Inhibitory CCK+ basket synapse defects in mouse models of dystroglycanopathy

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ABSTRACT

Dystroglycan (Dag1) is a transmembrane glycoprotein that links the extracellular

matrix to the actin cytoskeleton. Mutations in *Dag1* or the genes required for its

glycosylation result in dystroglycanopathy, a type of congenital muscular dystrophy

characterized by a wide range of phenotypes including muscle weakness, brain defects,

and cognitive impairment. We investigated interneuron (IN) development, synaptic

function, and associated seizure susceptibility in multiple mouse models that reflect the

wide phenotypic range of dystroglycanopathy neuropathology. Mice that model severe

dystroglycanopathy due to forebrain deletion of *Dag1* or *Pomt2*, which is required for

Dystroglycan glycosylation, show significant impairment of CCK^+/CB_1R^+ IN

development. CCK^+/CB_1R^+ IN axons failed to properly target the somatodendritic

compartment of pyramidal neurons in the hippocampus, resulting in synaptic defects

and increased seizure susceptibility. Mice lacking the intracellular domain of

Dystroglycan have milder defects in $CCK^+/CB1R^+$ IN axon targeting, but exhibit

dramatic changes in inhibitory synaptic function, indicating a critical postsynaptic role of

this domain. In contrast, CCK^+/CB_1R^+ IN synaptic function and seizure susceptibility was

normal in mice that model mild dystroglycanopathy due to partially reduced

Dystroglycan glycosylation. Collectively, these data show that inhibitory synaptic defects

and elevated seizure susceptibility are hallmarks of severe dystroglycanopathy, and

show that Dystroglycan plays an important role in organizing functional inhibitory

synapse assembly.

INTRODUCTION

The formation of neural circuits is a multistep process involving proliferation, migration, axon guidance, maturation of neuronal subtypes, and establishment of functional synaptic connections between neurons. The cell adhesion molecule Dystroglycan is widely expressed in muscle and brain. Within the forebrain, Dystroglycan is expressed in neuroepithelial cells, pyramidal neurons, astrocytes, oligodendrocytes, and vascular endothelial cells where it plays important roles in the formation of basement membranes during early brain development (Colognato et al., 2007; Nguyen et al., 2014; Nickolls & Bönnemann, 2018; Tian et al., 1996; Zaccaria et al., 2001). At later developmental stages, Dystroglycan is present at multiple synapses, including at photoreceptor ribbon synapses in the retina (Omori et al., 2012; Orlandi et al., 2018), inhibitory synapses in the cerebellum (Briatore et al., 2010, 2020; Patrizi et al., 2008), and inhibitory synapses onto pyramidal neurons (Brünig et al., 2002; Lévi et al., 2002).

Dystroglycan is a central component of the dystrophin-glycoprotein complex (DGC) known primarily for its role in the etiology of neuromuscular diseases including Duchenne muscular dystrophy (DMD), limb-girdle muscular dystrophy (LGMD), and congenital muscular dystrophy (CMD). The gene encoding *Dystroglycan* (*Dag1*) yields two subunits, the extracellular alpha Dystroglycan (α-Dag1) and the transmembrane beta Dystroglycan (β-Dag1). These two subunits are non-covalently bound, allowing Dystroglycan to function as a link between extracellular ligands and cytoskeletal and signaling proteins (Ervasti & Campbell, 1991; Holt et al., 2000; Ibraghimov-Beskrovnaya et al., 1992; C. J. Moore & Winder, 2010). Extracellular α-Dag1 interacts with multiple

proteins in the nervous system through its extensive glycan chains (Jahncke & Wright,

2023). Mutations in any of the 19 genes involved in α-Dag1 glycosylation impair

Dystroglycan function through reduced ligand binding and leads to a class of congenital

muscular dystrophy termed dystroglycanopathy (Blaeser et al., 2013). Patients with

severe forms of dystroglycanopathy frequently present with structural brain

abnormalities and experience seizures and cognitive impairments (Barresi & Campbell,

2006; Muntoni et al., 2011; Taniguchi-Ikeda et al., 2016). Dystroglycanopathy patients

with moderate severity can exhibit cognitive impairments even in the absence of

identifiable brain malformations, suggesting that Dystroglycan functions at later stages

of neural circuit formation such as synapse formation and/or maintenance (Clement et

al., 2008; Godfrey et al., 2007).

