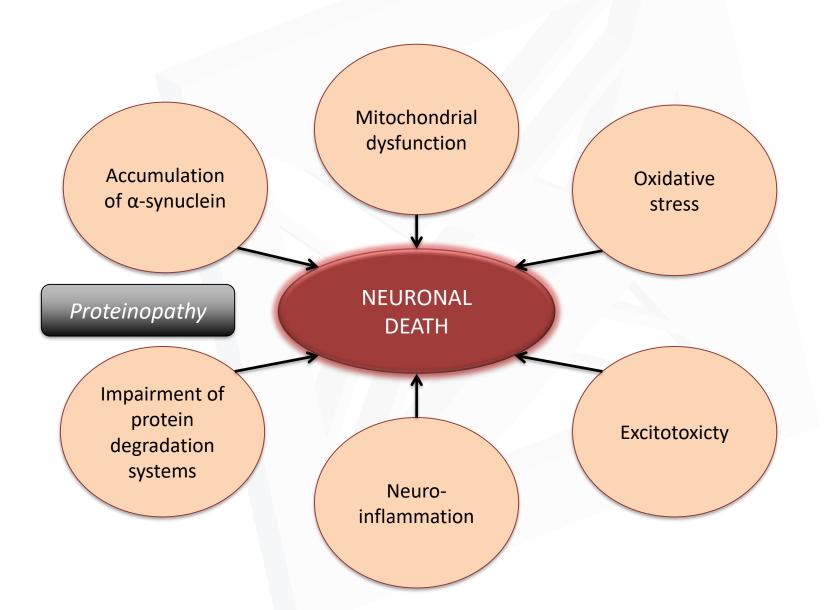
DBS (surgical procedure)

Most common targets: subthalamic nucleus (STN) globus pallidus interna (GPi)

