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Biomarker-driven phenotyping in Parkinson disease: a translational missing link in disease-modifying clinical trials

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Abstract

Past clinical trials of putative neuroprotective therapies have targeted Parkinson disease (PD) as a single pathogenic disease entity. From an Oslerian clinico-pathologic perspective, the wide complexity of PD converges into Lewy bodies and justifies a reductionist approach to PD: a single-mechanism therapy can affect most of those sharing the classic pathologic hallmark. From a systems-biology perspective, PD is a group of disorders that, while related by sharing the feature of nigral dopamine-neuron degeneration, exhibit unique genetic, biological and molecular abnormalities, which probably respond differentially to a given therapeutic approach, particularly for strategies aimed at neuroprotection. Under this model, only biomarker-defined, homogenous subtypes of PD are likely to respond optimally to therapies proven to affect the biological processes within each subtype. Therefore, we suggest that precision medicine applied to PD requires a reevaluation of the biomarker-discovery effort. This effort is currently centered on correlating biological measures to clinical features of PD and on identifying factors that predict whether various prodromal states will convert into the classical movement disorder. We suggest, instead, that subtyping of PD requires the reverse view, where abnormal biological signals (i.e., biomarkers) rather than clinical definitions are used to define disease phenotypes. Successful development of disease-modifying strategies will depend on how relevant the specific biological processes addressed by an intervention are to the pathogenetic mechanisms *in the subgroup of targeted patients*. This precision-medicine approach will likely yield smaller but well-defined subsets of PD amenable to successful neuroprotection.

Keywords

Parkinson disease; biomarkers; neuroprotection; systems biology

Introduction

The elusive and highest priority therapeutic frontier in Parkinson disease (PD) remains the development of disease-modifying or neuroprotective interventions. Neuroprotection using a precision medicine paradigm would ideally occur (1) prior to or at the earliest stages of a diagnosable form of the disease, (2) with interventions targeting specific biological processes associated with disease progression, and (3) in a PD subgroup where such key abnormal processes have been confirmed through validated biomarkers. A perfect set of

biomarkers would not only serve to select appropriate patients for a specific disease-modifying intervention, but also reflect disease progression and response to therapy. Therapeutic progress for disease modification would be accelerated by focusing on disease subgroups sharing similar abnormal molecular and biological characteristics.[1]

Biomarker-validated populations have remained a missing link in the translational efforts of putative disease-modifying therapies over the past two decades. Ongoing biomarker-discovery efforts have been designed based on consensus clinical criteria for PD and its subtypes (e.g., tremor-dominant PD). We will here briefly review the pitfalls associated with anchoring the development of biomarkers on clinical criteria and suggest that devoting the next decade to the generation of unbiased biomarker-driven subtyping (rather than clinical phenotype-driven biomarker validation) will help identify possibly smaller, and biologically more homogenous, subsets of PD patients that are more likely to be amenable to specific molecular targeting.

The short history of failures in neuroprotective efforts

Treating PD as a single disease has greatly served the development of symptomatic therapies based on dopaminergic enhancement, given the common denominator of all its variants: dopamine deficiency. This model, however, has consistently failed when testing potential disease-modifying interventions.[2] Indeed, drugs that have effectively targeted putative pathogenetic mechanisms in animal models of PD have consistently failed to accomplish disease modification in PD patients. The range of arguments justifying the translational failures range from inappropriate clinical trial designs, insufficiently sensitive endpoints, inadequate target engagement of putative neuroprotective interventions, patients recruited at an advanced disease stage, and, animal models (on which these interventions were developed) that do not “recapitulate the complexity of the human disease.”[3] But a critical step in the translational efforts deserves greater recognition: the same biological mechanisms identified as critical for the drugs shown to be neuroprotective in animal models must be criticial in the group of PD patients targeted by the clinical trials of those drugs.

