REVIEW

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The genetic background of Parkinson's disease and novel therapeutic targets

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ABSTRACT

Introduction: Parkinson's disease (PD) is the second most common neurodegenerative disease worldwide. The median age of disease onset is around 60 years. From a genetic point of view, PD is basically considered a sporadic, idiopathic disease, however, hereditary components can be detected in 5–10% of patients. Expanding data are available regarding the targeted molecular therapy of the disease. **Areas covered:** The aim of this current review article is to provide brief clinical and molecular insight into three important genetic forms (LRRK2, SNCA, GBA) of hereditary PD subtypes and to present the

human clinical trials in relation to these forms of the disease. **Expert opinion:** These small hereditary subgroups are crucially important in drug development, because the general trend is that clinical trials that treat PD patients as a large group, without any separation, do not meet expectations. As a result, no long term conclusions can currently be drawn regarding the effectiveness of the molecules tested in these phase 1 and 2 studies. Further precise studies are needed in the near future. ARTICLE HISTORY Received 22 July 2022 Accepted 25 November 2022

KEYWORDS GBA; genetic; LRRK2; Parkinson's disease; SNCA

1. Introduction

Parkinson's disease (PD) is the second most common neuro-degenerative disease worldwide [1].

The disease affects around 2–3% of the population \geq 65 years of age [1]. The primary feature of PD is the degeneration and loss of dopaminergic neurons in the substantia nigra, which results in a striatal dopaminergic deficit [1]. The median age of onset of clinical symptoms (bradykinesia, rigidity and/or rest tremor) is around 60 years [2]. From a genetic point of view, PD is basically considered a sporadic disease, but 5-10% of patients have a positive family history. However, confirmed hereditary cases following Mendelian inheritance are rare [3]. Clinical differentiation of sporadic and hereditary forms of PD is very challenging and sometimes impossible [2]. Nevertheless, it can be stated that genetic variations underlying monogenic forms of PD can be identified more often in early-onset cases [3]. To date, the number of genetically confirmed genes and loci causing PD in monogenic form is thirteen (PARK1, -2, -6-10, -12-17). Furthermore, four, so far unconfirmed, PARK loci are known as well (PARK3, -5, -11, -18) [4]. In terms of inheritance, these genes show autosomal dominant (e.g. LRRK2, SNCA), recessive (e.g. PRKN, PINK1, DJ-1) and X-linked (e.g. RAB39B) patterns [5]. Furthermore, GBA mutations in heterozygous form are the most important risk factors for developing PD [6]. Table 1 illustrates the main characteristics of the most important hereditary disease forms (Table 1).

The gold standard for treatment of PD is still levodopa [7]. Although levodopa is an excellent symptomatic drug, it does not slow or reverse the progression of the disease. Considering that since the introduction of dopaminergic therapy decades ago, no further significant breakthrough in the pharmacotherapy of PD has been made, alternative approaches have come to the fore. However, clinical trials aimed at the treatment of heterogeneous PD groups often fail. These results increasingly emphasize the importance of targeted therapies in certain genetically diagnosed groups of PD patients. As the number of patients carrying one of these genetic alterations is low, clinical trials have been started within the framework of international collaborations [8].

The aim of this current review article is to provide brief clinical and molecular insight into three important genetic forms of hereditary PD subtypes and to present the human clinical trials in relation to these forms of the condition.

1.1. Leucine-rich repeat kinase 2 (*LRRK2*) – targeted therapies

LRRK2 gene mutations are one of the most common genetic alterations behind familial forms of PD [2]. From a clinical perspective, the onset of motor symptoms is quite variable. Although mutations in this gene are mostly detected in late-onset cases (mean age of onset: 58–61 years), they can be found in younger patients as well [2]. *LRRK2*-associated PD is levodopa responsive [2]. It tends to have a milder progression and some non-motor symptoms are unusual (e.g. cognitive deterioration, psychiatric disturbances) [2,5]. The neuropathological picture of the disease is variable, because Lewy body pathology and pure forms of substantia nigra degeneration

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Article highlights

- Parkinson's disease (PD) is the second most common neurodegenerative disease worldwide.
- The median age of clinical symptoms (bradykinesia, rigidity and/or rest tremor) onset is around 60 years.
- Positive family history is found in 5-10% of patients.
- Three important genetically determined forms are *LRRK2-, SNCA-* and *GBA-* related subtypes.
- Phase 1 and 2 targeted studies are currently underway for this three genetic subtypes.
- No long-term conclusions can currently be drawn regarding the effectiveness of the molecules tested, further precise studies are needed in the near future.

without Lewy bodies have both been described, as well as the varying presence of neurofibrillary tangles [9].