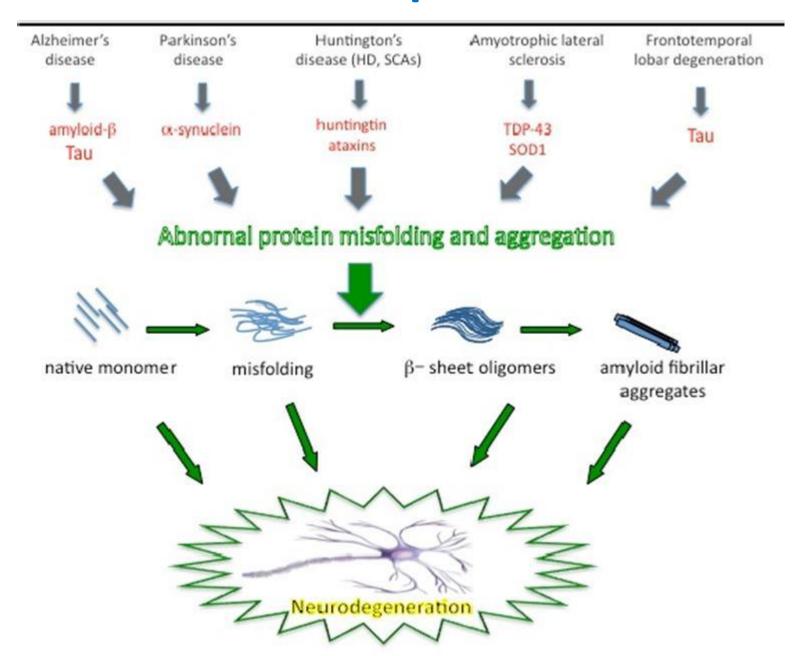
Deep Brain Stimulation



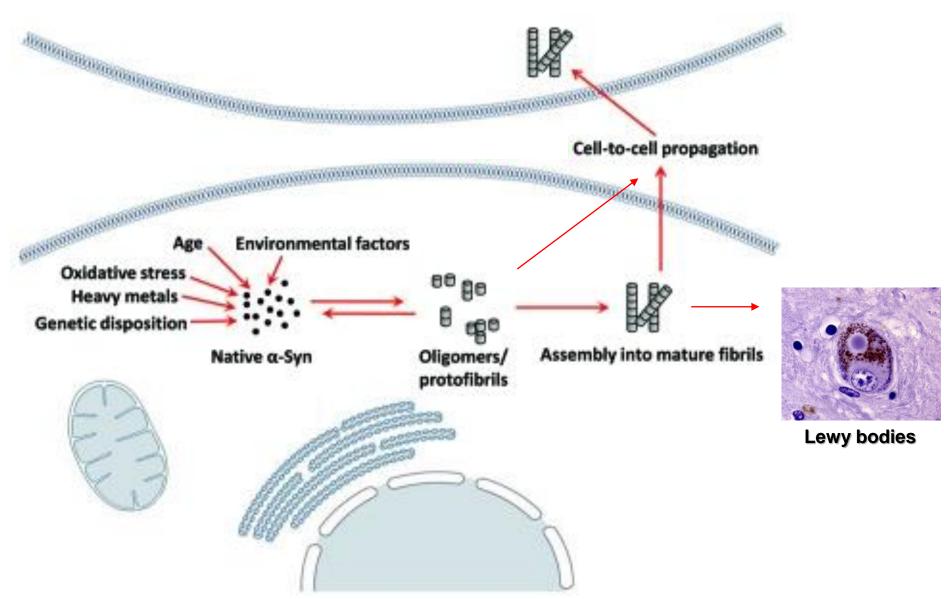
Pathogenic mechanisms



Proteinopathies

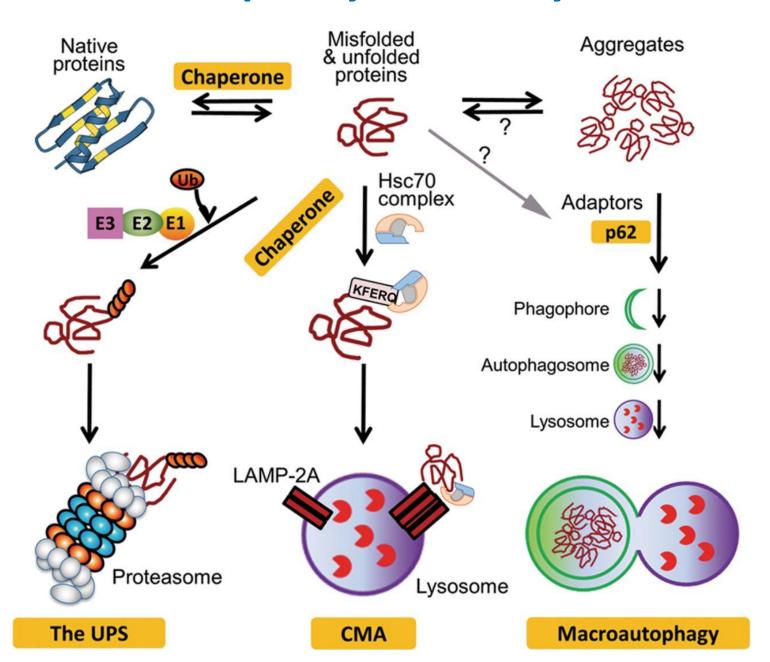


Alpha-synuclein toxicity and PD

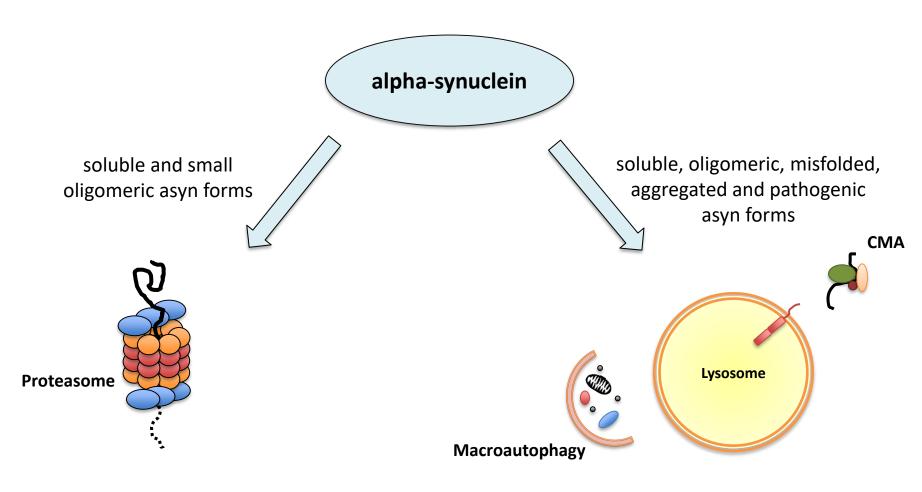


modified from: Pemberton and Melki, Commun Integr Biol. 2012 January 1; 5(1): 94-95