Two approaches to PD offer radically different outlooks for neuroprotection. On the one hand, the model of PD as a complex, heterogeneous disease assumes that all the clinical, genetic, and molecular variability can be traced to a unifying pathological core, namely aggregated α-synuclein found in Lewy bodies and neurites. On the other hand, the very complexity of PD, which has led to the notion that there exist different Parkinson *diseases*[4] which represent unique pathophysiologic entities, even if Lewy bodies are a common pathologic end-product and there are sufficient clinical elements to group them under the same diagnostic umbrella. The former model assumes that a drug may act on most patients with PD if the mechanism of action is *sufficiently common* or *dominant* across all clinical subtypes. Dopamine replacement strategies have been well served by this model because dopamine deficiency, predominantly from nigrostriatal neurodegeneration, is a dominant feature in all subtypes of PD. However, alterations in basic underlying biological processes such as mitochondrial, proteostatic, lysosomal, and inflammatory mechanisms may differ substantially among PD subtypes. Under the PD-as-several-diseases model, selected mitochondrial enhancement strategies (e.g., to enhance mitophagy or restore electron

transport chain activity) would be expected to succeed only in the subgroup of PD patients where mitochondrial dysfunction is an upstream event rather than a downstream byproduct of other molecular abnormalities. Clinical trials of drugs enhancing mitochondrial function will continue to fail if they include a substantial number of patients for whom mitochondrial dysfunction is not central.

In conclusion, the prevailing one-disease approach to PD has unsuccessfully predicted that clinical trials targeting a single pathogenic mechanism will mitigate disease progression in patients who share a clinical diagnosis but are heterogeneous regarding underlying molecular pathogenesis. Conversely, in the emerging precision-medicine model of neuroprotection, therapies can best succeed in the select subgroup of patients that share the biological aberrations such therapies were demonstrated to mechanistically alter.

The lessons from oncology

In the mirror-image field of oncology, where cells abnormally proliferate rather than degenerate, cancer was long viewed as a single, if heterogeneous disease. Breast cancer, for instance, was to be approached in a similarly aggressive fashion, with radical mastectomy, because it was equally malignant regardless of age or any other clinical variables.[5] In the 1950s and 1960s the application of breast-conserving surgery (“quadrantectomy” or “lumpectomy”) was widely believed as inappropriate compared to radical surgery. Only toward the late 1970s and early 1980s, after the first randomized clinical trial comparing these procedures demonstrated no difference in survival,[6, 7] breast cancer began to be reconsidered as a cluster of several diseases and a search for its biological subtypes was initiated.

The last three decades of cancer research redefined cancer entirely, using a systems-biology approach to guide its nosology and disease-modifying treatment. Under this paradigm in breast cancer, a combination of nine histological types (e.g., tubular, ductal, mucinous, etc. for invasive and in-situ carcinomas) with any combination of validated molecular markers (mainly, estrogen receptor [ER], progesterone receptor [PR], human epidermal growth factor receptor 2 (HER2), and others [e.g., ErbB2, p53, Ki67]) yields nearly 20 breast cancer subtypes, each with a distinct survival curve and response to therapy.[8] For example, the drug cocktail that is most effective for patients with HER2-positive breast cancer may be ineffective or harmful for patients with HER2-negative cancer.[9] Within this sophisticated layering of nosological data created to guide therapy, there still are subtypes of breast cancer that remain biologically difficult to characterize (e.g., the malignant “triple negative” [ER-negative, PR-negative, and HER2-negative] basal-like subtype).[10]

Unlike oncology, the field of neurodegenerative diseases does not have ready access to affected tissue for histopathology and this has contributed to the long dominance of clinical (and more recently, imaging) criteria for biomarker development. An oncologist examines several biomarkers in order to individualize a rational disease-modifying anti-cancer treatment: the specific histologic type, the plausible genetic mutations, the presence of ER/PR/HER2 receptors, and the anatomical spread. Only then is a rational therapeutic cocktail administered, addressing known mechanisms and preempting plausible alternative

mechanisms of cancer development for that specific patient. Neurologists involved in research of neurodegenerative diseases have remained committed to the reductionist model of PD (and, for that matter, Alzheimer disease (AD) and other disorders) as a single “but complex” disease, in the same manner as oncologists viewed cancer until the late 1970s.