The *LRRK2* gene contains 51 exons, which encode a 2527 amino acid long protein [5]. The LRRK2 protein is a homodimer with GTPase and kinase functions, harboring the following domains: (1) protein-protein interaction domains: armadillo (ARM), ankyrin-like (ANK), leucine-rich repeat (LRR) and WD40; (2) serine-threonine kinase domain; (3) Ras of complex protein (Roc) – C-terminal of Roc (COR) tandem domain [10]. The vast majority of pathogenic mutations identified to date are located close to the carboxyl terminus of the protein [10]. The most frequent mutation is c.6055 G > A (p.G2019S) [10]. The penetrance of mutations in the *LRRK2* gene is variable. The biological function of the LRRK2 protein is not yet known in detail, however, it may have an effect on cell signaling and subcellular transport processes [10].

All common *LRRK2* mutations result in increased kinase activity, so the pharmaceutical industry has focused on kinase inhibitors. During the development of the LRRK2 kinase inhibitor, possible pulmonary damage arose as an important safety issue in rodents and non-human primate animal studies. However, the toxic pathomechanism, involving primarily type II pneumocytes and resulting in a deposition of lamellar bodies, is presumably reversible, so the testing of individual LRRK2 kinase inhibitor compounds in clinical phases still occurred [11,12]. Regarding clinical trials, six relevant studies

were performed (Table 2, 3). DNL201 was the first clinically tested small, selective LRRK2 kinase inhibitor, which can penetrate the central nervous system. 122 healthy volunteers and 28 PD patients were involved in a phase 1b study (NCT03710707) [13]. DNL201 was tested for 28 days at low and high doses [13]. The molecule inhibited LRRK2 kinase activity, and it improved lysosomal function as well [13]. During the testing period no relevant safety issues appeared [13]. In the second, 28 day long, relevant clinical trial (NCT04056689), another LRRK2 kinase inhibitor (DNL151) was tested in three doses. 34 PD patients were enrolled in the phase 1b study [14]. Although the results are not yet fully available, the safety of the molecule, which was monitored along with the detection of lysosomal biomarkers, appeared satisfactory [14]. No serious adverse event occurred [14]. A different, larger study (NCT04557800, phase 1, 186 healthy volunteers) further strengthened the previous results, i.e. DNL151 is a safe and well-tolerated molecule. Further clinical trials are currently underway (antisense oligonucleotide – BIIB094 – Phase 1 – NCT03976349; LRRK2 inhibitor – BIIB122 (other name: DNL151) - Phase 2 - NCT05348785; LRRK2 inhibitor – BIIB122 (other name: DNL151) – Phase 3 – LIGHTHOUSE study), for which exact results are not yet known.

1.2. Alpha-synuclein (SNCA) – targeted therapies

Although the incidence of PD associated with a mutation in the *SNCA* gene is much lower than *LRRK2*-associated cases (about 140 reported cases), it is a population of critical importance for a more precise understanding of the pathomechanism of the disease [12]. Clinically, *SNCA*-associated PD is an early-onset (< 50 years) form, which shows rapid progression [5,19]. The presence of neurocognitive disturbance is very common [19]. This form shows a dramatic levodopa response after treatment initiation; however, this effect diminishes over the course of the disease [5]. In the scientific literature, some atypical presentations have also been reported (myoclonus, central hypoventilation, pyramidal signs, cerebellar signs) [2,5]. Lewy bodies are present in various important brain regions associated with movement control and movement organization (e.g. substantia nigra, cerebral cortex) [20].

Table 1. Comparison of the main hereditary subtypes associated with Parkinson's disease.