Protein quality control systems



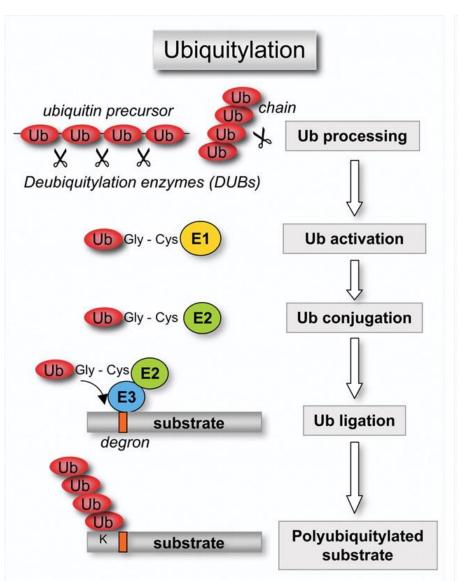
Alpha-synuclein catabolic systems

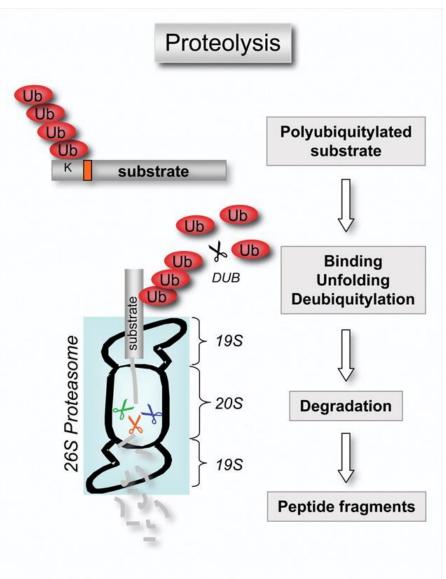


Ubiquitin-Proteasome System (UPS)

Autophagy-Lysosome Pathway (ALP)

Ubiquitin-proteasome system (UPS)





UPS alterations and PD

- Lewy bodies are ubiquitin-positive
- Genetics of PD:
 - Parkin (PARK2) is an E3 ubiquitin-ligase
 - UCHL1 (PARK5) is a DUB
- ↓ function/expression of 20S subunit in SNc of PD patients
- UPS inhibitors → animal models of PD