Clinical phenotype to biomarkers: Pitfalls in the current model

The success of future neuroprotective therapies in PD and other neurodegenerative disorders will depend on the extent to which biomarkers of disease subtypes and subtype-specific progression will help identify suitable populations for promising molecular interventions. The current model for biomarker development is anchored on a traditional definition of PD, as recently refined by the International Parkinson and Movement Disorders Society.[11] This phenotype-driven biomarker development program is based on the assumed existence of biological/molecular underpinnings for each diagnostic entity, as well as the corresponding prodromal state. The most important effort based on this premise is the Parkinson’s Progression Markers Initiative (PPMI), launched in 2011 by the Michael J. Fox Foundation for Parkinson’s Research.[12]

After a clinical diagnosis is made, the current approach to biomarker research (Figure 1A) evaluates how biological markers correlate with the clinical diagnosis (“state biomarkers”) or evolution (“rate biomarkers”). The most recent analysis of the PPMI CSF data found that PD subjects (n = 412) have lower alpha-synuclein (α-syn), total tau (t-tau), and phosphorylated tau (p-tau), but not lower amyloid-β1–42 (Aβ1–42) compared to healthy controls (n = 189).[13] As such, α-syn, t-tau, and p-tau could be considered biomarkers of disease, even if their individual diagnostic value for PD diagnosis is limited due to the large overlap with healthy controls. Nevertheless, these may be considered for use at a population level if confirmed in other cohorts. However, in the *De Novo Parkinson* or DeNoPa cohort (n = 123 PD; 106 age-matched healthy controls) neither t-tau nor p-tau in CSF segregated PD from controls.[14] Only α-syn was lower at baseline but it did not change over a 2-year period, suggesting it is not useful for monitoring disease progression.[14] Thus, CSF biomarkers from clinically defined phenotypes exhibit substantial signal overlap and the outcomes may vary between cohorts. Furthermore, this model has left unanswered the question of which biomarkers might help assist in individualizing molecular therapy in a precision-medicine future.

Extensively used clinical phenotypes include tremor-dominant (TD), postural instability-gait disorder (PIGD), non-motor mild cognitive impairment (PD-MCI), and dementia (PDD) subtypes.[15] In clinical epidemiologic studies, the motor PIGD phenotype is associated with greater likelihood of evolving into the PD-MCI and PDD phenotypes.[16] Segregating these clinical phenotypes based on Unified Parkinson Disease Rating Scale (UPDRS)[17] data collected in the PPMI, only low α-syn, but not changes in this or other biomarkers, was associated with the PIGD phenotype and also with worse cognitive performance (e.g, PD-MCI/PDD).[13] In another PPMI analysis, however, the 2-year conversion to PD-MCI (n= 286 participants without MCI at baseline) was associated with lower mean baseline CSF β-amyloid 1–42 (343.8 vs. 380.4 pg/mL, $p < 0.01$) but not α-syn.[18] These conflicting data have been suggested to reflect “disease heterogeneity”, but have not yet forced a

reconsideration of the *clinical phenotype* → *biomarker* model for validating both the disease subtypes and the corresponding presumed biomarkers.

Importantly, the separation of PD from other disorders on clinical grounds is challenged by the finding that molecular elements traditionally considered a domain of other neurodegenerative disorders may "explain some of the variability in PD." For example, amyloid as measured by CSF Aβ1–42 is present in 17% of dopamine transporter scan-positive PD patients within two years from diagnosis.[19] These patients are older, more cognitively impaired, and have more cortical atrophy in medial temporal, frontal and brainstem structures.[19] Thus, this small but significantly different group of patients exhibiting a PD-AD hybrid (two diseases or a defined molecular/pathology subtype?) defies the "neat" clinical separation between α-syn and amyloid/tau pathologies, or between PD and AD clinical phenotypes.

Lastly, a major problem with biomarker discovery using clinical phenotypes as anchors is the "instability" of the clinical phenotypes themselves: Within a year of enrollment in the PPMI study, the mean values of the two common motor phenotypes, TD and PIGD, defined using the scoring of related sub-items from the UPDRS,[20] shifted by nearly 40% and 20%, respectively, regardless of dopaminergic treatment.[21] This cast further doubt on the relevance of any molecular/biological derangements presumed to be associated with each of these clinical phenotypes.

