



REVIEW

Remembering your A, B, C's: Alzheimer's disease and ABCA1



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Abstract The function of ATP binding cassette protein A1 (ABCA1) is central to cholesterol mobilization. Reduced ABCA1 expression or activity is implicated in Alzheimer's disease (AD) and other disorders. Therapeutic approaches to boost ABCA1 activity have yet to be translated successfully to the clinic. The risk factors for AD development and progression, including comorbid disorders such as type 2 diabetes and cardiovascular disease, highlight the intersection of cholesterol transport and inflammation. Upregulation of ABCA1 can positively impact APOE lipidation, insulin sensitivity, peripheral vascular and blood–brain barrier integrity, and anti-inflammatory signaling. Various strategies towards ABCA1-boosting compounds have been described, with a bias toward nuclear hormone receptor (NHR) agonists. These agonists display beneficial preclinical effects; however, important side effects have limited development. In particular, ligands that bind liver X receptor (LXR), the primary NHR that controls ABCA1 expression, have shown positive effects in AD mouse models; however, lipogenesis and unwanted increases in triglyceride production are often observed. The longstanding approach, focusing on LXR β vs. LXR α selectivity, is over-simplistic and has failed. Novel approaches such as phenotypic screening may lead to small molecule NHR modulators that elevate ABCA1 function without inducing lipogenesis and are clinically translatable.

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1. Introduction

Alzheimer's disease (AD) is the most prevalent form of dementia in the US and worldwide, and it is currently the sixth leading cause of death in the US^{1,2}. Age is the greatest risk factor for AD, which will translate to an increase in disease prevalence with increasing life expectancy globally: current estimates indicate the number of diagnosed cases in the US increasing from six million to fourteen million by 2050. The widespread prevalence of AD is contrasted by the dearth of available treatments. There are five FDA-approved small molecule drugs: donepezil, rivastigmine, and galantamine inhibit the acetylcholinesterase enzyme; memantine antagonizes the NMDA glutamate receptor; and a combination donepezil–memantine pill performs both functions. However, these treatments provide only temporary symptomatic improvement. They do not prevent, slow the progression, or alter the fatal prognosis of AD^{3,4}. The AD clinical trial failure rate (99.6% in the decade from 2002 to 2012) is the highest of any disease state, and there is an urgent need to discover and develop effective new therapies^{5–7}. The extremely high risk and cost of failure has led pharmaceutical companies to divest of AD drug development before Phase 2 proof-of-concept and pivotal Phase 3 clinical trials, which likely has led to premature abandonment of promising therapeutic strategies.

Diagnosis of AD rests on specialized tests for cognitive function combined with post-mortem histological analysis for hallmark AD pathology: a) extracellular amyloid plaques formed from amyloid- β (A β) peptide fragments and b) intracellular neurofibrillary tangles (NFT) composed of atypically phosphorylated tau protein. Inhibition of A β and tau peptide aggregation dominated early therapeutic approaches to AD, and the approval of aducanumab, in June 2021, is likely to revive these and other approaches targeting the removal of hallmark pathology. Although almost all disease-modifying AD therapeutics have failed in clinical trials, many targeted at A β have reported significant reductions in A β in these trials. This disconnect between attenuated A β without improved cognitive function has been explained by the need to treat patients in the prodromal stage of the disease. Longitudinal imaging studies have estimated that A β and NFT pathology develop up to three decades before symptoms, with brain atrophy (diminished hippocampal volume) and neuronal hypo-function (reduced glucose metabolism) preceding clinical onset by roughly ten years⁸. Unfortunately, the move “to treat before clinical symptoms” is stymied by the lack of predictive diagnostics. In 2020, the Lancet Commission on “Dementia prevention, intervention, and care” concluded that imaging techniques for hallmark A β and tau pathology (and blood tests for A β) have not reached clinical significance for predicting cognitive decline⁹. Indeed, it was concluded that most cognitively normal people with brain and/or plasma biomarkers for AD do not develop dementia within a clinically relevant timeframe.

Aducanumab, like other antibodies targeted at A β , dose-dependently reduced brain A β , as visualized by PET imaging. The FDA approval of aducanumab for prodromal AD, under the agency's accelerated approval pathway, requires substantial evidence of effect on an intermediate biomarker (in this case A β) and reasonable likelihood of a meaningful clinical benefit, which the FDA hopes will be achieved in post-market clinical trials. The approval of aducanumab is highly controversial because of unproven efficacy and direct contradiction of the Lancet Commission's findings on predictive biomarkers; however, it will likely maintain focus on clearance of A β as a clinical endpoint.

Many people develop a heavy A β burden but never suffer from cognitive decline¹⁰. In addition, the brains of patients who suffer cognitive decline and are diagnosed with AD show a wide range of pathologies post-mortem, including Lewy bodies, microinfarcts, and TDP-43 aggregates; some do not show a heavy A β or NFT burden^{11–13}. The acronym ADRD (AD and related dementia) conveniently describes the disease from which the majority of those with dementia will die. Cognition declines with age, and ADRD may represent an accelerated version of normal aging phenomena driven by idiosyncratic loss of neural reserve¹⁴. Extensive ongoing research aims to define lifestyle, clinical, and physiological factors that underlie the susceptibility or, conversely, the resilience to dementia during aging¹⁵. Recent genome-wide association study (GWAS) reports highlighted pathways, such as lipid metabolism and immune signaling in the liver, distinct from traditional AD-associated genes and pathology that are associated with resilience to clinical dementia^{16,17}.

In contrast to the difficulty of assessing pathological progression toward AD prior to diagnosis, there are documented risk factors for clinical AD, which are readily measurable. These risk factors include innate genetic traits, such as *APOE4* (apolipoprotein E $\epsilon 4$ genotype), unmodifiable risk factors, such as aging, and modifiable environmental or behavioral factors that can be quantified in a clinical setting (e.g., blood pressure). As detailed above, targeting a drug to an amyloid plaque has yet to produce a robust clinical cognitive benefit, whereas neutralizing a risk factor could provide a profound therapeutic impact on ADRD development and progression. This paradigm has been used successfully in cardiovascular disease (CVD) with low-density lipoprotein (LDL) lowering statins and anti-hypertensive medications reducing risk and improving disease-free survival.

The Lancet Commission report on risk factors for ADRD stated that reducing the dementia risk created from diseases such as type 2 diabetes (T2D) and obesity would have a significant impact on healthy aging with cognition intact⁹. In recent years, appreciation has grown for the role of other pathophysiological factors, such as insulin resistance, neuroinflammation, and dyslipidemia, leading to ADRD progression; thus, new drug strategies should consider these facets of the disease^{18–21}. Chronic metabolic diseases, including T2D and CVD, represent a growing health burden driven by increasing obesity. T2D is a significant risk factor for comorbidity with ADRD^{22,23}, with dementia risk paralleling the duration and severity of T2D²⁴. Specifically, insulin resistance, impaired glucose metabolism, mitochondrial dysfunction, inflammation, dyslipidemia, and impaired cholesterol mobilization may be common underlying pathogenic promoters of dementia in T2D and ADRD. T2D is a major risk factor for CVD and recent findings demonstrate that risk factors contributing to CVD, including high LDL-cholesterol and blood pressure, also increase risk of developing AD^{25,26}. Insulin resistance contributes to AD pathogenesis even in patients without overt diabetes²⁷. In addition, the major genetic risk factor for ADRD, *APOE4*, shows significant association with T2D in several studies and contributes to increased LDL cholesterol levels that drive CVD progression^{28,29}.

In this review article, we will demonstrate that boosting ATP binding cassette A1 (ABCA1) levels fulfills many of the objectives introduced above (Fig. 1). Evidence suggests that increased ABCA1 activity is beneficial for CVD, T2D, and ADRD. Moreover, several mechanisms link ABCA1 function to A β clearance and to mechanisms associated with heightened risk associated with *APOE4*. Therapeutic approaches to increasing levels of

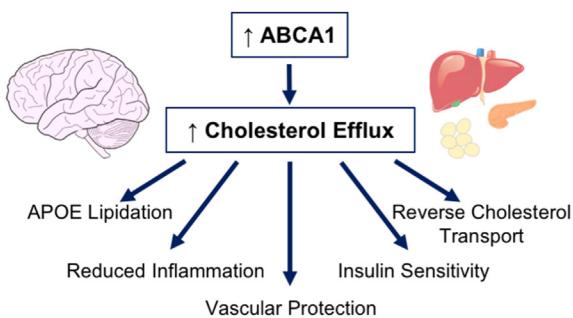


Figure 1 Proposed beneficial roles of ABCA1 in AD, ADRD, and comorbidities. ABCA1 mediates cellular cholesterol efflux, such that increased ABCA1 expression would be expected to produce several direct and indirect beneficial effects *via* an enhancement of efflux activity. These effects would provide therapeutic efficacy both in the brain and in peripheral tissues.

ABCA1 in the brain will be discussed along with results from studies in preclinical models of AD.

2. ADRD and risk factors

2.1. Late onset AD versus rare familial AD (FAD)

ADRD is a disease of aging: incidence increases nearly twenty-fold from ages 65 to 90, and roughly one in every three over the age of 90 suffer from dementia^{30,31}. Mild cognitive impairment (MCI) can be seen as a normal consequence of aging; however, not all MCI transitions to ADRD. Oxidative damage to DNA, lipids, and proteins accumulates with aging against a background of weakened repair and clearance mechanisms^{32,33}, leading to attenuation of essential cellular functions, particularly in metabolism and mitochondrial function³⁴. With the exception of FAD, caused by inherited mutations in amyloid precursor protein (*APP*) or presenilin (*PSEN*) 1 or 2 genes that account for $\leq 1\%$ of all cases, clinical diagnosis comes during the seventh decade of life or later³⁵.