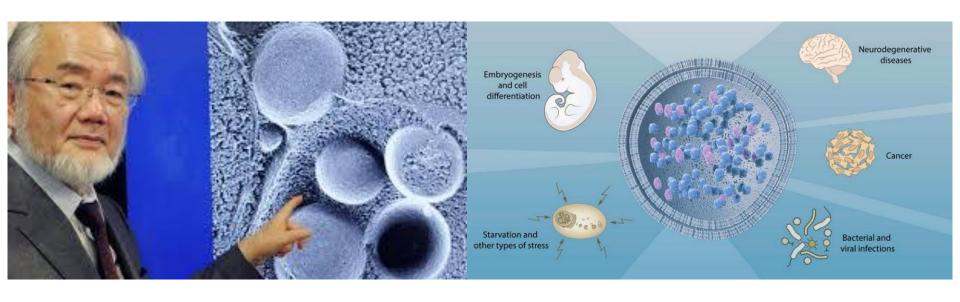
The 2016 Nobel Prize in Medicine



Yoshinori Ohsumi,

Tokyo Institute of Technology

Autophagy



International Award «Lombardia è Ricerca» - 2019

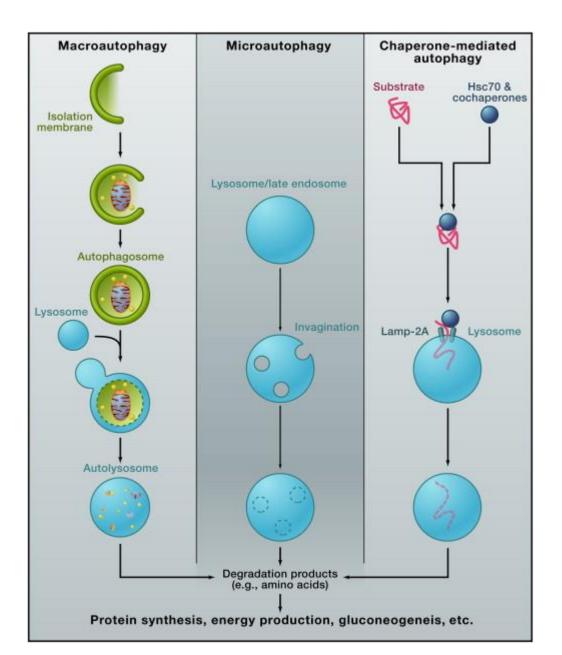


Caloric restriction → ↑ autophagy → ↑ longevity

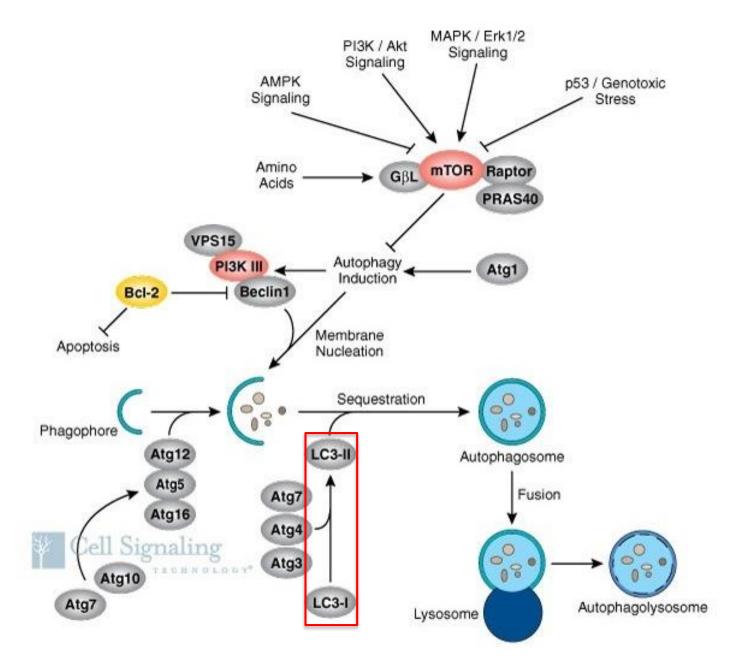




Types of autophagy



(Macro)autophagy



Macroautophagy alterations and PD

 autophagosome accumulation in SNc of PD patients and in animal and cell models of PD

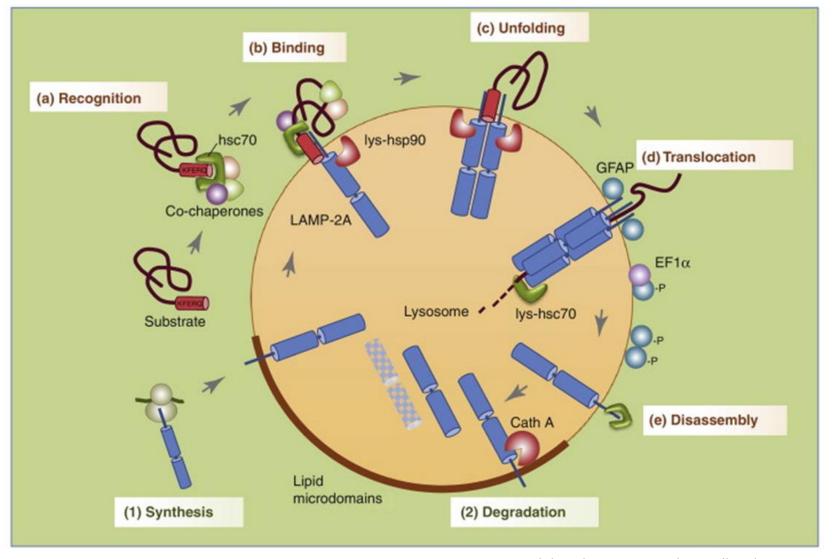
PINK1, parkin: key role in mitophagy

• LRKK2 ...