Biomarkers to clinical phenotype: Ideal model

The desirable approach (Figure 1B), based on a systems-biology model, assumes that PD is a point-of-entry diagnosis encompassing patients with several genetic, biological and pathophysiologic abnormalities. The ideal biomarker discovery program is based on large, aging populations with or without a neurological diagnosis at baseline. Some of these individuals will be diagnosed with PD, some with AD, some with other neurodegenerative disorders, and some will remain neurologically healthy. The statistical analysis would not be dependent on the clinical diagnoses as the independent variable but, rather, on the biological and molecular abnormalities. Identification of abnormal biological processes would occur in an unbiased manner, detached from any preconceived notion of whether it correlates with a clinically defined disease. Abnormally high and low signals would then be used, in isolation or in combination, to determine the extent to which they correlate with specific clinical features and with the progression of motor or non-motor disability. While some biomarkers may correlate with previously defined PD subtypes (e.g., PD-MCI), others will most likely segregate with previously unrecognized phenotypes (e.g., prominent postural tremor and a non-neurological impairment, such as arthritis), for which we have no current consensus clinical criteria. Many will not be associated with a clearcut clinical phenotype. For example, biomarker pairs A&B and C&D may be associated with parkinsonism, and A&B may include early dementia in 50% and C&D may include early dementia in 30%. Even if distinct biomarker patterns were not to lead to distinctive clinical phenotypes (as it may be theoretically expected based on current evidence: for instance, patients with *GBA* mutations do indeed have more dementia and these mutations may be associated with the clinical picture of dementia with Lewy bodies but many patients behave no differently from those

without a clear disturbance of lysosomal function[22]), the biological homogeneity of these PD subtypes would represent suitable targets for the application of "personalized" disease-modifying therapies. A potentially powerful way to implement this *biomarker → clinical phenotype* model is through an exploratory, unbiased, non-hypothesis-driven approach to biomarker development, with a reverse analytic plan to that applied in the PPMI and other biomarker validation cohorts. An exponentially larger sample of aging adults than available in those cohorts would be required to have adequate power because an unbiased biomarker development program would concentrate on recognizing the phenotype of those whose biological signals represent unique patterns (rather than simple 'positive-negative' biomarkers based on a given cutoff of "positivity") or are outliers in the measurement spectrum in order to discriminate subgroups ideal for potentially neuroprotective molecular therapies.

Implications for clinical trials

It is critical for the biological action of therapies with promising neuroprotective potential, confirmed to engage relevant molecular targets, to be considered only in patients with the appropriate biomarker signatures. Without biomarkers of disease (for patient selection) and progression (for response monitoring), the chances for success in neuroprotection trials are limited. In the immediate future, clinical trials of drugs with neuroprotective properties may succeed, in the absence of biomarkers to assist in the selection of a suitable cohort, only if the mechanisms of action of the interventions are of sufficiently broad applicability in Lewy body PD. For instance, despite the lack of a biomarker for propagation of α-syn pathology, it is conceivable that immunotherapies aimed at disrupting this mechanism of disease progression may be applicable to a large proportion of PD patients. Future clinical trials may also target selected genetic (e.g., at-risk or manifest *LRRK2* mutation carriers for initial trials of LRRK2 kinase inhibition,[23] and GBA mutation carriers for trials of glucosylceramide synthase inhibitor to influence glucocerebrosidase activity[24]) or polysomnography-defined pre-motor REM sleep behavior disorder subtypes.[25] An ongoing example of the use of a biomarker to define a clinical trial cohort is the SURE-PD3 study, in which inosine, a precursor of urate, is only given to patients with low baseline urate, a molecular biomarker that predicts the rate of disease progression.[26]