Genetic subtype	Mean age of onset range	Inheritance	Mutation type	Clinical characteristics	Response to levodopa and deep brain stimulation treatments
LRRK2	4th-10th decade	Autosomal dominant	Missense	Milder progression. Some non-motor symptoms are unusual.	Levodopa responsive. Excellent motor response to subthalamic nucleus DBS.
SNCA	2nd-7th decade	Autosomal dominant	Missense/ multiplications	Frequent cognitive decline, psychiatric disturbances. Some atypical presentations were also reported (myoclonus, central hypoventilation, pyramidal signs, cerebellar signs).	Variable levodopa responsiveness. DBS: improvement of motor symptoms. Higher rate of cognitive complications.
GBA	4th-8th decade	Autosomal dominant	Missense/deletions	Frequent presence of postural instability with gait difficulty, neurocognitive disorder, dysautonomia and other psychiatric disturbances.	Levodopa responsive. DBS: can be beneficial, but cognitive complications are common.

(Abbreviations: DBS – deep brain stimulation; GBA – glucocerebrosidase gene; LRRK2 – Leucine-rich repeat kinase 2 gene; SNCA – α-synuclein gene.)

Table 2. Completed major clinical trials related to LRRK2, SNCA and GBA.

	Reference	has Jennings <i>et al.</i> , 2022 [13]	clinicaltrials. gov	ell Volc <i>et al.</i> , e 2020 [22]	Schenk <i>et al.</i> , 2017 [23]	her Pagano <i>et al.</i> , 2022 [24]	clinicaltrials. gov	Lang <i>et al.</i> , es 2022 [25]	Levin <i>et al.</i> , 2022 [15]	vell Stamler <i>et al.</i> , 2019 [16]	clinicaltrials. gov	Pagan <i>et al.</i> , 2016 [17]	Pagan <i>et al.</i> , 2019 [18]	Simuni <i>et al.</i> , 2020 [26]	clinicaltrials. gov	clinicaltrials. gov	clinicaltrials. gov
	Main results	DNL201 is safe and well tolerated. It appears that it has the ability to correct lysosomal dysfunction.	DNL151 was safe and generally well tolerated.	Repeated administrations of PD01A were safe and well tolerated. It caused a measurable humoral immune response.	Good safety and tolerability. The serum level of the alpha-synuclein was reduced.	Prasinezumab therapy had no meaningful effect (neither clinically nor radiologically /DaT-SPECT/).	Terminated	The trial was terminated, because of lack of efficacy (UPDRS). DaT-SPECT imaging showed no differences between placebo and cinpanemab group.	Good safety and tolerability.	PBT434 has proportional pharmacokinetics and was well tolerated in healthy volunteers.	Terminated	Good safety and tolerability.	Reduced plasma and CSF level of alpha-synuclein.	Poor CSF penetration. No clinical improvement.	Good safety and tolerability.	Good safety and tolerability.	Good safety and tolerability.
(treatment period or time frame of	the study)	28 days	14 and 28 days	221–259 weeks	3 months	52 weeks	72 weeks	52 weeks	~ 90 days	8 days	48 weeks	6 months	12 months	6 months	26 days	8 days	4 weeks
	Participants	28 PD	186 healthy volunteers	24 PD	40 participants	316 participants	24 participants	357 participants	68 participants	18 healthy volunteers	47 participants	12 participants	75 participants	76 participants	24 participants	18 participants	60 participants
	Target, effect	LRRK2 inhibitor	LRRK2 inhibitor	Active immunization	Passive immunization	Passive immunization	Passive immunization	Passive immunization	Disruption of α- synuclein aggregation	lron attenuating agent	Enhancing autophagic activity	Enhancing autophagic activity	Enhancing autophagic activity	Enhancing autophagic activity	Enhancing autophagic activity	Enhancing autophagic activity	Enhancing autophagic activity
	Tested molecule	DNL201; low and high doses	DNL151; single daily doses (from 15 mg to 300 mg – 28 days)/ twice daily doses (up to 400 mg – 14 days)	PD01A	Prasinezumab (/PRX002/ R07046015)	Prasinezumab	BIIB054 (/cinpanemab)	BIIB054 (/cinpanemab)	Anle138b	PBT434	Rapamycin (sirolimus)	Nilotinib	Nilotinib	Nilotinib	K0706/SCC-138	K0706/SCC-138	K0706/SCC-138
	Phase	1b 1	-	-	1b 1	2	-	7	-	-	2	-	2	2	-	-	-
	Clinical trial	NCT03710707	NCT04557800	2011–002650-31, 2013–001774-20, 2014–002489-54, 2015–004854-16	NCT02095171	NCT03100149 (PASADENA)	NCT03716570	NCT03318523 (SPARK)	NCT04208152	n.a.	NCT03589976	NCT02281474	NCT02954978	NCT03205488	NCT03316820	NCT03445338	NCT02970019
Genetic	subtype	LRRK2		SNCA													