Nevertheless, FAD transgenic (FAD-Tg) mice that overexpress these mutant forms of human *APP*, *PSEN1*, or *PSEN2* alone or in combination, remain dominant in AD drug discovery, because FAD-Tg mice develop amyloid neuropathology similar to that seen in AD patients^{36–44}. FAD-Tg mice are generally studied as young adults (at 3–12 months of age) and do not reproduce NFT pathology, nor do the FAD-Tg mice that also express mutations in the human gene responsible for tau protein expression (*e.g.*, 3xTg mice) faithfully model human AD^{45–50}. This inability to reproduce the complexity of human AD in mouse models has been discussed extensively in other recent reviews^{51,52}. The heavy focus on amyloid mutations in these models naturally biased AD drug development toward agents (*e.g.*, aducanumab and several others) that could reverse the development of amyloid pathology in these mice, which, as discussed above, have not shown beneficial clinical effects.

FAD-Tg models still play a key role in AD drug discovery because some can model aspects of AD beyond amyloid pathology, such as the altered metabolism and mitochondrial function that are central to late-onset AD. They can also replicate some of the effects of AD risk factors, such as sex and other genetic variations⁵². Meanwhile, additional models are being generated and

characterized using the vast amount of genomic and proteomic data that has rapidly become available over the past decade⁵³. The recent overall trend in ADRD research has been to emphasize factors that drive the early stages of the disease, even before $A\beta$ and NFT pathology appear. Better understanding of these factors, improved modeling of their pathophysiology in animal species, and development of therapeutic agents to target them may ultimately yield disease-modifying therapies for late-onset dementia, if appropriate clinical biomarkers can be found. In the following pages, we detail these key factors that promote ADRD onset and progression.

2.2. Genetic risk factors and *APOE*

Dozens of loci linked to AD development have been identified by GWAS^{16,54}. These rare, risk-driving polymorphisms include variants in microglial genes *TREM2* and *ABCA7*. *TREM2* (trigger receptor expressed on myeloid cells 2) protein mediates the microglial stress response and the R47H missense mutation significantly increases AD risk^{55,56}. *ABCA7* plays a role in cholesterol transport and microglial phagocytosis, and loss-of-function mutations at this locus also enhance AD risk^{57,58}. Both the understanding of the physiologic implications of these mutations and their occurrence are low⁴⁴; for example, the frequency of *TREM2**R47H is $<0.5\%$ in Caucasians and even lower in Chinese and African-American populations^{59–64}. The interaction of these rare genetic variants with other AD risk factors is poorly understood.

Conversely, the *APOE4* allele is much more common. The protein encoded by this gene, *APOE* (34 kDa, 299 amino acids), is required for the formation of lipoprotein particles in the brain⁶⁵. The critical function of transporting cholesterol and phospholipids throughout the central nervous system (CNS) is performed by these particles, which share similarities to high-density lipoprotein particles (HDL) in the periphery. Across human *APOE* isoforms, the only amino acids that differ are residues 112 and 158⁶⁵. The E2, E3 and E4 isoforms contain Cys/Cys, Cys/Arg, and Arg/Arg mutations of these residues, respectively. Despite these small differences, *APOE* genotype profoundly affects AD pathogenesis in a dose and allele-dependent manner⁶⁶. Although the frequency of *APOE4* allele is less than 14% in the global human population, the allele frequency in AD patients is 40%⁶⁷. Carriers of one *APOE4* allele have a $\sim 50\%$ chance of developing AD, whereas in homozygotes the risk is $>90\%$. Moreover, compared to non-carriers (mean age of onset = 84), *APOE4* heterozygotes and homozygotes develop AD roughly 8 and 16 years earlier, respectively⁶⁸.

APOE4 is a “loss-of-function” isoform: restoration of function to that of *APOE2* or *APOE3* would ameliorate AD pathology in *APOE4* carriers⁶⁸. This outcome holds true even if the alternative “gain of toxic function” hypothesis holds true. A proposed unique feature of the *APOE4* isoform is increased intrinsic disorder, termed the “molten globule” state^{69,70}. Most proteins contain intrinsically disordered regions, and these proteins are often stabilized by protein–protein interactions with scaffold proteins and chaperones. In the absence of stabilization, these proteins, including *APOE4*, are more susceptible to proteolytic degradation. Consequently, there is less *APOE4* than *APOE3* available for apolipoprotein formation; *APOE4*-containing lipoproteins are poorly lipidated and are less stable^{71–74}.

The structural and functional *APOE* isoform-specific differences contribute to profound pathologic effects of *APOE4*. Thus, therapeutic approaches that correct *APOE4*-mediated pathologic

mechanisms or render neutral the risk relative to APOE3 should be prioritized. This conclusion is amplified by a recent observation on one rare APOE variant with a significant impact on AD risk. As part of a study on an FAD population in Colombia, a woman was identified who developed MCI in her seventies, compared to a mean of 45 years old for her relatives; protection in this patient was derived from being homozygous for an ultra-rare *APOE*-Christchurch variant characterized by a single, R136S amino acid substitution⁷⁵. Reduced NFT pathology and neurodegeneration were observed, despite high A β levels characteristic of FAD being present⁷⁶. This case emphasizes the profound role of APOE in modulating neurodegeneration and progression to dementia in AD. Several studies have demonstrated an interplay of female sex with APOE4 in accentuating AD risk. In one meta-analysis, female *APOE3/E4* heterozygotes exhibited odds ratios ranging from 2 to 4, compared to the odds ratio for male *APOE3/E4* heterozygotes of <1.5⁶⁷. Subsequent studies have demonstrated significant, but more modest, effects of sex on *APOE4*-mediated AD risk^{77,78}.

2.3. Connectedness of APOE, T2D, CVD, and ADRD

Outside the CNS, two major chronic conditions—T2D and CVD—strongly drive risk of AD. T2D and CVD share close metabolic links, and their influence on AD is similarly driven by these metabolic factors. Epidemiological studies, systematic reviews, and meta-analyses have firmly established T2D as a risk factor for AD and related dementias, even after correction for underlying drivers such as obesity or physical inactivity^{24,79,80}. Changes to glucose homeostasis and insulin signaling significantly impact the brain. Excess insulin may compete with A β peptides for degradation by insulin-degrading enzyme⁸¹. The connection between insulin resistance and AD pathogenesis is further bolstered by shared perturbations in cellular metabolism, inflammation secondary to deposition of advanced glycation end-products, and direct vascular damage^{82–84}. The links between CVD pathology and AD risk are similarly multifaceted. Elevations in cholesterol and blood pressure promote atherosclerosis in cerebral vessels, resulting in stiff, narrow vasculature that reduces cerebral perfusion and precipitates A β and NFT pathology formation^{85,86}. This hypoperfusion can be exacerbated, chronically, by heart arrhythmias, or, acutely and severely, by myocardial infarctions. Sudden brain ischemia causes immediate neuronal loss while also enhancing ongoing AD pathological processes^{87,88}.

Of particular interest is that T2D²⁹, CVD⁸⁹, TBI⁹⁰, and even behavioral risk factors, such as smoking status⁹¹ and exercise⁹², drive AD risk in a synergistic fashion when combined with the *APOE4* allele. *APOE4* correlates with increased plasma LDL levels, which may partially explain its connection with T2D/CVD in AD risk^{93–95}. In some studies, relative risks increased from 1.5 to 2 for single risk factors up to 5–10 when *APOE4* is present. The magnitude of this synergism highlights the importance of understanding the molecular basis of *APOE4*-mediated deficits and of the interactions among *APOE4*, other risk factors, and dementia.

There are two major pathophysiologic commonalities that tie together the biological traits of *APOE4* and aging, comorbid conditions such as TBI, CVD, and T2D, and even lifestyle factors such as obesity and smoking: disrupted lipid homeostasis and chronically heightened inflammation. This conclusion is supported by GWAS evidence that has associated loci relating to cholesterol metabolism and immune function with AD and dementia^{17,96,97}.

Drug candidates that impact the intersection of these two pathological mediators would provide impactful, pleiotropic efficacy. This consideration has led us and others to suggest the ATP-binding cassette family member A1 (ABCA1) protein as a compelling therapeutic target for AD.

3. Roles of ABCA1 in health and disease

3.1. ABCA1 and its broad physiological roles

ABCA1 is expressed ubiquitously throughout the human body, with peripheral levels highest in liver hepatocytes⁹⁸. In the CNS, ABCA1 is found in neurons, astrocytes, and microglia⁹⁹. Human ABCA1, consisting of 2261 amino acids, is an integral membrane protein that utilizes ATP to transport cholesterol, phospholipids, and other lipid molecules to apolipoprotein carriers^{100–102}. In the plasma membrane and in intracellular organelles, including endosomes and lysosomes, ABCA1 associates with cholesterol-rich membrane domains¹⁰³, where it may serve to protect cells from excessive and potentially cytotoxic accumulation of free cholesterol. ABCA1 interacts with many of the protein components of HDL, namely APOA1, APOA2, APOA4, APOC1–3, and APOE¹⁰⁴, particularly when these apolipoproteins are minimally lipidated¹⁰⁵. ABCA1 is uniquely suited to add lipid to lipid-poor apolipoproteins, whereas other ABC family members (*e.g.*, ABCG1/G4) and cholesterol transporters (*e.g.*, SR-B1) interact with already-lipidated forms^{103,106}. In addition to this putative direct transfer function, ABCA1 has many indirect functions resulting from its influence on cellular cholesterol homeostasis. These effects, which are depicted in Fig. 1 and elaborated in greater detail in the following sections, help explain why ABCA1 represents such a promising target for therapeutics that might broadly attenuate pathophysiological processes shared between ADRD and its many underlying risk factors.