There are several major challenges in ushering the era of precision medicine for PD through biomarker development programs. Besides assay variability, population heterogeneity, differing power to detect a range of biological effects, we will need to: (1) differentiate between specific *and early* biomarkers (linked to causative pathological mechanisms and therefore targetable for therapy development) vs. non-specific *or late* biomarkers (reflecting reactive plasticity or self-perpetuating neurodegenerative cycles and unwarranted for therapeutic targeting) vs. biomarkers reflecting a physiological response to injury; (2) understand the extent to which identifiable biomarkers may be "unstable" (transient) or constant throughout the course of the disease. This will require a ranking of biomarkers related to the phenotypic staging they represent and the early-versus-late relevance in the neurodegenerative processes: This may take many years to ascertain, particularly if our starting point, due to logistical and power issues, will need to be restricted to large PD cohorts (advanced as well as *de novo* and prodromal, as in PPMI) rather than even larger

population-based cohorts. Thus, we need to take a large, unbiased step back to invest the next decade laying the groundwork for biomarker-driven clinico-molecular phenotyping in PD to inform the development of clinical trials targeting smaller, but better defined, biologically homogeneous PD subtypes, one at a time. This will imply reconsidering the wisdom of further phenotype-based biomarker development programs and current clinical diagnostic criteria to select patients for disease-modifying clinical trials. Such an expensive, time consuming but transformational effort will require the engagement of the entire research community, with substantial investments from foundations, industry and government.

Authors' roles

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2. Manuscript Preparation: A. Writing of the first draft, B. Review and Critique

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Appendix

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Appendix

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References

1. Espay AJ, Brundin P, Lang AE. Precision medicine for disease modification in parkinson disease. Nat Rev Neurol. 2017 in press.
2. Athauda D, Foltynie T. The ongoing pursuit of neuroprotective therapies in parkinson disease. Nat Rev Neurol. 2015; 11:25–40. [PubMed: 25447485]
3. Park A, Stacy M. Disease-modifying drugs in parkinson's disease. Drugs. 2015; 75:2065–2071. [PubMed: 26581672]
4. Calne DB, Mizuno Y. The neuromythology of parkinson's disease. Parkinsonism Relat Disord. 2004; 10:319–322. [PubMed: 15196512]
5. Halsted WSI. A clinical and histological study of certain adenocarcinomata of the breast: And a brief consideration of the supraclavicular operation and of the results of operations for cancer of the breast from 1889 to 1898 at the johns hopkins hospital. Ann Surg. 1898; 28:557–576.
6. Veronesi U, Saccozzi R, Del Vecchio M, Banfi A, Clemente C, De Lena M, et al. Comparing radical mastectomy with quadrantectomy, axillary dissection, and radiotherapy in patients with small cancers of the breast. N Engl J Med. 1981; 305:6–11. [PubMed: 7015141]
7. Veronesi U, Cascinelli N, Mariani L, Greco M, Saccozzi R, Luini A, et al. Twenty-year follow-up of a randomized study comparing breast-conserving surgery with radical mastectomy for early breast cancer. N Engl J Med. 2002; 347:1227–1232. [PubMed: 12393819]
8. Malhotra GK, Zhao X, Band H, Band V. Histological, molecular and functional subtypes of breast cancers. Cancer Biol Ther. 2010; 10:955–960. [PubMed: 21057215]
9. Mendes D, Alves C, Afonso N, Cardoso F, Passos-Coelho JL, Costa L, et al. The benefit of her2-targeted therapies on overall survival of patients with metastatic her2-positive breast cancer--a systematic review. Breast Cancer Res. 2015; 17:140. [PubMed: 26578067]
10. Bianchini G, Balko JM, Mayer IA, Sanders ME, Gianni L. Triple-negative breast cancer: Challenges and opportunities of a heterogeneous disease. Nat Rev Clin Oncol. 2016
11. Postuma RB, Berg D, Stern M, Poewe W, Olanow CW, Oertel W, et al. Mds clinical diagnostic criteria for parkinson's disease. Mov Disord. 2015; 30:1591–1601. [PubMed: 26474316]
12. Parkinson Progression Marker I. The parkinson progression marker initiative (ppmi). Prog Neurobiol. 2011; 95:629–635. [PubMed: 21930184]
13. Kang JH, Mollenhauer B, Coffey CS, Toledo JB, Weintraub D, Galasko DR, et al. Csf biomarkers associated with disease heterogeneity in early parkinson's disease: The parkinson's progression markers initiative study. Acta Neuropathol. 2016; 131:935–949. [PubMed: 27021906]
14. Mollenhauer B, Zimmermann J, Sixel-Doring F, Focke NK, Wicke T, Ebentheuer J, et al. Monitoring of 30 marker candidates in early parkinson disease as progression markers. Neurology. 2016
15. Thenganatt MA, Jankovic J. Parkinson disease subtypes. JAMA Neurol. 2014; 71:499–504. [PubMed: 24514863]
16. Zhu K, van Hilten JJ, Marinus J. Predictors of dementia in parkinson's disease; findings from a 5-year prospective study using the scopa-cog. Parkinsonism Relat Disord. 2014; 20:980–985. [PubMed: 25024059]
17. Goetz CG, Tilley BC, Shaftman SR, Stebbins GT, Fahn S, Martinez-Martin P, et al. Movement disorder society-sponsored revision of the unified parkinson's disease rating scale (mds-updrs): Scale presentation and clinimetric testing results. Mov Disord. 2008; 23:2129–2170. [PubMed: 19025984]
18. Terrelonge M Jr, Marder KS, Weintraub D, Alcalay RN. Csf beta-amyloid 1–42 predicts progression to cognitive impairment in newly diagnosed parkinson disease. J Mol Neurosci. 2016; 58:88–92. [PubMed: 26330275]