Reference	Mullin <i>et al.</i> , 2020 [30]	clinicaltrials. gov	Schneider <i>et al.</i> , 2020 [19]	ind Schneider
Main results	It was well-tolerated and safe. Glucocerebrosidase level Mullin was elevated in CSF, there was a significant decrease <i>et a</i> in CSF a-synuclein concentration. Motor scores 202 improved.	Terminated	There were no safety events. Good tolerability.	2 gene; n.a. – not available; PD – Parkinson's disease; SNCA – α-synuclein gene.) (Table 2 is based on the work of Jasutkar [21] and Schneider
Duration (treatment period or time frame of the study)	6 months	36 weeks	n.a.	disease; SNCA – α-synı
Participants	18 PD	273 participants	~ 40 participants	able; PD – Parkinson's
Target, effect	Increasing glucocerebrosidase activity	Glucosylceramide synthase inhibitor	Increasing glucocerebrosidase activity	cinase 2 gene; n.a. – not avail
Tested molecule	Ambroxol	Venglustat	LTI-291	Abbreviations: <i>GBA</i> – glucocerebrosidase gene; <i>LRRK2</i> – Leucine-rich repeat kinase [19], as well as data from clinicaltrials.gov.)
Phase	7	2	-	sidase ge trials.gov
Clinical trial	NCT02941822	NCT02906020	NTR6598 and NTR6705	Abbreviations: <i>GBA</i> – glucocerebrosidase gen [19], as well as data from clinicaltrials.gov.)
Genetic subtype	GBA			(Abbreviat [19], as ¹

Table 2. (Continued).