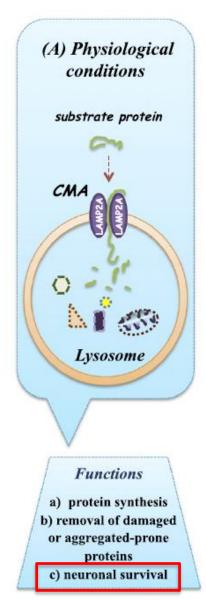
 $\begin{tabular}{ll} \textbf{Table 1} \\ \textbf{Familial and other genes involved in Parkinson's disease}^a \ and \ their roles in the autophagy-lysosomal pathway. \end{tabular}$

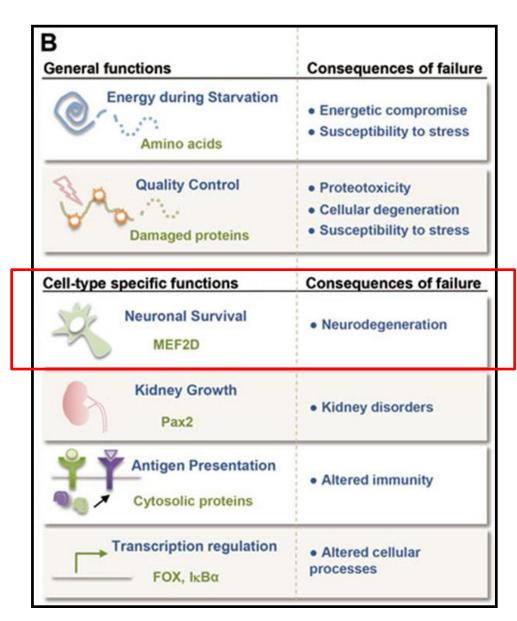
Gene	Genetic and clinical features	Role in ALP
Autosomal dom	ninant PD genes	
SNCA	Rare point mutations and gene multiplication lead to EOPD. Several point mutations and gene duplication associated with LOPD.	Degraded by the ALP; overexpression or point mutations may lead to dysfunction of CMA, microautophagy and macroautophagy.
LRRK2	Several mutations were reported, most common is p.G2019S. Typical phenotype, with lower rates of non-motor symptoms.	Regulates endolysosomal transport, lysosomal function and potentially mitophagy.
VPS35	Very rare, only one mutation (p.D620 N) was reliably confirmed as associated with PD. Typical phenotype, potentially with earlier age at onset.	Involved in endolysosomal transport regulation.
Autosomal rece	essive PD genes	
PRKN (Parkin)	Bi-allelic mutations are the most common recessive genetic cause of EOPD. Dystonia is common, early onset but slowly progressive.	Regulates mitophagy through interaction with PINK1 and targeting of dysfunctional mitochondria for degradation by the lysosome.
PINK1	The second most common recessive genetic cause of EOPD. Anxiety may be more common	Regulation of mitophagy through the same pathway as PRKN
PARK7 (DJ-1)	Rare cause of recessive EOPD. Early onset, more dystonia at presentation	Regulation of mitophagy in a parallel pathway to that of PRKN/PINK1
VPS13C	Very rare mutations were reported. Early onset, rapidly progressive PD with rapid cognitive decline.	Activates the PRKN/PINK1 mitophagy pathway.
Other genes, in	ivolved in PD and lysosomal storage disorders	
GBA	More than 100 mutations were reported in PD. Typical PD with earlier onset on average, and wide spectrum of non-motor symptoms. Prominent cognitive decline and neuropsychiatric features	A lysosomal hydrolase involved in degradation of glycosphingolipids. Bi-allelic mutations may cause Gaucher disease.
SMPD1	Rare mutations, mainly in Ashkenazi Jews, were associated with PD in different studies. Typical PD, possibly with earlier onset.	A lysosomal hydrolase involved in degradation of sphingolipids. Bi-allelic mutations may cause Niemann-Pick type A/B disease.
ASAH1	Burden analysis suggested association with PD, yet this association needs to be replicated. No information on clinical presentation is available.	A lysosomal enzyme responsible for the degradation of ceramide. Bi-allelic mutations may cause Farber disease or spinal muscular atrophy with progressive myoclonic epilepsy.
GLA	No genetic evidence for involvement, yet enzymatic activity is reduced in PD patients. No information on clinical presentation is available.	A lysosomal hydrolase involved in glycolipid degradation. Bi-allelic mutations may cause Fabry disease.