The dramatic structural and anatomical phenotypes of global *Dag1* deletion in

mice has often precluded analysis of Dystroglycan's synaptic functions (Myshrall et al.,

2012; Satz et al., 2008, 2010). Recent studies show that when *Dag1* is selectively

deleted from postmitotic pyramidal neurons, neuronal migration and lamination is

normal, however CCK^+/CB_1R^+ interneurons (INs) fail to populate the forebrain or form

synapses in these mice (Früh et al., 2016; Miller & Wright, 2021). Furthermore,

conditional deletion of *Dag1* from cerebellar Purkinje neurons leads to impaired

inhibitory synaptic transmission and a reduction in the number of inhibitory synapses in

cerebellar cortex (Briatore et al., 2020). These studies establish a role for Dystroglycan

function at a subset of inhibitory synapses in the brain, but the critical features of

Dystroglycan necessary for these functions, and the relationship between inhibitory

synaptogenesis and neurological phenotypes in dystroglycanopathy, remains

undefined.

Here, we use multiple mouse models that recapitulate the full range of

dystroglycanopathy neuropathology to address several outstanding questions related to

the role of Dystroglycan at inhibitory synapses. We find that CCK$^+$/CB$_1$R$^+$ IN axon

targeting, synapse formation, and synapse function requires both glycosylation of α-

Dag1 and interactions through the intracellular domain of β-Dag1, and that defects in

synaptic structure and function is associated with increased seizure susceptibility in

mouse models of dystroglycanopathy.

RESULTS

Characterizing Dystroglycan localization and glycosylation in multiple models of

dystroglycanopathy

While conditional deletion of *Dag1* from pyramidal neurons causes a loss of

CCK$^+$/CB$_1$R$^+$ IN innervation in the forebrain, this has not been examined in

dystroglycanopathy relevant mouse models exhibiting more widespread loss of

functional Dystroglycan. We therefore generated five distinct mouse models; three to

provide mechanistic insight into Dystroglycan function and two of which model mild

dystroglycanopathy (schematized in **Fig. 1A**). Since complete loss of *Dag1* results in

early embryonic lethality in mice, we generated forebrain-specific conditional knockouts

by crossing *Emx1^{Cre}* with *Dystroglycan* floxed mice (*Dag1$^{F/F}$*), to drive recombination in

neuroepithelial cells in the dorsal forebrain beginning at embryonic day 10.5 (E10.5)

(Gorski et al., 2002; Liang et al., 2012). We verified the recombination pattern of

Emx1^{Cre} with the mCherry reporter *Rosa26$^{Lox-STOP-Lox-H2B:mCherry}$*. H2B:mCherry signal

was present in all excitatory neurons and astrocytes throughout the forebrain (**Fig. 1**

Supp. 1A, B, D) but not microglia or interneurons (**Fig. 1 Supp. 1C, E**).

To model loss of Dystroglycan glycosylation, $Emx1^{Cre}$ was crossed with $Pomt2^{F/F}$

conditional mice to generate $Pomt2^{cKOs}$. Pomt2 (protein O-mannosyltransferase 2) is a

glycosyltransferase that functions in a heterocomplex with Pomt1 to add O-mannose at

the beginning of the Dystroglycan glycan chain (Manya et al., 2004). Without the initial

O-mannose, no additional sugar moieties can be added to the glycan chain, resulting in

near complete loss of Dystroglycan glycosylation. This is lethal embryonically in a global

$Pomt2$ knockout, however $Emx1^{Cre}$;$Pomt2^{cKO}$ mice are viable and survive into adulthood

(Hu et al., 2016; Reeuwijk et al., 2005; Yanagisawa et al., 2007).

In addition to binding extracellular ligands, Dystroglycan binds cytoskeletal

proteins and signals through the intracellular tail of its β-subunit. To determine whether

the intracellular domain of Dystroglycan is required for synaptic development and/or

function, we examined mice in which one copy of $Dag1$ was deleted, and the other copy

lacks the intracellular domain of β-Dag1 ($Dag1^{cyto/-}$). These mice develop muscular

dystrophy but show normal neuronal migration and axon guidance in regions throughout

the central nervous system where Dystroglycan glycosylation is required (Lindenmaier

et al., 2019; Satz et al., 2009, 2010).