6MCCl Classing10ULT Stated dates: route dub. up 10: 300 mgERUL In the interaction of the i	Genetic subtype	Clinical trial P	Phase	Tested molecule	Target, effect	Participants	Duration (treatment period or time frame of the study)	Main results	Reference
NCT037549 1 BIBD04, single and multiple does Antenses officuencies (6, 2 PD) D.A. Dealls forsity are not operation in the operation operation in the operation operation operation. Dealls (5, 2 PD) Deall operation operation operation operation operation operation. Deall operation operation operation operation operation operation operation. Deall operation operatindut operatindut operation operation operation operatingoperaction	.RRK2	NCT04056689	1b	DNL151; 3 tested doses; once daily, up to 300 mg.	LRRK2 inhibitor	34 PD	28 days	Detailed results are not available.	Ding and Ren, 2020 [14]
NCT0334305 2b BB13.2 LBRX inhibitor 640 participants 64 weeks Deatlide results are not available. UGHT101CE 3 BB13.2 LBRX inhibitor 640 participants 56 weeks Deatlide results are not available. UGHT101CE 3 BB13.2 LBRX inhibitor 20 participants 56 weeks Deatlide results are not available. NCU205188 1 PD01A Active immuniation 32 participants 12 months na. 61 NCU205188 1< PD01A		NCT03976349	-	BIIB094; single and multiple doses	Antisense oligonucleotide; LRRK2 degradation	82 participants (62 PD)	n.a.	Detailed results are not available.	clinicaltrials.gov
UGHTHOUK 3 BIB12.2 UBRV2.3 BIB12.2 UBRV2.3 BIB12.2 UBRV2.3 BIB12.3 Distribution Standing Distribution Standing Distribution Distribution <thdistribution< td=""><td></td><td>NCT05348785</td><td>2b</td><td>BIIB122</td><td>LRRK2 inhibitor</td><td>640 participants</td><td>48 weeks</td><td>Detailed results are not available.</td><td>Pharmaceutical company sites</td></thdistribution<>		NCT05348785	2b	BIIB122	LRRK2 inhibitor	640 participants	48 weeks	Detailed results are not available.	Pharmaceutical company sites
		LIGHTHOUSE study	m	BIIB122	LRRK2 inhibitor	400 participants	96 weeks	Detailed results are not available.	Pharmaceutical company sites
KC038504 1 POUA Active Immunization 30 participants 52 weeks 1.a. 61 KC02257343 1 POUA Active Immunization 30 participants 17 months 1.a. 61 KC02257343 1 POUA Active Immunization 30 participants 12 months 1.a. 61 KC00375731 2 Prainezmab (PRX002/P0046015) Pasive Immunization 30 participants 12 months 1.a. 61 KC0047535 1 Lu AF8242 Pasive Immunization 35 participants 30 weeks 1.a. 61 KC0045555 1 Lu AF8242 Pasive Immunization 35 participants 30 weeks 1.a. 61 KC0045555 1 Lu AF8242 Pasive Immunization 35 participants 30 weeks 1.a. 61 KC0045555 1 Lu AF8242 Pasive Immunization 57 participants 30 wieks 1.a. 61 KC0045555 1 Lu AF8242 Pasive Immunization 57 participants 30 wieks 1.a.<	VCA	NCT02618941	-	PD01A	Active immunization	26 participants	12 months	n.a.	clinicaltrials.gov
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NCT0327156 MED1341 Passive immunication 50 participants 13 weeks n.a. 01 NCT03351565 1 MED1341 Passive immunication 25 participants 28 weeks n.a. 01 NCT03361565 1 ME1382 Passive immunication 25 participants 28 weeks n.a. 01 NCT03361565 1 MPT200-11 Disruption of c-synuclein 48 participants 30 days n.a. 01 NCT03366682 1 NPT200-11 Disruption of c-synuclein 55 participants 30 days n.a. 01 NCT03361563 2 ENT-01 Disruption of c-synuclein 55 participants 10 months n.a. 01 NCT033781791 2 ENT-01 Disruption of c-synuclein 35 participants 10 weeks n.a. 01 NCT033817201 1 YX-739 Sterryton of c-synuclein 35 participants 10 weeks n.a. 01 NCT03913612 2 ENT-01 Disruption of c-synuclein 35 participants 10 weeks		NCT04777331	2	Prasinezumab (/PRX002/RO7046015)	Passive immunization	575 participants	76 weeks	n.a.	clinicaltrials.gov
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NCT03611566 I LM R842 Passive immunization 74 participants 84 days n.a. 61 NCT03601565 1 Anle138b Disruption of c-synuclein 74 participants 30 days n.a. 61 NCT036047525 2 ENT-01 Disruption of c-synuclein 55 participants 30 days n.a. 61 NCT03604753 2 ENT-01 Disruption of c-synuclein 56 participants 10 months n.a. 61 NCT03604753 2 ENT-01 Disruption of c-synuclein 58 participants 14 weeks n.a. 61 NCT0361791 2 ENT-01 Disruption of c-synuclein 28 participants 14 weeks n.a. 61 NCT0361791 2 ENT-01 Disruption of c-synuclein 24 participants 14 weeks n.a. 61 NCT03655236 2 KV706/SCC-138 Enhancing autophagic activity 50 participants 14 weeks n.a. 61 NCT03655236 2 KV706/SCC-138 Enhancing autophagic activity 50 particip		NCT04449484	-	MEDI1341	Passive immunization	25 participants	28 weeks	n.a.	clinicaltrials.gov
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2 Ambroxol Increasing glucocerebrosidase 15 participants 52 weeks n.a. activity		NCT04588285	2	Ambroxol	Increasing glucocerebrosidase activity	172 participants	18 months	n.a.	clinicaltrials.gov
		NCT04405596	2	Ambroxol	Increasing glucocerebrosidase activity	15 participants	52 weeks	n.a.	clinicaltrials.gov

(Continued)

Table 3. (Continued).

Reference	Schneider <i>et al.</i> , 2020 [19]	clinicaltrials.gov	Jasutkar <i>et al.</i> , 2022 [21]
Main results	n.a.	n.a.	n.a.
Duration (treatment period or time frame of the study)	n.a.	5 years	n.a.
Participants	45 PD	ment 24 participants	n.a.
Target, effect	TORC1 inhibitor	AAV9-mediated GBA replacement 24 participants	S1P5 receptor agonist
Tested molecule			
Phase	1b/2a RTB101	1/2a PR001	1 ESB-1609
Genetic subtype Clinical trial Phase	n.a.	NCT04127578 1/2a	n.a.
Genetic subtype			

(Abbreviations: *GBA* – glucocerebrosidase gene; *LRRK2* – Leucine-rich repeat kinase 2 gene; n.a. – not available; PD – Parkinson's disease; *SNCA* – α-synuclein gene.) (Table 3 is based on the work of Jasutkar [21] and Schneider [19], as well as data on clinicaltrials.gov.)