3.2. ABCA1 and CNS lipid transport

Cholesterol homeostasis is vital to CNS function. The brain contains 2% of the total mass of an adult human yet holds nearly 20% of the total cholesterol^{107,108}. Most brain cholesterol resides stably in specialized myelin membranes, but roughly 30% is found in cellular membranes of neurons and glial cells, where it actively moves or is metabolized within and between cells¹⁰⁸. Importantly, CNS and peripheral cholesterol pools are separated by the blood–brain barrier (BBB); thus, all CNS cholesterol is synthesized, transported, and recycled *in situ*. In adult brains, cholesterol synthesis and turnover occurs at a low, yet nonzero, rate¹⁰⁹. Although neurons and astrocytes both express cholesterol synthetic enzymes^{110,111}, neurons exhibit functional dependence on astrocytes for cholesterol delivery¹¹².

CNS cholesterol transport occurs *via* formation of APOE-containing lipoproteins (Fig. 2). Although APOE can be, and often is, synthesized by other cell types^{113,114}, astrocytes serve as the primary source of brain lipoproteins¹¹⁵. Newly-synthesized APOE receives cholesterol and phospholipids *via* ABCA1, then is secreted into brain parenchyma as discoidal lipoproteins. Cells with “excess” cholesterol complete additional lipid transfer to promote maturation of this lipoprotein particle, which can ultimately be internalized by cells “deficient” in cholesterol, a process mediated by proteins such as LDL receptor or LDL receptor-related protein 1 (LRP1)¹¹⁶.

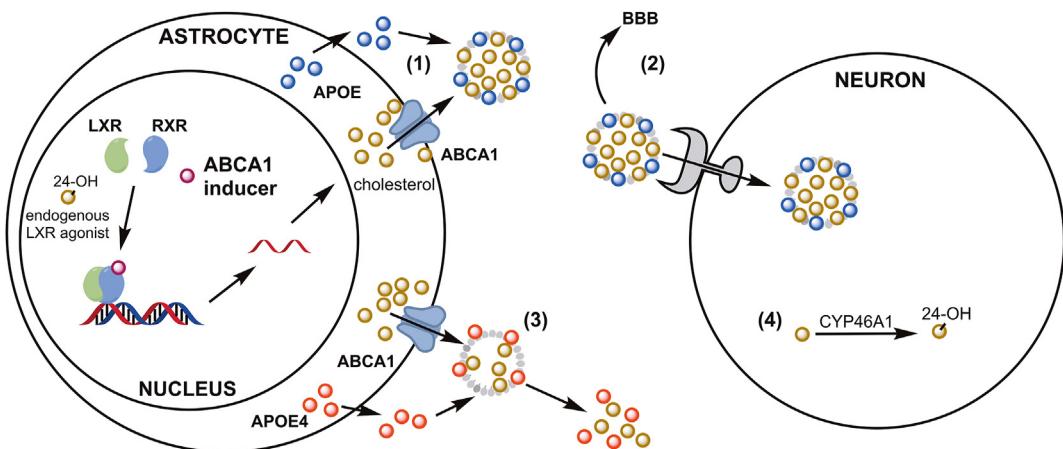


Figure 2 Brain cholesterol transport by ABCA1 and APOE. ABCA1 transports cholesterol out of cells to promote lipidation of secreted APOE to form lipoprotein particles (1), which are either internalized by cholesterol-deficient cells or transported across the BBB to maintain brain cholesterol homeostasis (2). Poorly lipidated APOE4 (compared to APOE3 or APOE2) is prone to degradation, disrupting this homeostasis and contributing to AD pathology (3). Internal CNS control of cholesterol homeostasis is regulated by neuronal expression of CYP46A1 enzyme, which converts excess cholesterol to 24-hydroxycholesterol (4). This form can cross the BBB (unlike cholesterol itself), and it acts as an endogenous agonist of LXR to promote expression of the cholesterol transport machinery. This endogenous control mechanism is disrupted in AD, predisposing brain cells to cholesterol overload. Small molecule ABCA1 inducers may elicit therapeutic effects against AD by boosting cholesterol transport, particularly *via* increased APOE lipidation in APOE4 carriers.

Neuronal cholesterol homeostasis is under tight control to allow adequate function and growth while preventing accumulation of cytotoxic free cholesterol. Internalization of lipoproteins *via* LRP1 is a critical source of cholesterol for neurite outgrowth, synaptogenesis, and remodeling¹¹⁷; but LRP1 also exerts negative feedback to limit intracellular cholesterol concentrations¹¹⁸. Lipoprotein receptors expressed at the BBB can promote cholesterol egress from the CNS¹¹⁹. A second efflux mechanism occurs *via* CYP46A1, an enzyme that converts cholesterol to 24-hydroxycholesterol (24HC), which, unlike cholesterol itself, is BBB-permeable¹²⁰. 24HC is also an endogenous agonist of the liver X receptor (LXR) that drives transcription of key genes such as ABCA1, ABCG1, and APOE (Fig. 2).

3.3. Restoration of brain cholesterol homeostasis by boosting ABCA1

CNS cholesterol homeostasis is a critical and tightly regulated process dependent on APOE and strongly influenced by APOE isoform. As stated above, APOE4 represents a loss-of-function allele relative to the common, risk neutral APOE3 variant. Human plasma and cerebrospinal fluid¹²¹, along with brain parenchyma of APOE targeted-replacement mice¹²², exhibit isoform-dependent concentrations of APOE (APOE2 > E3 > E4). A similar isoform dependence occurs for APOE-promoted cholesterol efflux from CNS cells¹²³. In human iPSC-derived CNS models, APOE4 broadly disrupts cholesterol metabolism¹²⁴. Together, these deficits associated with APOE4 lead to smaller lipoproteins that contain less cholesterol^{125,126}. In fact, APOE3-containing lipoproteins carry up to three times as much cholesterol per gram of protein as their APOE4-containing counterparts¹²⁷.

Reduced lipidation of APOE4 produces broad functional consequences. Lipidation of APOE alters protein morphology to expose residues used for receptor binding and prevents toxic aggregation of unlipidated APOE^{128,129}. Poorly lipidated APOE4 is

unstable and, hence, susceptible to proteolytic degradation leading to generation of neurotoxic fragments^{73,130}, and less efficient clearance of toxic A β species¹³¹. Overloading membrane cholesterol in neurons reproduces AD phenotypes, including A β overproduction and disrupted axonal transport¹³². In brain tissue from human AD patients, APOE4 is associated with heightened A β deposition, soluble oligomeric A β (oA β) levels, and amyloid plaque pathology^{133–136}, in addition to elevated tau pathology^{137,138}.

Based on the evidence elaborated above, a primary hypothesis for therapeutically boosting ABCA1 is relatively straightforward: *increasing cholesterol efflux to APOE, via induction of ABCA1, will restore lipidation of APOE4 and correct other AD-related phenotypes*. Genetic knockout of *Abca1* in mice dramatically reduces brain APOE lipidation and secretion and disturbs cholesterol homeostasis^{139–142}. Murine ABCA1 overexpression enhances lipidation and reduces aggregation of APOE^{143,144}. Treating mice with LXR agonist, elaborated in detail below, likewise raises APOE protein levels *via* ABCA1 action¹⁴⁵. Increased lipidated APOE, particularly improvement in APOE4 lipidation, plays a significant role in clearance and detoxification of A β species^{146–148}.

Moreover, ABCA1 induction may be beneficial for AD cholesterol homeostasis regardless of APOE4 status, as AD brain samples reveal plasma membrane cholesterol enrichment with disease progression¹⁴⁹. Endogenous control mechanisms that respond to excess cholesterol to promote ABCA1 expression are dysfunctional in AD patients: both circulating levels of 24HC and neuronal CYP46A1 expression are reduced^{150,151}. Consequently, cholesterol efflux capacity in AD patients is reduced by 30%, independent of APOE genotype¹⁵². Studies of genetic polymorphisms in ABCA1 have revealed increased or decreased risk of AD, possibly in a sex-dependent manner, associated with certain variants that alter cholesterol transport capacity^{153–155}. One specific loss-of-function mutation, *ABCA1*N1800H*, increased AD risk fourfold¹⁵⁶. Together, these data strongly support

the hypothesis that enhancement of ABCA1 expression and function could restore CNS cholesterol homeostasis and reverse AD phenotypes.