19. McMillan CT, Wolk DA. Presence of cerebral amyloid modulates phenotype and pattern of neurodegeneration in early parkinson's disease. J Neurol Neurosurg Psychiatry. 2016
20. Stebbins GT, Goetz CG, Burn DJ, Jankovic J, Khoo TK, Tilley BC. How to identify tremor dominant and postural instability/gait difficulty groups with the movement disorder society unified parkinson's disease rating scale: Comparison with the unified parkinson's disease rating scale. Mov Disord. 2013; 28:668–670. [PubMed: 23408503]
21. Simuni T, Caspell-Garcia C, Coffey C, Lasch S, Tanner C, Marek K, et al. How stable are parkinson's disease subtypes in de novo patients: Analysis of the ppmi cohort? Parkinsonism Relat Disord. 2016; 28:62–67. [PubMed: 27132498]
22. Bras J, Guerreiro R, Darwent L, Parkkinen L, Ansorge O, Escott-Price V, et al. Genetic analysis implicates apoe, snca and suggests lysosomal dysfunction in the etiology of dementia with lewy bodies. Hum Mol Genet. 2014; 23:6139–6146. [PubMed: 24973356]
23. West AB. Ten years and counting: Moving leucine-rich repeat kinase 2 inhibitors to the clinic. Mov Disord. 2015; 30:180–189. [PubMed: 25448543]
24. Alcalay RN, Levy OA, Waters CC, Fahn S, Ford B, Kuo SH, et al. Glucocerebrosidase activity in parkinson's disease with and without gba mutations. Brain. 2015; 138:2648–2658. [PubMed: 26117366]
25. Postuma RB, Gagnon JF, Bertrand JA, Genier Marchand D, Montplaisir JY. Parkinson risk in idiopathic rem sleep behavior disorder: Preparing for neuroprotective trials. Neurology. 2015; 84:1104–1113. [PubMed: 25681454]
26. Schwarzschild MA, Ascherio A, Beal MF, Cudkowicz ME, Curhan GC, et al. The Parkinson Study Group S-PDI. Inosine to increase serum and cerebrospinal fluid urate in parkinson disease: A randomized clinical trial. JAMA Neurol. 2013