Chaperone-mediated autophagy (CMA): a selective form of autophagy

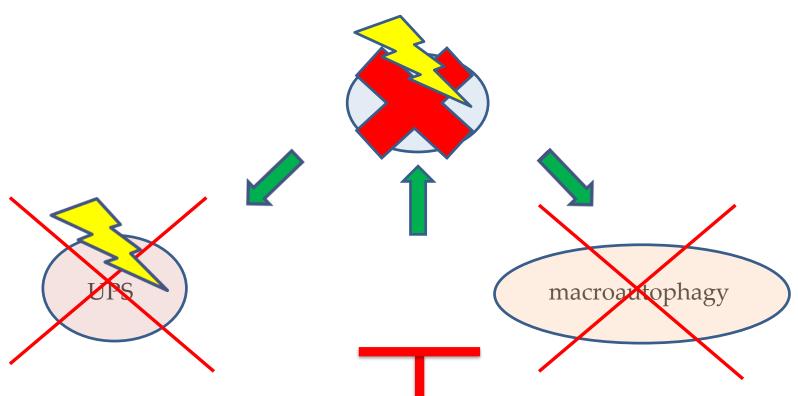


Physiological functions of CMA





Cross talk between different proteolytic systems



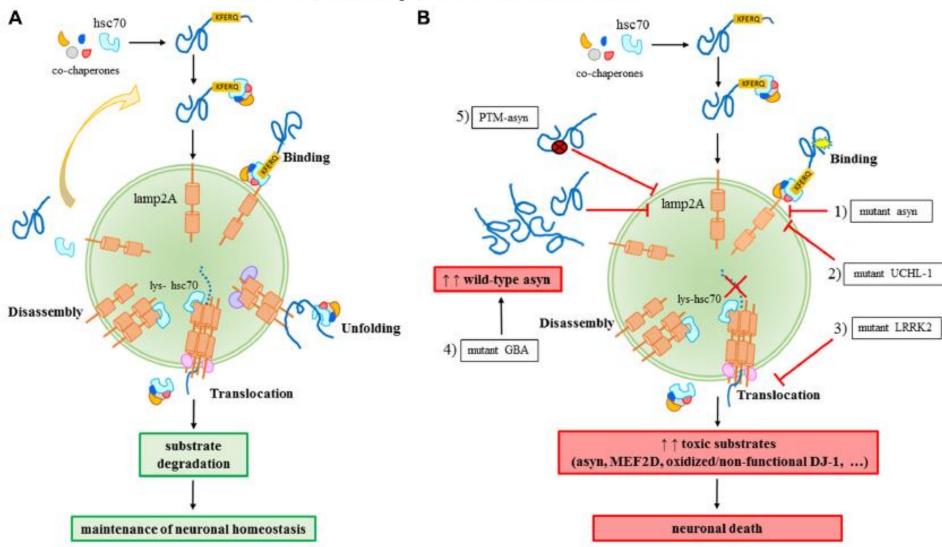
- defects in macroautophagy or UPS → ↑ CMA
- CMA blockage → ↑ macroautophagy
- CMA alterations → UPS perturbation

AGING

Role of Chaperone-Mediated Autophagy Dysfunctions in the Pathogenesis of Parkinson's Disease

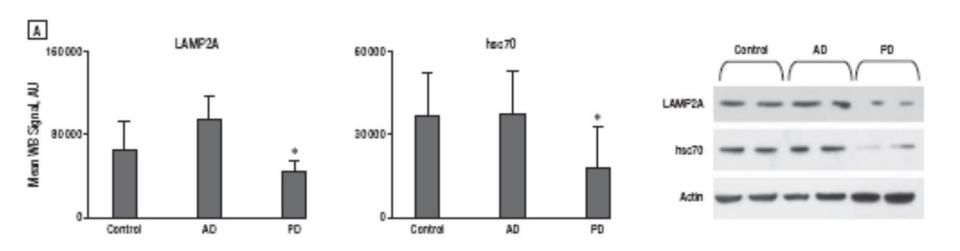


Gessica Sala1*, Daniele Marinig1,2, Alessandro Arosio1 and Carlo Ferrarese1,3



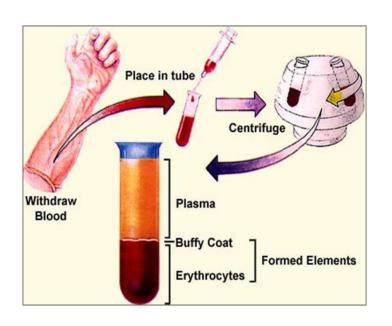
CMA alterations in PD patients

- Jamp2A and hsc70 levels in advanced stages in dopaminergic neurons of PD patients (Alvarez-Erviti et al., Arch Neurol 2010)