A new type of microglia, lipid droplet-accumulating microglia, resembling foamy macrophages in atherosclerotic lesions, has recently been shown to accumulate in the aging brain and to be associated with neurodegenerative disease^{157–159}. Intracellular lipid droplets, containing glycerolipids and cholesterol, are markers of inflammation. The compromised cholesterol trafficking of astrocytes underlies the detrimental effect of APOE4 on lipid metabolism and lipid trafficking between astrocytes and neurons¹²⁶. In astrocytes and neurons from *APOE3* and *APOE4* knock-in mice, APOE4-expressing astrocytes are also less able to metabolize fatty acids and both to transport and to internalize fatty acids from neurons, a process mediated by APOE-lipid particles (Fig. 3)¹⁶⁰. The APOE4-induced defects in lipid transport and metabolism in neurons and glial cells leads to accumulation of

lipid droplets, lipotoxicity, and decreased mitochondrial function; which can be reversed by ABCA1 activation. Similar observations on astrocyte-neuron dysfunction were made when neurons were subject to excitotoxicity induced by NMDA¹⁶¹.

3.4. ABCA1 and peripheral lipid transport

Although APOE and cholesterol cannot cross the blood–brain barrier, peripheral lipid transport plays an important role in AD pathogenesis. It has been proposed that the protective role of ABCA1 in AD may derive from enhancing plasma HDL, APOA1, and APOE, equally as from direct CNS actions^{162,163}. This importance of peripheral actions is often neglected when evaluating AD drug development strategies. Plasma lipoprotein metabolism is more varied than in the CNS, in which APOE dominates. Several lipoprotein particles contribute to vascular cholesterol deposition, inflammation, and atherogenesis to drive

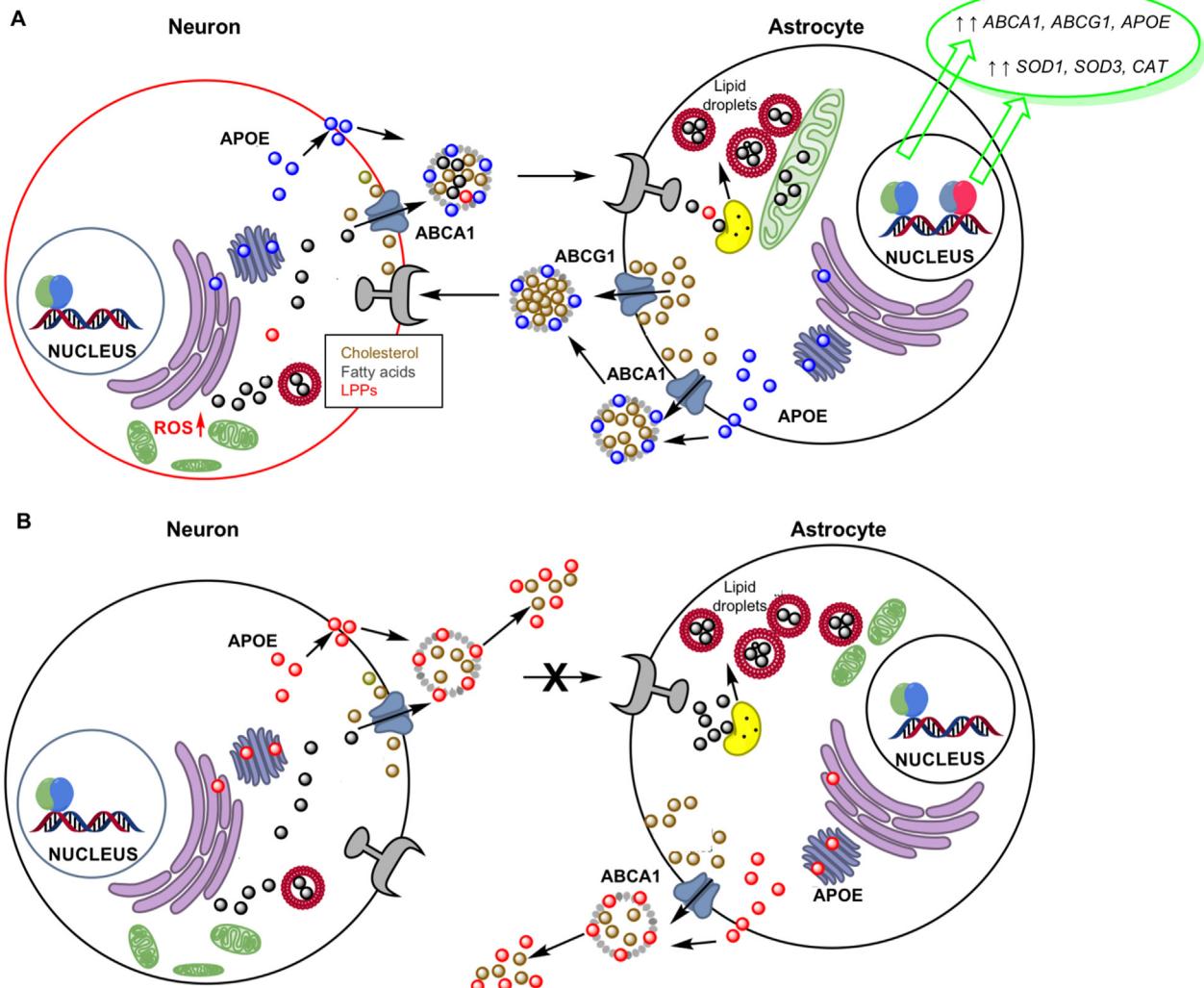


Figure 3 APOE, ABCA1, and inflammation. (A) Neuronal NMDA stimulation increased fatty acid and triglycerides (TGs) leading to decreased mitochondrial respiration, lipid peroxidation, and increased reactive oxygen species (ROS); in turn leading to lipotoxicity and neuronal death. Transport of fatty acids, TGs and lipid peroxidation products (LPPs) from neurons to astrocytes by lipidated APOE rescued neurons by lysosomal catabolism of fatty acids, storage in lipid droplets, and use for mitochondrial oxidative phosphorylation; which was accompanied by transcriptional upregulation of LXR and NRF2 target genes. (B) APOE4 neurons showed 36% lower APOE, reduced neurite branching, elevated fatty acids and TGs, and decreased mitochondrial function and glucose metabolism. APOE4 astrocytes were less efficient at transporting lipids and fatty acids from neurons and at fatty acid catabolism and energy conversion, containing fragmented mitochondria and elevated TGs.

atherosclerosis^{164–166}. Conversely, HDL particles are anti-atherogenic. HDL facilitates removal of cholesterol from vascular walls and peripheral tissues *via* reverse cholesterol transport (RCT), thereby preventing formation of cytotoxic oxidized lipid species and reducing inflammation and atherogenic lesion formation¹⁶⁷. ABCA1 contributes to formation of particles termed pre-βHDL^{101,106,168}, and ABCA1/ABCG1 promote formation of mature HDL particles¹⁶⁹. Reduced plasma cholesterol efflux capacity, which is directly tied to ABCA1 and ABCG1 expression, synergizes with other components of metabolic syndrome to promote atherosclerosis¹⁷⁰. Pathological changes that occur during atherosclerosis, such as oxidation of LDL, down-regulate ABCA1 expression^{171,172}. Tangier disease, characterized by *ABCA1* loss-of-function mutations, leads to premature atherosclerosis¹⁷³, and *ABCA1* variants that increase AD risk also have been associated with T2D and CVD risk^{174–176}. Increased peripheral atheroprotection *via* ABCA1 induction would promote cerebral vascular health, preserving BBB integrity and function^{177,178}, and, ultimately, protect against AD.

3.5. *ABCA1* and insulin resistance

Insulin resistance plays a key role in the brain during AD pathogenesis. AD brains exhibit altered insulin-related gene expression and diminished phosphorylation of AKT and GSK3 β ¹⁷⁹, even in patients not diagnosed with T2D¹⁸⁰. Altered glucose homeostasis (*i.e.*, cerebral hypometabolism) in neurons predates cognitive decline in AD patients⁸. Synaptic plasticity relies on insulin signaling^{181,182}, and insulin protects neurons from oA β -induced toxicity¹⁸³. Several large, long-term cohort studies demonstrated an association of use of metformin, an insulin sensitizing drug, with a significantly reduced risk of developing MCI or dementia in patients with diabetes^{184–186}. Two small, short-term pilot studies with metformin in non-diabetic patients with MCI or early AD showed improvements in cognitive performance^{187,188}, but long-term data are lacking. A larger Phase 2/3 trial is currently enrolling patients with MCI to study the effect of metformin on progression to AD (NCT04098666). Similarly, intranasal insulin improved cognition in pilot studies in early-stage AD patients¹⁸⁹. However, Phase 3 clinical trials with anti-diabetes agents rosiglitazone and pioglitazone demonstrated no efficacy in AD patients¹⁹⁰, although this may be associated with insufficient bioavailability¹⁹¹. Thus, the description of AD as “type 3 diabetes” is an oversimplification¹⁹²; however, therapeutic strategies that improve insulin sensitivity hold promise in AD. Boosting ABCA1 expression represents one such strategy. Tangier disease causes disrupted insulin homeostasis¹⁹³, and *ABCA1* deletion in pancreatic β -cells and insulin target tissues reduces insulin release and sensitivity, respectively^{194–197}. Patients with pre-diabetes or T2D exhibit reduced adipose and liver ABCA1 expression and diminished cholesterol efflux capacity^{198,199}. These studies support pharmacological enhancement of ABCA1 as a therapeutic strategy to correct deficits in cholesterol transport and insulin resistance.