The SNCA gene contains six exons which encode the 140 amino acid long α -synuclein protein. The protein has three domains: (1) amino-terminal region (1–60); (2) central hydrophobic domain (61–95); (3) carboxy-terminal domain (96–140) [5]. So far, a few recurrent genetic alterations have been described in the scientific literature: three missense mutations (p.A53T, p.A30P, p.E46K), duplications and triplications [5]. The three missense point mutations disrupt the amino-terminal region and modify the conformation of the protein (leading to the formation of more stable beta sheets), so they can be considered toxic gain of function mutations [5]. The Lewy bodies detected during neuropathological examinations are presumably remnants of the degenerative process, but the exact pathomechanism is still unknown [5].

The mechanisms of drug action used in clinical trials can be classified as follows: (1) immunotherapy – active or passive; (2) disruption of α -synuclein aggregations; (3) promotion of the degradation of α -synuclein; (4) targeting other diseased-related genes, which may aggravate α -synuclein production (this fourth part is detailed in other subsections) [21].

During active immunization, an antigen is administered into the body via vaccination to induce an immune response. In contrast, during passive immunization, antibodies are directly administered [19]. The hypothesis is that the injected or produced antibody binds to the pathological extracellular proteins, resulting in their removal, which alleviates disease progression [19]. To date, more than 15 relevant clinical trials have been performed with active and passive immunization in PD [21]. The following synthetic peptide molecules were tested in active immunotherapy studies: PD01A (2011-002650-31, 2013-001774-20, 2014-002489-54, 2015-004854-16, NCT02618941, NCT01885494, NCT02216188, NCT01568099), PD03A (NCT02267434) and UB-312 (NCT0407 5318). For detailed results, please see Tables 2 and 3. The overall conclusion of the above-mentioned studies is that PD01A and PD03A resulted in a measurable immune response and these molecules are generally safe and well-tolerated (the UB-312 study is currently active, no results are available) [22]. Five molecules were tested in passive immunization trials: Prasinezumab (/PRX002/RO7046015) (NCT02095171, NCT03100149 (PASADE NA), NCT04777331), BIIB054 or cinpanemab (NCT03716570, NCT03318523 (SPARK)), MEDI1341 (NCT03272165, NCT04449484) and Lu AF82422 (NCT03611569). Prasinezumab is a humanized IgG1 monoclonal antibody. The results of the phase 1 study showed that it has a good safety and tolerability profile [23]. The serum level of a-synuclein was reduced. The PASADENA study was terminated because prasinezumab therapy had no meaningful effect (either clinically or radiologically /DaT-SPECT/) [24]. The results of the other prasinezumab (NCT04777331) phase 2 study are not yet available. The two BIIB054 (cinpanemab) studies (NCT03716570, NCT03318523 (SPARK)) were terminated because they did not meet primary and secondary outcome measures [25]. The results of the MEDI131 and Lu AF8242 studies have not yet been published.

The following molecules belong to the second group, which disrupt α -synuclein aggregation [21]. Anle138b (NCT04208152, NCT04685265); NPT200-11 (NCT02606682); ENT-01 (NCT03047629, NCT04483479, NCT03781791); PBT434 and YTX-7739. Anle138b, NPT200-11 and ENT-01 inhibit alpha-synuclein formation through the disturbance of oligomerization and by

displacing α -synuclein from membranes. PBT434 also blocks α synuclein aggregation by lowering iron levels (a novel quinazolinone compound with a moderate affinity metal-binding motif). In contrast, YTX-7739 works via the inhibition of the stearoyl-CoA desaturase enzyme. Despite the limited availability of study results, we know that Anle138b and PBT434 are safe and tolerated in phase 1 clinical trials.