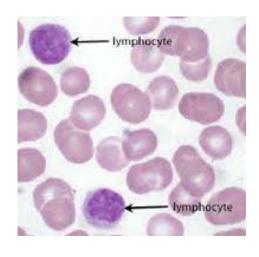


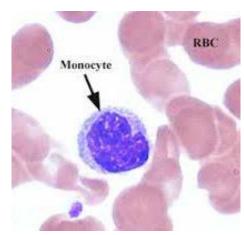
Possible role for deregulation of microRNA (Alvarez-Erviti et al., Cell Death Dis 2013) and sequence variation in lamp2 promoter region (Pang, Neurosci Lett 2012)

Aim 1: to search for autophagy dysfunctions in ex vivo cells from PD patients











Identification of new PD biomarkers

- early diagnosis
- personalized therapy
- monitoring of drug efficacy in clinical trials

Methods

PBMCs isolation through density gradient centrifugation



Protein expression

WB
IF
FRA (insoluble proteins)
Dot blot (soluble proteins)

Gene expression

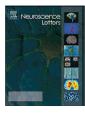
→ real time PCR



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Alpha-synuclein nitration and autophagy response are induced in peripheral blood cells from patients with Parkinson disease

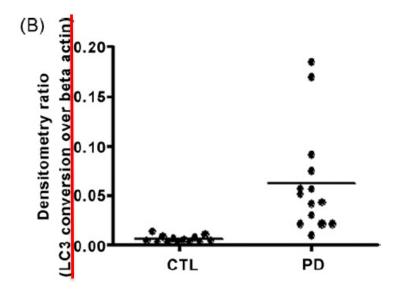
Alessandro Prigione^{a,1}, Fabrizio Piazza^a, Laura Brighina^{a,b}, Barbara Begni^a, Alessio Galbussera^b, Jacopo C. DiFrancesco^{a,b}, Simona Andreoni^a, Roberto Piolti^b, Carlo Ferrarese^{a,b,c,*}

Table 1 Subject demographic.

	PD patients	Controls
Number	25	30
Sex (M/F)	12/13	18/12
Age at study (years)	65 ± 9.9	60.1 ± 13
Age at onset (years)	58 ± 9.8	
UPDRS III score	29.2 ± 12	
Hoehn and Yahr stage	2.4 ± 0.9	
MMSE score	24.4 ± 5.6	
GDS score	5.3 ± 4.1	
Levodopa dosage (mg/die)	460 ± 197	
REP1 259 bp ^a	22	18
REP1 261 bp ^a	22	41
REP1 263 bp ^a	6	1

Values are expressed as mean \pm standard deviation.

^a REP1 allele number (2 per participant); allele frequencies (the number of participants is half the number of alleles indicated).



↑ autophagosomes in PD PBMCs

^a Laboratory of Neurobiology, Department of Neuroscience and Biomedical Technologies, University of Milan-Bicocca, Italy

^b Department of Neurology, University of Milan-Bicocca, San Gerardo Hospital, Monza, Italy

c Scientific Institute "E. Medea", Bosisio Parini, Italy



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Research Report

Reduced expression of the chaperone-mediated autophagy carrier hsc70 protein in lymphomonocytes of patients with Parkinson's disease

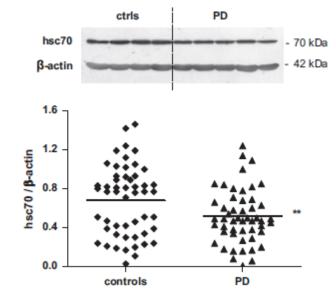
Gessica Sala^{a,*}, Giovanni Stefanoni^{a,b}, Alessandro Arosio^{a,c}, Chiara Riva^a, Laura Melchionda^a, Enrico Saracchi^{a,b}, Silvia Fermi^{a,b}, Laura Brighina^b, Carlo Ferrarese^{a,b}

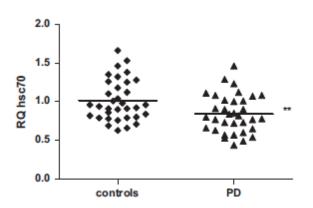


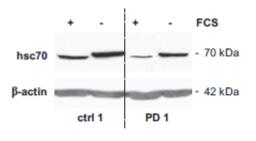
Table 1 – Demographic and clinical characteristics of the enrolled population.