3.6. Inflammation: Role of ABCA1 and implications for ADRD

An increasing body of evidence suggests that a sustained, inappropriate inflammatory response is a driving mechanism behind AD pathology that underlies connections between peripheral risk factors and AD^{27,200–204}. The neural reserve or cognitive resilience in individuals that develop A β pathology without cognitive

decline may be associated with resilience to neuroinflammation^{205,206}. Inflammation in the CNS and periphery is strongly associated with AD. A meta-analysis combining forty individual studies revealed higher plasma levels of cytokines (TNF α , IL1 β , IL6, IL12, IL18, and TGF β) in AD patients *versus* healthy controls²⁰⁷. These cytokines may cross the BBB, inducing neuroinflammatory responses²⁰⁸, or damage the BBB itself²⁰⁹, further enhancing immune cell infiltration and reducing glucose transport into the brain^{210,211}. Microglia and astrocytes are the major mediators of immune response in the CNS. Microglial phagocytosis of toxic A β species is hypothesized to be beneficial during early AD pathogenesis²¹². However, as disease progresses, microglial phagocytosis may be overwhelmed, without diminishing cytokine production^{213,214}, resulting in more immune cells being recruited to sites of inflammation, where they produce additional cytokines²⁰⁰. Proinflammatory cytokines increase brain insulin resistance²¹⁵, damage synapses²¹⁶, and induce neuronal death²¹⁷. Neuroinflammation, particularly in response to A β pathology, is exacerbated in the presence of APOE4^{218–222}.

Murine genetic deletion of brain *Abca1* enhances neuroinflammation and astrogliosis²²³. In humans with *ABCA1* mutations, plasma levels and immune cell expression of cytokines are elevated compared to healthy controls²²⁴. This pro-inflammatory profile associated with diminished ABCA1 expression stems from excess free membrane cholesterol, which promotes mobilization of inflammatory mediators, such as toll-like receptors, to lipid rafts^{225–227}. Independent of cholesterol mobilization, interaction of ABCA1 with APOA1 activates JAK2/STAT3 to suppress proinflammatory cytokine production²²⁸. Thus, pharmacologic enhancement of ABCA1 expression may attenuate proinflammatory states associated with AD pathogenesis.

4. Pharmacological approaches to boosting ABCA1 for ADRD therapy

4.1. Overview

The broad therapeutic efficacy expected from pharmacological enhancement of ABCA1 expression and function has led to numerous therapeutic strategies; however, no candidate has been successfully translated to clinical use. A brief overview will be presented, with a more detailed analysis of LXR agonists.

4.2. Apolipoprotein peptide mimetics

HDL peptide mimetics were developed that enhanced HDL levels and prevented atherogenic lesion formation^{229,230}. It was later determined that these peptides promoted ABCA1-mediated cholesterol efflux²³¹. The many apolipoprotein mimetics²³², can be grouped into two classes: APOA1 and APOE mimetics²³³. The initial model for APOA1 mimetics was a peptide named 18A (containing 18 amino-acids)²³⁴ that forms an amphipathic helix mimicking the structure of APOA1. Modifications of this peptide led to compounds with atheroprotective properties in mice^{235–237}. In AD models, D-4F enhanced APOE lipidation by ABCA1 and was anti-inflammatory and pro-cognitive^{238–240}. APOE-mimetic peptides include: COG1410, consisting of APOE residues 138–149²⁴¹; COG112, consisting of APOE residues 133–149²⁴²; Ac-hE-18A-NH₂, comprised of 18A linked to APOE residues 141–150²⁴³; and CS-2563, consisting of the modified C-terminal APOE domain (aa238–266)^{244,245}. Only CS-2563 directly

stimulates ABCA1-mediated cholesterol efflux. Despite anti-inflammatory and neuroprotective effects in models of neurodegeneration, these mimetics share poor CNS bioavailability. A smaller peptide of only five amino acids, termed CN-105, demonstrated improved brain bioavailability in humans and was reported to reduce A β pathology and cognitive deficits in APOE4-expressing FAD mice^{246,247}. This peptide is in Phase 2A clinical trials for intracerebral hemorrhage (NCT03168581) and post-operative cognitive decline (NCT03802396).

4.3. Small molecule approaches to ABCA1 induction

Humans express 48 unique nuclear hormone receptors (NHRs) that share a common ancestral gene and, therefore, possess common structural motifs that include an N-terminal transcriptional transactivation domain, a conserved DNA-binding domain, and a C-terminal ligand-binding domain^{248,249}. Some of these receptors are well-characterized and have been exploited clinically (*e.g.*, estrogen receptor α ; ER α), while a handful still possess the designation of “orphan receptor” because an endogenous ligand has yet to be identified²⁵⁰. ABCA1 expression is regulated primarily by LXR, retinoid X receptors (RXR), and peroxisome-proliferator activated receptors (PPAR). These represent the most well-studied therapeutic targets for ABCA1 induction by small molecules. Additional, non-NHR approaches are briefly summarized below:

- (1) cAMP analogs, PKA activators, phosphodiesterase inhibitors, and adenosine A_{2A} receptor agonists are all designed to enhance the cAMP/PKA pathway, to increase ABCA1 expression and cholesterol efflux for anti-atherogenic and anti-inflammatory effects^{251,252}.
- (2) Anti-hypertensive agents and targets have also been widely explored in AD; mechanisms include ABCA1-mediated cholesterol mobilization. Angiotensin II promotes intracellular cholesterol accumulation by reducing *ABCA1* transcription via NHR downregulation, promoting foam cell formation and hampering glucose-stimulated insulin secretion from pancreatic β cells^{253,254}, indicating beneficial roles for angiotensin-converting enzyme inhibitors and angiotensin-receptor blockers. Calcium channel blockers are also used clinically for hypertension and CVD: two have been shown to increase ABCA1 expression: nifedipine, which activated PPAR γ via an ERK1/2-dependent mechanism at a clinically relevant concentration²⁵⁵, and verapamil, which stimulated *ABCA1* promoter activation independent from LXR, albeit at supratherapeutic concentrations of 10–30 μ mol/L²⁵⁶.
- (3) AMP-activated protein kinase (AMPK) is a major metabolic regulator²⁵⁷, which provides antioxidant functions, plays a role in CVD, and is an indirect target of T2D drug metformin²⁵⁸. Two studies showed that AMPK agonists increased *Abca1* and/or *Abcg1* mRNA and cholesterol efflux to APOA1, although they disagreed on whether this effect was LXR-dependent or -independent^{259,260}.
- (4) Glucagon-like peptide-1 (GLP1) is a short peptide hormone classically associated with simulating insulin release and attenuating glucagon release to lower plasma glucose²⁶¹. GLP1 receptor agonists and inhibitors of the GLP1-degrading enzyme are used clinically in T2D. GLP1 is neuroprotective and GLP1 therapeutics were shown to upregulate cholesterol transporters, enhance cholesterol

efflux, and reduced proinflammatory cytokine release in cell models²⁶², although the mechanism is not fully defined^{263–265}. Liraglutide, a GLP1 analog, is currently in a Phase 2 trial of patients with mild AD²⁶⁶.

- (5) The clinical use of the vitamin niacin (nicotinic acid) in hyperlipidemia and hypertriglyceridemia has been decreasing over the years: niacin increases HDL and reduces levels of LDL and VLDL²⁶⁷. Niacin influences a vast number of biological mechanisms, one of which is activation of the G-protein coupled receptor GPR109A²⁶⁸. Niacin increases ABCA1 expression *via* multiple pathways^{269–271}.
- (6) CYP46A1 catalyzes the conversion of cholesterol to 24HC, which permits BBB efflux and activates LXR endogenously²⁷². Increasing CYP46A1 activity to promote ABCA1 activity and restore CNS cholesterol homeostasis has been proposed in AD²⁷³. The HIV drug efavirenz induces *CYP46A1* at a dose below that used in HIV patients and is in clinical trial for AD (NCT03706885). CYP46A1 expression is brain-specific, thereby minimizing peripheral side effects; however, direct activators of CYP46A1 may interact with other CYPs because of structural similarity^{274,275}. Efavirenz analogs and CYP46A1 activators are in early development²⁷⁶.
- (7) Histone deacetylase inhibitors (HDACi) have been studied extensively in preclinical and early clinical trials in AD. HDACs are epigenetic erasers modulating histone-mediated chromatin control and transcriptional activation. HDACs have many non-histone protein substrates, which have often been found to mediate observed activity. Pan-HDACi trichostatin A upregulates ABCA1 and ABCG1 expression and stimulates cellular cholesterol efflux *via* induction of PPAR γ ^{277–279}. Similarly, Class I HDACi were shown to promote astrocytic APOE secretion and upregulate ABCA1 expression²⁸⁰.