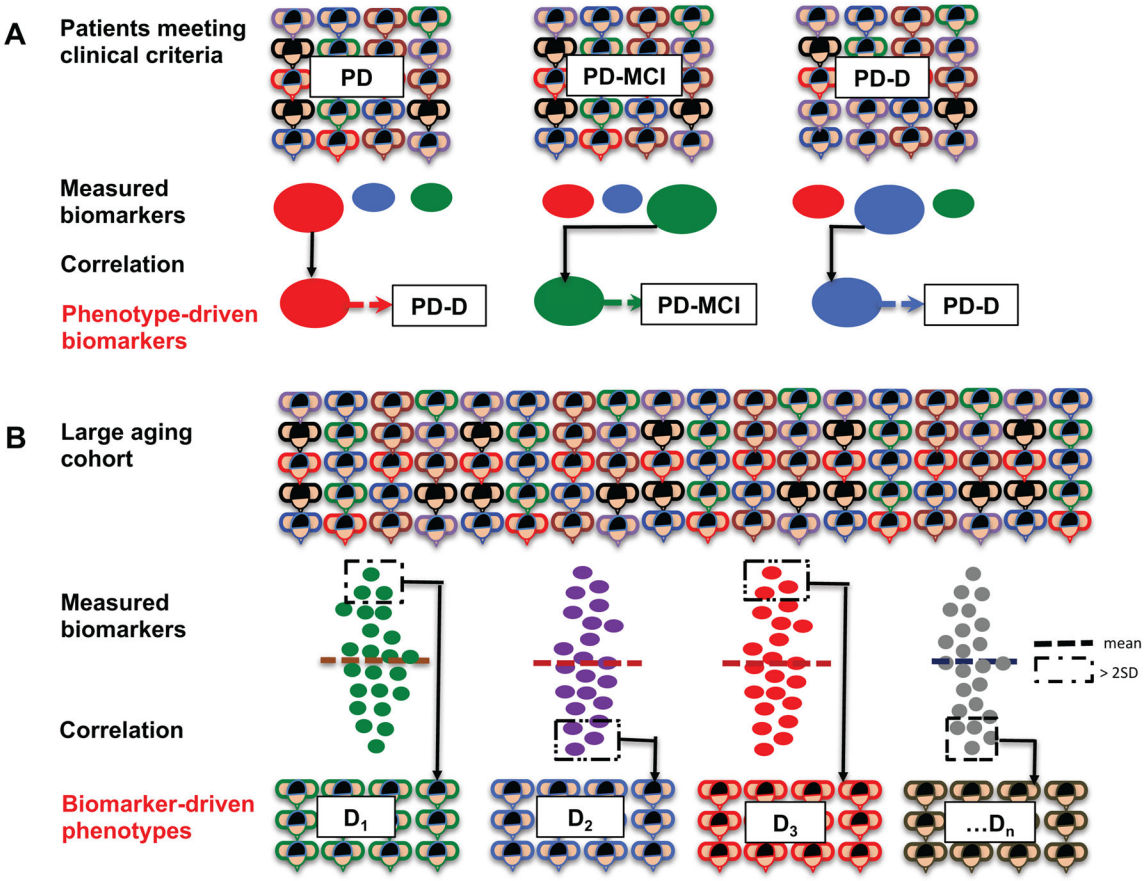

Figure 1. Biomarker development models

A. Clinical phenotype → Biomarker validation. Under this model, clinical phenotypes are established as the "truth" against which biomarkers are validated. After defining the clinical constructs (e.g., PD-MCI), statistical analyses determine the strength of correlation with a variety of abnormal biological signals. In this example, the "green" signal becomes a biomarker of PD-MCI. **B. Biological/molecular abnormalities → Biomarker-driven phenotypes.** Under this model, the "truth" is unknown and the analysis is non-hypothesis driven (exploratory). Biological/molecular signals are examined within a large cohort of individuals, including criteria-meeting "PD" but also individuals with other PD-like diagnoses and those aging without overt disease. The biomarker-driven phenotypes (D_1, D_2…D_n, where D stands for "disease") share strong biological homogeneity, even if not clinically, as they are generated based on abnormal biological signals (exemplified as >2 standard deviations above the mean for green and red signal; and >2 SD below the mean for purple and a theoretical gray "n" signal).