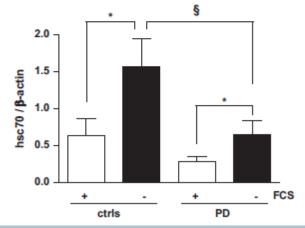
	Controls	PD patients
Number	53	53
Age at study (years)	66.1 ± 7.2	66.9 ± 9.7
Sex (M/F)	34/19	36/17
Age at onset (years)	n.a.	64.6 ± 9.6
Disease duration (years)	n.a.	2.5±2.6
UPDRS III score	n.a.	15.6 ± 10.3
Hoehn and Yahr stage	n.a.	1.7±0.7
MMSE score	29.20±1.3	28.3 ± 2
Treated/untreated	n.a.	39/14
(L-Dopa)		(26)
(Dopamine agonists)		(14)
(Rasagiline)		(5)

n.a.=not applicable.

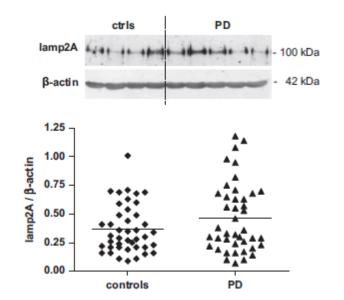


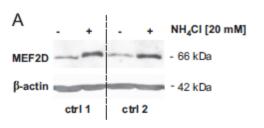


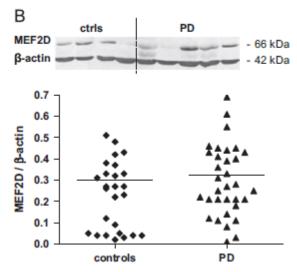




↓ hsc70 in PD PBMCs after starvation



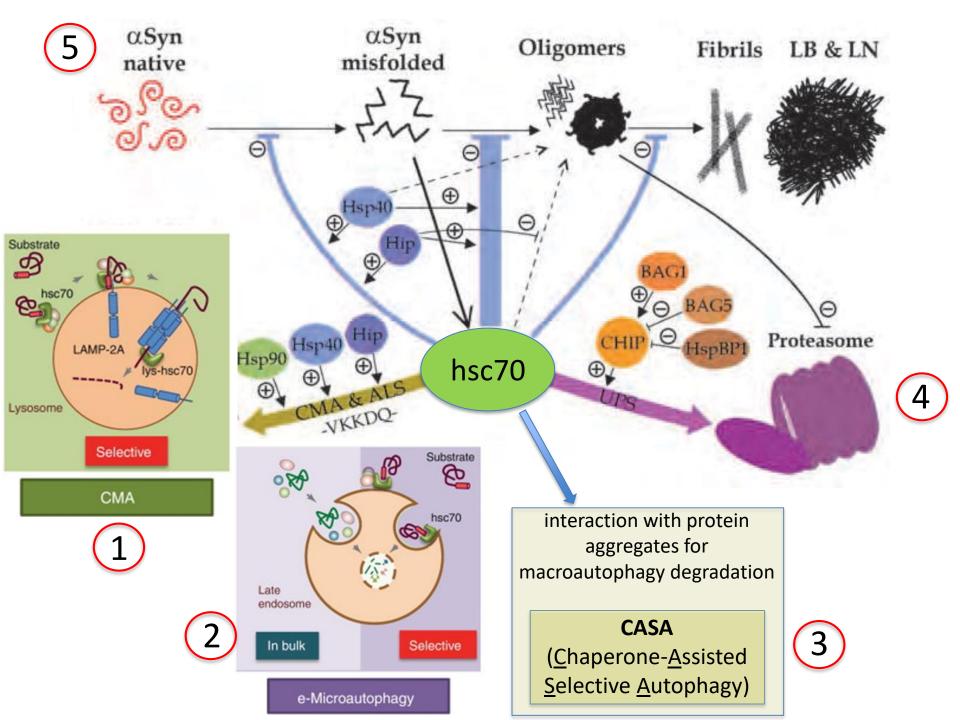




= lamp2A and MEF2D mRNA levels no correlation hsc70-clinical characteristics

systemic ↓ of hsc70
↓

possible 'trait' biomarker for PD



↓ hsc70



↑ cell susceptibility to stressors
↑ protein accumulation/aggregation



hsc70 up-regulation as therapeutic approach