4.4. Nuclear hormone receptor signaling: RXR

RXRs function as heterodimeric binding partners not only with LXRs, but also with all other class II nuclear hormone receptors (NR1 subfamily), which include PPAR, retinoic acid receptors (RAR), constitutive androstane receptors, pregnane X receptor, farnesoid X receptor (FXR), vitamin D receptor, and thyroid hormone receptors²⁸¹. Most of these heterodimers function as permissive pairs, meaning that ligand activation of either RXR or its binding partner elicits similar effects²⁸². Profiling of binding sites across the genome illustrated two key phenomena associated with this function: first, that most sites of LXR–DNA binding are shared with RXR but only a fraction of RXR binding sites are shared with LXR; and second, that these whole-genome binding profiles are quite different across cell types²⁸³. RXR agonists have been shown to increase ABCA1 expression^{284,285}, but they also elicit lipogenic side effects. The prototypical RXR agonist bexarotene demonstrated this combination, with induction of ABCA1/ABCG1 in certain tissues, but not others, that was accompanied by increased hepatic lipogenesis^{286–288}. Additionally, a landmark study demonstrated enhanced cholesterol transport, A β clearance, and cognition in FAD mice²⁸⁹, but follow-up studies were unable to fully replicate these results^{290–294}. In humans, bexarotene had no efficacy in AD clinical trials and increased TGs^{295,296}. Recent reports described novel RXR agonists that boost ABCA1 expression and improve pathology in FAD

mice, without TG-related liver effects^{297,298}. Based on the many heterodimer interactions of RXR, biased agonism to induce ABCA1 in certain cells and tissues while avoiding hepatic lipogenesis appears feasible, possibly by selectively activating RXR–FXR or RXR–RAR heterodimers in preference to RXR–LXR α ^{299–301}.

4.5. Nuclear hormone receptor signaling: PPAR

PPARs function via heterodimer formation with RXR and are activated endogenously by oxidized fatty acids. The three PPAR isoforms perform overlapping yet distinct functions compared with each other and with LXR isoforms. PPAR α is most prominent in fatty acid metabolism, PPAR γ in glucose metabolism and anti-inflammation, and the less well-studied PPAR β/δ in fatty acid metabolism and anti-inflammation³⁰². All three isoforms have been shown to modulate ABCA1 expression levels^{303,304}, although this effect may require LXR α . PPAR γ /RXR dimers have been proposed to control LXR α transcription by direct promoter binding²⁸⁴. Various PPAR agonists have been used clinically in T2D and CVD. Gemfibrozil and other PPAR α -selective agonists increase ABCA1 activity, improve HDL and TG levels in pre-clinical and clinical studies, and demonstrate efficacy in mouse AD models^{305–307}. Rosiglitazone and pioglitazone, used clinically in T2D, failed to show efficacy in AD clinical trials¹⁹⁰. Recently-developed PPAR γ agonists continue to show positive effects on ABCA1 expression^{308,309}, and a PPAR β/δ agonist that increases ABCA1 has also been described³¹⁰. Various PPAR ligands have been described that interact with other NHRs^{311,312}. Furthermore, selective PPAR modulators (SPPARMs) have been explored^{313,314}.

4.6. Nuclear hormone receptor signaling: LXR

LXR is the primary NHR target for pharmacologic induction of ABCA1 expression. Humans express two isoforms: LXR α that is highly expressed in liver, small intestine, and adipose, and LXR β that demonstrates ubiquitous expression, including brain tissue^{106,315–317}. Endogenous oxysterols, e.g., 24HC, activate LXR, which acts via LXR response elements consisting of two direct repeats of a consensus sequence (*i.e.*, ATTGCA) occurring in the promoter regions of dozens of genes. LXR–DNA binding results in transactivation or transrepression of various target genes related to cholesterol transport (*e.g.*, ABCA1) and synthesis, glucose metabolism, and inflammatory signaling^{318,319}. A final set of LXR target genes consists of the machinery that controls TG synthesis, both via direct transcriptional activation and through upregulation of sterol-response element binding protein 1c (SREBP1c)³²⁰. The earliest synthetic LXR agonist, T0901317 (T0), elicited potent responses in all of these transcriptional functions, demonstrating phenotypic improvements in mouse models, while also provoking TG overproduction and steatohepatitis^{321–327}.

Treatment of *Lxra*^{−/−} and *Lxrb*^{−/−} mice with T0 demonstrated that hypertriglyceridemia was dependent on LXR α ³²⁸; thus, development of LXR β -selective agonists was prioritized. The first such “selective” agonist was GW3965; however, this compound ultimately was not phenotypically selective as it increased TGs in mouse models^{329,330}. Groups from Wyeth^{331,332}, Merck³³³, Tokyo New Drug Research Laboratories^{334–336}, Vitae^{337,338}, and Bristol–Myers Squibb^{339–341} developed compounds highly selective for LXR β in receptor binding assays. BMS-852927 was originally described as an

LXR β -selective partial agonist; and indeed, several LXR ligands show partial agonist activity at LXR α ^{339–342}.

The results of development and characterization of LXR ligands in preclinical AD animal model studies are provided in Table 1. To summarize, early agonists T0 and GW3965 have been studied in multiple FAD models at doses ranging from 2.5 to 50 mg/kg/day and for treatment durations ranging from 6 days to 24 weeks, analyzed via a host of behavioral, immunohistochemical, and biochemical techniques. Despite markedly varied treatment paradigms, these two compounds consistently increased ABCA1 and APOE expression, reduced A β and inflammatory marker levels, and improved cognitive performance. Inclusion of ABCA1 KO mice in some studies revealed that many of the observed therapeutic effects were dependent on ABCA1 expression. Newer, LXR β -selective ligands have primarily been tested in mouse models of atherosclerosis, but those evaluated for preclinical AD efficacy have demonstrated promising CNS pharmacokinetic–pharmacodynamic profiles and similar effects on AD-related pathology.

Two LXR β agonists, BMS-852927 and LXR-623, entered human clinical trials, with both compounds raising ABCA1 and ABCG1 expression levels^{342,343}; however, CNS adverse events were observed with LXR-623; and peripheral side effects, including neutropenia and increased TG and LDL levels, were observed with BMS-852927. The findings with BMS-852927 are consistent with the differences between rodent and human lipid physiology that will need to be addressed in future LXR-based drug development efforts. Specifically, rodents lack the plasma cholesterol ester transfer protein (CETP) that humans express, and LXR produces a distinct response on inducible degrader of LDL (IDOL) protein in rodents *versus* humans^{342,344,345}.

4.7. LXR-based drug discovery strategies for boosting ABCA1

Approaches to modulate LXR should be informed by the clinically successful modulation of other NHRs, notably ER. Selective estrogen receptor modulators (SERMs) are clinically important ER α ligands that deliver diverse pharmacology that is tissue-selective^{360–362}. Selective androgen receptor modulators have not reached the clinic, but are drugs of abuse in sports because of muscle and bone building effects, purportedly without side effects associated with steroids³⁶³. SPPARMs have been introduced above. A similar concept has also been applied to label some LXR ligands as SLIMs (selective liver x receptor modulators)^{364,365}. For example, SR9238, described as a liver-selective LXR agonist, could be classed as a SLIM^{366,367}. The clinical relevance of NHR selective modulators rests on: a) enhancement of beneficial transcriptional events; without b) induction of transcriptional events associated with adverse effects. In this transcriptional context, the terms agonist and antagonist have little value. The transcriptional output of the NHR transcriptional complex depends on the cellular context (availability and binding of coregulators) and the ligand (differential stabilization of complexes)³⁶⁸. For example, IMB-808 binds both LXR isoforms, but, in contrast to T0, cholesterol efflux genes are selectively induced over lipogenic genes because IMB-808 and T0 recruit different coregulators³⁶⁹.

LXRs bind to LXR response elements that occur in the promoter regions of dozens of genes leading to transactivation or transrepression of genes related to (A) cholesterol transport (*e.g.*, ABCA1, APOE) and glucose metabolism; and (B) the cellular lipogenic machinery that controls triglyceride synthesis, both via direct transcriptional activation and through upregulation of SREBP1c^{318,319}. Biochemical measurement of ligand binding to

Table 1 *In vivo* studies of LXR agonists in preclinical AD models.