The general hypothesis in connection with the elimination of a-synuclein is that its soluble form is eliminated via the ubiquitin-proteasome system, while the autophagy/lysosomal system may be responsible for the breakdown of aggregates [21]. In the available clinical studies, the following molecules, acting primarily via the activation of the autophagy/lysosomal system, were tested [19,21]: Rapamycin (sirolimus) (NCT03589976), Nilotinib (NCT02281474, NCT02954978, NCT03205488), K0706/SCC-(NCT03316820, NCT03445338, NCT02970019, 138 NCT03655236, NCT03996460), Radotinib (NCT04691661), FB101 (NCT04165837), ikT-148009 (NCT04350177), Bosutinib (NCT03888222). The first tested drug, namely rapamycin, acts via enhancing autophagic processes by inhibiting the mechanistic target of rapamycin (mTOR). Despite the first promising results, the applicability of rapamycin appears to be limited, given that severe side effects are expected due to the broad cellular usage of the mTOR signaling pathway. Nilotinib, as a c-Abl tyrosine kinase inhibitor, has been studied in detail. However, despite initially promising data, the molecule showed poor CSF penetration and lacked meaningful clinical effects [26]. The phase 1 studies of K0706/SCC-138 showed good safety and tolerability, both in healthy and PD patients. Two phase 2 trials are currently underway. Detailed clinical results of trials related to Radotinib, FB101, ikT-148009 and Bosutinib molecules are not currently available.

1.3. Glucocerebrosidase (GBA) - targeted therapies

β-glucocerebrosidase (GBA) heterozygous mutations are one of the most well-established risk factors of PD with variable penetrance depending on age [5]. The GBA gene encodes the lysosomal enzyme β -glucocerebrosidase, which has important roles in glycolipid metabolism (breakdown of glucocerebroside and glucosylsphingosine). Both autosomal recessive and dominant mutations increase the possibility of developing parkinsonism, however, the autosomal recessive form is more severe, and is called Gaucher disease, which is the most common lysosomal storage disease (with annual incidence of 1/60.000) [27]. From a clinical perspective, GBAassociated PD starts between the 4th and 8th decade (mean age of onset: 56.8 years). In this form of the disease there is a higher occurrence of postural instability with gait difficulty, dementia, dysautonomia and other psychiatric disturbances [5]. Pathologically, the brain alterations of patients with heterozygous GBA mutations are very similar to idiopathic PD patients, however, the cortical spreading of Lewy bodies are more prominent in some cases [19].

The *GBA* gene contains 11 exons. The protein has three domains: (1) domain I (residues 1–27 and 383–414) – antiparallel β sheet and two disulfide bridges (residues 4–16 and 18–

23); (2) domain II (residues 30–75 and 431–497) – immunoglobulin-like domain; (3) domain III – catalytic domain (residues 76–381 and 416–430) [28]. The exact mechanism of how heterozygous *GBA* mutations lead to the increased risk of developing PD has not been fully elucidated, but the most widely accepted mechanism is a bidirectional feedback loop between glucocerebrosidase and α -synuclein. The abnormal functioning of the glucocerebrosidase enzyme disrupts the lysosomal protein degradation process, which results in the accumulation of α -synuclein. Furthermore, α -synuclein inhibits normal neuronal lysosomal-glucocerebrosidase interaction [21,29].

Regarding the treatment of GBA-associated PD, it is a great advantage that many clinical trials have already been conducted in connection with Gaucher disease. However, enzyme replacement therapy (ERT), which seems to be very effective in Gaucher disease, cannot be used in GBA-associated PD, since ERT does not cross the blood-brain barrier [19]. Currently the following targeted treatments were tested in this population [19,21]: (1) – ambroxol (AiM-PD study); (2) – venglustat (MOVES-PD study); (3) - RTB101; (4) LTI-291; (5) PR001; (6) ESB-1609. Ambroxol is a well-known mucolytic agent, which binds to the active site of glucocerebrosidase and increases its activity. In the AiM-PD study (NCT02941822), 17 PD patients (8 with GBA mutations) were involved and the drug was given for [30]. lt was well-tolerated 186 days and safe. Glucocerebrosidase level was elevated in cerebrospinal fluid (CSF), furthermore, there was a significant increase in CSF α synuclein concentration [19]. Currently, three (NCT02914366, NCT04588285, NCT04405596) clinical trials are in progress, in which specific subpopulations are being tested (PD dementia, Lewy body dementia). Another molecule, namely venglustat, is an oral glucosylceramide synthase inhibitor. Venglustat was tested in a phase 2 multicenter, randomized, double-blind, placebo-controlled study (NCT02906020 - MOVES-PD), however, the trial was terminated because the results did not meet the primary or secondary endpoints. Only limited data are available on the other four molecules (RTB101, LTI-291, PR001, ESB-1609 under testing). However, we know from documented personal communication that LTI-291 might have a good safety and tolerability profile [19].