Compd.	Animal system	Key finding	Ref.
Merck	Wistar Han Rats s.c. 4 days. Pharmacokinetics (PK) and peripheral lipids.	<u>Rats:</u> Plasma and liver TG not significantly increased by compound or GW3965. $CL = 87 \text{ mL/min/kg}$; $t_{1/2} = 2.9 \text{ h}$; $F (\%) = 71\%$; PPB = 98.2%	Stachet et al., 2016 ³³³
	Tg2576 FAD-Tg mice s.c. 3 weeks. PK, open field test (OFT), brain ABCA1, apoE, and A β .	<u>Mice:</u> PK comparable to rat. Increased ABCA1 and apoE. Decreased soluble A β . Reduced locomotion back to WT control.	
	Rhesus monkey <i>p.o.</i> 2-weeks. PK, CSF apoE and A β , peripheral lipids.	<u>Rhesus monkey:</u> ($CL = 18 \text{ mL/min/kg}$; $t_{1/2} = 2.0 \text{ h}$; $F (\%) = 77\%$; PPB = 99.3%). 3-fold increased apoE. CSF A β levels increased. No change in liver fat content.	
Vitae	C57BL/6 mice 3 mg/kg <i>p.o.</i> 4 h. PK and brain ABCA1.	LXR β EC ₅₀ = 38 nmol/L; 77% E _{max} ; LXRA EC ₅₀ = 166 nmol/L; 83% E _{max}	Tice et al., 2016 ³³⁸
	Sprague-Dawley rats <i>p.o.</i> 4 h (5 mg/kg) or 5 days (1, 3, or 10 mg/kg qd). Brain ABCA1, CSF and cerebral A β_{40} /A β_{42} .	<u>Mouse 4 h:</u> Plasma 1075 nmol/L, brain = 1018 nmol/L; ABCA1 induction = 3.1 \times <u>Rat 4 h:</u> Plasma = 1215 nmol/L, brain = 2282 nmol/L, ABCA1 induction = 2.8 \times <u>Rat 5 day:</u> Plasma = 187–2800 nmol/L, Brain = 641–5360 nmol/L, ABCA1 induction = 5–9 \times ; no significant changes in A β .	
	APP23 FAD-Tg mice <i>p.o.</i> 6 days. Measured A β . APP23 mice <i>p.o.</i> 20–25 days. Cortical and hippocampal A β , ABCA1 and apoE, and inflammatory markers (mRNA).	Increased ABCA1; A β_{40} and A β_{42} significantly decreased. Increased ABCA1 and apoE; significant reduction in insoluble A β with no effect on soluble A β . Inflammatory gene expression significantly decreased.	Koldamova et al., 2005 ³²⁴
T0901317	Tg2576 mice <i>p.o.</i> 7 days. Contextual fear conditioning and contextual memory tasks (CFT). Hippocampal and cortical apoE and ABCA1 (mRNA), A β , and APP; plasma A β .	Complete reversal of cognitive deficits in CFT. Increased hippocampal ABCA1 and apoE. Significant A β_{42} reduction. No significant effects on full-length APP or processed APP. No significant effect on plasma A β .	Riddell et al., 2007 ³⁴⁷
	APP23 mice <i>p.o.</i> 4 months with high-fat diet (HFD). Morris water maze (MWM) memory task. Cortical and hippocampal A β , apoE, ABCA1.	Reversal of MWM deficits caused by HFD. Reversal of increased insoluble A β due to HFD. Reduction of soluble A β beyond control diet levels. Increased ABCA1 and apoE.	Fitz et al., 2010 ³⁴⁸
	APP23 mice <i>p.o.</i> 7 weeks. MWM. Drug levels, forebrain A β , ABCA1, and apoE.	No significant change in MWM performance. Brain drug level 5 nmol/g vs. blood 2 nmol/mL. Soluble and insoluble A β reduced;	Terwel et al., 2011 ³⁴⁹

Table 1 (continued)

Compd.	Animal system	Key finding	Ref.
GW3965	APPswe/PS1 Δe9 (APP/PS1) mice <i>p.o.</i> 2 months. NOR and object location task. Brain and serum cholesterol profiles, hippocampal and cortical A β , ABCA1, and apoE. APP/PS1 mice <i>p.o.</i> 30 days. MWM. Hippocampal and cortical A β , GFAP, CD11b, ABCG1, apoJ, and inflammatory markers. Nucleus basalis ChAT.	ABCA1 and apoE increased. Improved cognitive performance. Increased cholesterol precursor levels. Increased ABCA1 and apoE. No change in A β plaque burden Improved MWM performance. Increased ABCG1 and apoJ, increased cholinergic neurons. Reduced astrocytosis and microgliosis, reduced COX2 and iNOS, reduced total A β .	Vannierlo et al., 2011 ³⁵⁰ Cui et al., 2012 ³⁵¹
	APP23 mice <i>p.o.</i> 50 days. Radial arm water maze (RWM) and CFT. Hippocampal and cortical A β , ABCA1, apoE; interstitial fluid A β and apoE. APP/PS1ΔE9/ABCA1 $^{+/+}$ /APOE-TR mice <i>p.o.</i> 28 days. Novel object recognition (NOR) and CFT. Cortical A β , ABCA1 and apoE; apoE lipidation (native PAGE).	Cognitive performance restored. No change in soluble or insoluble A β , but reduced A β in ISF. Increased ABCA1 and apoE, increased lipidation of ISF apoE. Increased ABCA1; increased apoE lipidation without change in total apoE. Significant reduction of soluble oA β in APOE4 but not APOE3 mice, no change in A β plaques. CFT improvement in APOE4 but not APOE3 mice; no change in NOR.	Fitz et al., 2014 ³⁵² Carter et al., 2017 ³⁵³
	Tg2576 mice <i>p.o.</i> 4 months (A β) or 6 days (CFT). APP/PS1 mice <i>p.o.</i> 8 or 24 weeks. NOR and Morris water maze (MWM). Cortical and hippocampal A β , ABCA1 and apoE.	Improved contextual memory, reduced A β plaque and peptide. Increased ABCA1 and apoE; increased CSF apoE lipidation. Reduced amyloid plaques and shifted A β from insoluble to soluble pool. Improved NOR and MWM performance.	Jiang et al., 2008 ¹⁴⁸ Donkin et al., 2010 ¹⁴⁵
	Tg2576 mice <i>p.o.</i> 2 weeks. Odor habituation task, electrophysiology, whole-brain A β . APP/PS1 (\pm ABCA1 KO) <i>p.o.</i> 8 weeks. Cortical, hippocampal, and CSF apoE and apoA1. 3xTg FAD mice <i>p.o.</i> 12 weeks. MWM. Hippocampal and cortical A β , NFT, ABCA1, apoE; dentate gyrus nestin and pH3.	Enhanced odor habituation. Restored odor-evoked neural activity circuits. Reduced soluble and insoluble A β . Cortical apoE and apoA1, hippocampal apoA1, and CSF apoA1 increased. Hippocampal and CSF apoE unchanged. Improved MWM performance. Soluble/insoluble A β and p-tau unchanged. Increased ABCA1 and apoE. Astro- and microgliosis reduced to WT baseline. Increased neurogenesis.	Wesson et al., 2011 ³⁵⁴ Stukas et al., 2012 ³⁵⁵ Sandoval-Hernandez et al., 2015 ³⁵⁶
	APP/PS1 mice <i>p.o.</i> 9 days. CFT. Hippocampal and cortical ABCA1, ABCG1, apoE, inflammatory markers, and A β .	CFT performance restored to level of WT control. ABCA1/G1 and apoE increased. Non-significant reductions in A β . Iba1 significantly reduced; TNF α and others non-significant.	Skerrett et al., 2015 ³⁵⁷

(continued on next page)

Table 1 (continued)

Compd.	Animal system	Key finding	Ref.
	3xTg mice <i>p.o.</i> 6 days. MWM, hippocampal A β , gene methylation, and synaptic proteins (JMN). Hippocampal GFAP/Iba1, LRP1, and lectin staining (<i>Neuro Lett</i>).	MWM retention restored to WT baseline; learning unaffected. No change in A β ; PSD95 and synapsin-1 increased; and DNA methylation of synaptic genes decreased. Reduced GFAP and altered morphology, no change in microglia; increased LRP1; decreased vascular tortuosity with reduced perivascular A β .	Sandoval-Hernandez et al., 2016 (split across two articles) ^{358,359}

truncated ligand-binding domains (LBD) of LXR does not reflect the influence of a ligand on transcriptional output, which includes expression of *ABCA1* and hundreds of other genes^{327,370–373}. Specifically, *ABCA1* and SREBP1c expression require distinct combinations of nuclear coregulator displacement/recruitment. LXR target genes are not controlled identically *via* the stabilization/derepression mechanism. *ABCA1* is controlled *via* derepression, in which LXR^{-/-} mice exhibit higher gene expression than LXR^{+/+} mice at baseline, whereas *SREBF1* (gene encoding SREBP1) is controlled by the classical nuclear receptor model of receptor recruitment to the DNA promoter upon ligand binding, with basal expression in LXR^{+/+} \geq LXR^{-/-}³⁷². Thus, unique ligands that are equipotent for LXR α and LXR β LBD-binding *in vitro* can elicit unique transcriptional and phenotypic responses in complex biological systems.

A recent seminal paper describes the challenge for LXR ligand design: specifically, this work was focused on nonlipogenic ABCA1 inducers using *in vivo* phenotypic outputs of intestinal ABCA1 *versus* plasma triglycerides as binary ligand descriptors for multivariate statistical correlation with: i) H/D-exchange mass spectrometry; surface plasmon resonance binding to coregulators; LXR-LBD affinity; LXR transactivation; and ii) computational modeling³⁷⁴. One clear observation from hydrogen–deuterium exchange and surface plasmon resonance data is that the almost identical ligand binding pockets of LXR α and LXR β are not an insurmountable barrier to design of LXR ligands with selective pharmacology: different chemical structures stabilized overlapping but nonidentical regions of LXR. More lipogenic ligands stabilized helix-12 (H12) and coactivator peptide binding (Fig. 4); whereas stabilization of the H3/H5 interface and corepressor peptide binding may bias towards ABCA1 inducers. As a corollary to this work, simply optimizing ligand affinity for LXR β -LBD *versus* LXR α -LBD will result in LXR β selectivity, but not necessarily nonlipogenic ABCA1 inducers. Structures for a variety of LXR complexes are shown (including one in a heterodimeric complex with RXR bound to DNA) and compared with ER complexes showing similarity between NHR architecture, ligand binding, and coregulator recruitment.

A final complexity in designing LXR ligands is the extensive cross-talk that occurs among NHRs, such that activation of one may amplify or depress the expression and/or functional output of another^{283,378–381}. In addition to cross-talk, cross-reactivity between LXR and other NHRs is not uncommon. To is used as a benchmark LXR agonist; however, it has off-target activity at FXR³⁸². The LXR agonist GSK2033 binds to PPARs³⁶⁶. Fibrates, used successfully to

treat hypertriglyceridemia, bind both PPAR α and LXR β , with inhibition of lipogenesis and SREBP1c expression attributed to “antagonist” action at LXR³⁸³. GSK2033, described as the first potent LXR antagonist (IC₅₀ = 31.8 nmol/L for LXR β)⁷⁶, also engages glucocorticoid receptor, pregnane X receptor, and FXR¹⁰⁹.