2. Conclusion

Although hereditary components can only be proven to be present in a very small number of cases of PD, these subpopulations are of particular importance regarding the development of personalized drugs. In this article, the three most relevant and widely tested hereditary subgroups were analyzed (*LRRK2, SNCA, GBA*). Overall, it can be concluded that many clinical studies have been carried out in connection with these targeted therapies, the vast majority being phase 1–2. From the perspective of *LRRK2*, the most promising compounds are DNL201 and DNL151. The results of clinical trials showed that these two molecules are safe and well tolerated. Among the *SNCA* immunization studies, it seems that within the active immunization procedures, PD01A may be relevant for future treatments. Anle138b, one of the α-synuclein disrupting agents, showed good tolerability and safety in the phase 1 trial, while K0706/SCC-138. Ambroxol and LTI-291 also showed good tolerability and safety during clinical trials in PD patients with the *GBA* heterozygous mutation. In conclusion, it can be declared that phase 2 and 3 studies in precisely defined subpopulations are mandatory in order to more accurately assess the effectiveness of the above-mentioned individual molecules.

3. Expert opinion

Although PD is still considered a sporadic disease, owing to the genes identified by genome-wide association studies (GWAS) it seems that a small portion of PD patients have a genetically determined etiology. These small hereditary subgroups are crucially important for drug development, because the general trend is that clinical trials involving a large heterogeneous group of PD patients, without any separation, do not meet expectations [31-33]. Our incomplete understanding of the disease mechanism, a lack of strong biomarkers which would make it possible to detect PD in the very early stages, and pathological, molecular, and environmental diversity make it difficult to identify future treatment options. Most of the clinical trials detailed in the manuscript are currently at phase 1 or 2 levels. As a result, at present no long-term conclusions can be drawn regarding the effectiveness of the molecules tested in these studies.

The main difficulty of future clinical trials on genetically defined subpopulations stems primarily from the small number of patients, so international collaborations and patient registry development are necessary. Additionally, considering that the individual forms of the disease are very rare, it can be challenging to assess the effectiveness with the often-used clinical condition assessment scales (e.g. Unified Parkinson's Disease Rating Scale). However, it seems that genetic testing is important, not only from the perspective of drug development, but also to provide a precise prognosis. The knowledge related to individual genetic subtypes is constantly increasing. The disease course, the effectiveness of levodopa and deep brain stimulation treatment can be predicted by specifying the exact genetic subtypes. With knowledge of that information, patients can receive personalized counseling and the opportunity to make individual decisions.

The organization of future clinical trials on a genetic basis presents many additional challenges. First of all, there is the question of which patients should be offered genetic testing in connection with PD before being involved in a clinical trial. Although early-onset of the disease, a characteristic phenotype, and a positive family history can help in making decisions, patients without these features may also have genetic backgrounds. A negative family history can be explained by a reduced penetrance, different age of onset, de novo mutations, etc. If genetic testing occurs, mainly in the form of clinical exome sequencing, the interpretation of the obtained results is often challenging. In the optimal case, a known pathogenic mutation in a disease-causing gene is confirmed, so there is no obstacle to patient inclusion in a targeted clinical trial. However, clinical settings are rarely so ideal. In most cases, unknown variants (variant of unknown significance – VUS) are detected or negative results are obtained. Although in a framework of international collaboration, it is possible to create a small number of patient groups in which the participants carry a mutation in the same gene, the phenotype of these patients and their responses to molecular therapy may still be different. Knowing this, pharmaceutical companies have the following options if they want to organize a precision clinical trial: (1) – during preclinical animal studies, they identify patients with mutations in the same gene that allow them to be classified into one clinical trial group; (2) – design drugs for hot-spot mutations (e.g. *LRRK2* Gly2019Ser).

In conclusion, the authors' opinion is that in the 21st century, genetic testing should be part of the workup of PD patients before exposing them to additional, non-conventional (e.g. targeted molecular therapies) treatments.

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Declaration of interest

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