4.8. Phenotypic drug discovery strategies

Phenotypic drug discovery for nonlipogenic ABCA1 inducers is likely to identify some LXR ligands that act as SLIMs and others that regulate NHRs, either by direct binding or by feedback modulation. Given the poor correlation of phenotype with binding affinity (for LXR α *versus* LXR β) and the complexity of NHR feedback, phenotypic screening is the logical approach to discover nonlipogenic ABCA1 inducers. A target-agnostic approach that prioritizes phenotype allows for identification of compounds that engage novel targets or, potentially, multiple targets to produce the desired effect. Notably, both PPAR agonist E3317 and the HDACi trichostatin A, described above, were identified as ABCA1 inducers *via* phenotypic approaches^{277,309}.

A number of phenotypic screening efforts have been reported focusing on APOE transcription or secretion as the primary readout, some with ABCA1 upregulation as a secondary readout^{384–386}. However, in one case, the counterscreen was designed to remove ABCA1 inducers³⁸⁷. The perceived lipogenic risk associated with LXR agonists led Pfizer, Astra Zeneca, and others to screen CCF-STTG1 astrocytoma cells to identify hits that increase APOE, counterscreening to triage LXR ligands, although subsequent validation of resulting compounds in animal models is lacking^{384–386,388,389}. We recently described a luciferase-based phenotypic strategy employing an *ABCA1* promoter to identify ABCA1 boosting compounds and a *SREBF1* promoter to counterscreen against lipogenesis in HepG2 cells. This approach yielded multiple compounds with ABCA1-boosting, non-lipogenic profiles both *in vitro* and *in vivo*³⁹⁰. Chemical optimization resulted in a lead compound that had beneficial effects in an obesogenic mouse model of T2D. The broad metabolic effects observed prompted further investigation, revealing a binding profile of full agonist activity at LXR β and partial agonist activity at LXR α , with weak antagonism of PPAR and RXR isoforms³⁹¹. This strategy did not preclude LXR ligands from being identified; indeed, based on the promoter sequence, it was biased towards LXR ligands. Furthermore, this ABCA1-inducing LXR agonist was not only nonlipogenic, but also reduced triglycerides in the obesogenic mouse model.

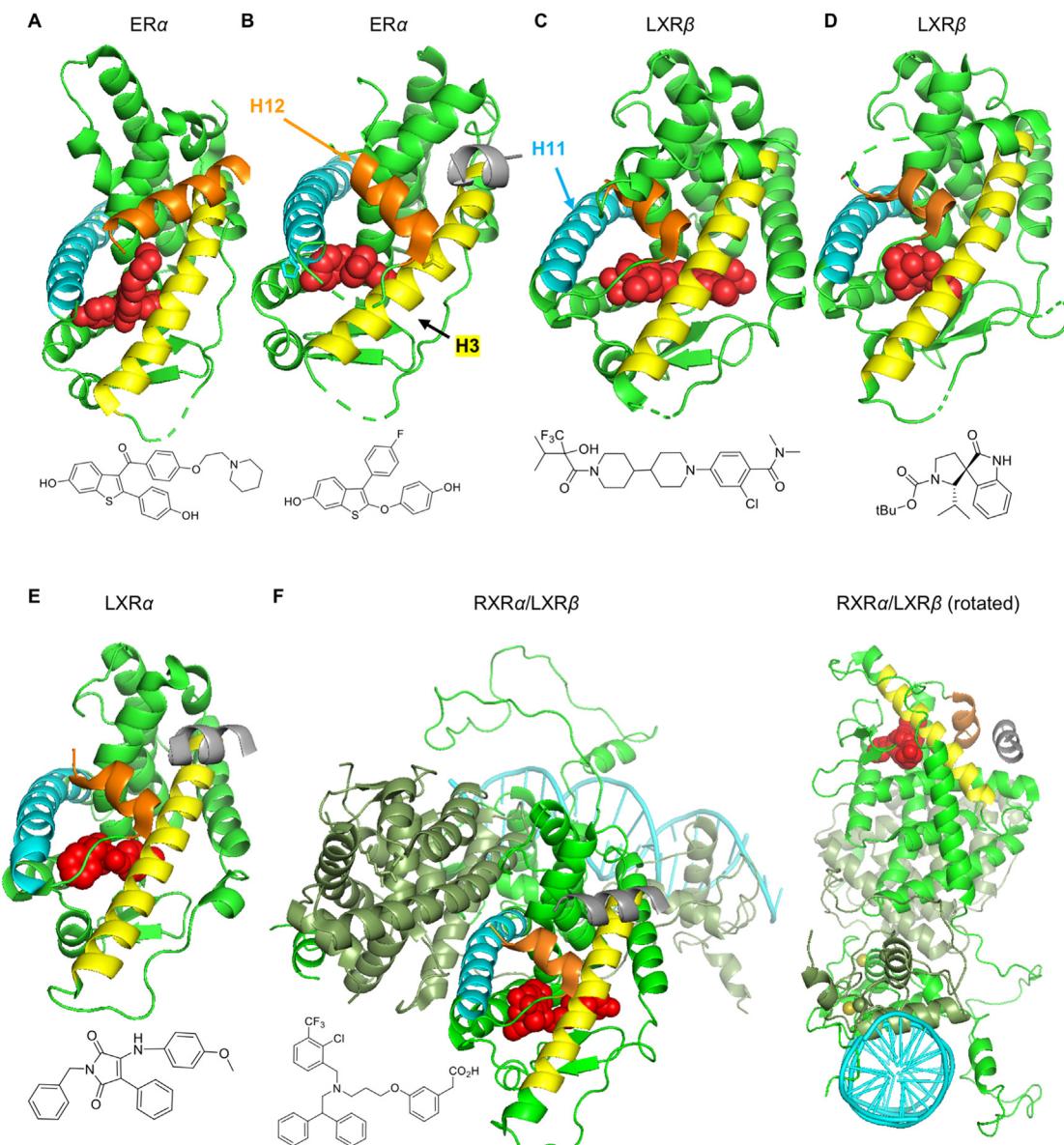


Figure 4 NHR and ligand structures (H12 orange; H3 yellow; H11 blue; ligand red; coregulator silver). (A) ER α in “antagonist conformation” with SERM raloxifene displacing H12 (PDB 2JFA). (B) ER α in “agonist conformation” with TTC-352 inducing closure, stabilizing H12, and binding the coactivator NCOA2 (PDB 7JHD). (C) Merck Comp9 LXR agonist (LXR β ; PDB 5HJP). (D) LXR “inverse agonist” (LXR β ; PDB 6K9M)³⁷⁵. (E) GSK3986 (LXR α ; PDB 2ACL with NCOA1 bound): showing similarity with ER agonist conformation forming AF-2; and similar binding poses with both LXR isoforms and with agonists and inverse agonists. (F) LXR β :RXR α heterodimer bound to DR-4 DNA element including LBDs, coregulator, and DNA-binding domains (4NQA)³⁷⁶: although containing more components of the transcriptional complex, intrinsically disordered N-terminal domains (containing AF-1) are absent. Tissue selectivity of NR ligands is widely believed to result from cell-specific coregulator expression³⁷⁰; however, the ligand is dominant as the linchpin in allosteric communication between coregulators and DNA³⁷⁷.

5. Conclusions

AD and related metabolic conditions are among the top causes of morbidity and mortality in the United States and worldwide, with existing therapies demonstrating minimal efficacy at reversing the progression of or enhancing survival from AD. Cholesterol metabolism and transport in both the CNS and periphery are central to the pathophysiology of AD and related diseases such as T2D and CVD, impacting such processes as A β and NFT production and deposition, atherosclerosis, inflammatory signaling, and insulin resistance. Because of this critical importance of

cholesterol homeostasis in these conditions, boosting expression or function of the primary cholesterol transport protein ABCA1 has been proposed as a therapeutic target. Drug development efforts to enhance ABCA1 have focused on nuclear hormone receptor—particularly, liver X receptor—agonists. These agonists have demonstrated promising results in preclinical AD models; however, their development and translation to the clinic has been hampered by an inability to avoid undesirable effects on triglyceride biogenesis. Recent research in LXR biology, as well as experience from drug discovery at other NHRs, suggests that the central paradigms that have driven LXR/ABCA1-based drug

development are overly simplistic. In particular, the focus on developing agonists selective for LXR β vs. LXR α isoforms will not yield non-lipogenic ABCA1 inducers as was previously thought. Rather, future medicinal chemistry efforts should strive to produce selective receptor modulators (*e.g.*, SLIMs or SPPARMs described above) that elicit only a small fraction of biological effects regardless of activity in receptor binding assays. Phenotypic, instead of target-based, drug discovery approaches are well-suited to approach this challenge; indeed, several *in vitro* and early preclinical screens using various phenotypic assays have yielded numerous promising development candidates.

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Author contributions

Cutler T. Lewandowski wrote the original draft, produced figures and tables, and contributed to revisions. Megan S. Laham produced tables and figures and contributed to revisions. Gregory R.J. Thatcher provided supervision, acquired research funding, and contributed to revisions.

Conflicts of interest

Gregory R. J. Thatcher is an inventor on patents owned by the University of Illinois. The other authors have no competing interests or relationships to disclose.

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