To model mild forms of dystroglycanopathy, we examined mice expressing

missense mutations in $B4gat1$ $(β$-1,4-glucuronyltransferase, $B4gat1^{M155T}$) and $Fkrp$

(fukutin related protein, $Fkrp^{P448L}$), two genes required for Dystroglycan glycosylation.

$B4gat1^{M155T}$ mice were initially identified in a forward genetic screen and develop mild

muscular dystrophy and have diminished ligand binding capacity due to reduced

Dystroglycan glycosylation (Wright et al., 2012). The $Fkrp^{P448L}$ missense mutation

models a mutation found in a patient with dystroglycanopathy (Brockington et al., 2001).

In mice, the $Fkrp^{P448L}$ mutation leads to reduced glycosylation and mild muscular

dystrophy, but no gross brain or eye malformations (Blaeser et al., 2013). While it is

possible that *Pomt2*, *B4gat1*, and *Fkrp* could play a role in the glycosylation of proteins

other than Dystroglycan, the identity of these proteins has not been described in

neurons to date and we did not observe any emergent phenotypes that have not been

observed in *Dag1* mutants (Gerin et al., 2016; Larsen, Narimatsu, Joshi, Siukstaite, et

al., 2017; Larsen, Narimatsu, Joshi, Yang, et al., 2017; Willer et al., 2014).

We first examined the pattern of Dystroglycan localization in pyramidal neurons

in CA1 of hippocampus in each of the five models by immunostaining adult (P30) mice

with the IIH6 antibody, which detects the terminal matriglycan repeats on the glycan

chain on α-Dag1 (Sheikh et al., 2022; Yoshida-Moriguchi & Campbell, 2015). In wild-

type (WT) mice, punctate IIH6 immunoreactivity was evident in the somatic and

perisomatic compartment of CA1 pyramidal neurons (**Fig. 1A**). Immunoreactivity was

also present in blood vessels, where *Dag1* is also expressed (Durbeej et al., 1998;

Zaccaria et al., 2001). Neuronal immunoreactivity was undetectable in

$Emx1^{Cre}$;$Dag1^{cKOs}$ and $Emx1^{Cre}$;$Pomt2^{cKOs}$, whereas blood vessel expression was

maintained, illustrating the specificity of the conditional deletion (**Fig. 1A**). Punctate

perisomatic IIH6 immunoreactivity was present in $Dag1^{cyto/-}$, $B4gat1^{M155T/M155T}$, and

$Fkrp^{P448L/P448L}$ mice (**Fig. 1A**). To assess Dystroglycan localization in $Emx1^{Cre}$;$Pomt2^{cKOs}$

we used an antibody that recognizes the intracellular C-terminus of β-Dag1. Although

immunoreactivity for β-Dag1 was present and elevated above $Emx1^{Cre}$;$Dag1^{cKO}$ or

Dag1$^{cyto/-}$ levels, Dag1 localization did not appear punctate in *Emx1^{Cre};Pomt2^{cKOs}* (**Fig. 1**

Supp. 2A). This apparent difference implies that Dag1 glycosylation, and by extension

the extracellular interactions that matriglycan mediates, is required for proper Dag1

synaptic localization.

We next prepared WGA-enriched lysate from neonatal (P0) forebrain and

immunoblotted for (1) IIH6, to quantify the degree of α-Dag1 glycosylation and (2) β-

Dag1, to measure total Dystroglycan protein levels (**Fig. 1B**). Dag1 glycosylation was

significantly reduced in *Emx1^{Cre};Dag1^{cKOs}*, *Emx1^{Cre};Pomt2^{cKOs}*, *Dag1$^{cyto/-}$*,

B4gat1$^{M155T/M155T}$, and *Fkrp$^{P448L/P448L}$* mice; however, the reduction in *Fkrp$^{P448L/P448L}$* mice

was less severe than the other models (**Fig. 1C**). The reduction in glycosylation

observed in the *Dag1$^{cyto/-}$* mice is surprising given that the mutation is restricted to the

intracellular domain. *Dystroglycan* heterozygotes (*Dag1$^{+/-}$*) show no reduction in IIH6

levels compared to wild-types (data not shown), so the reduction in *Dag1$^{cyto/-}$* mice can

be presumed to be due to the intracellular deletion. It is possible that the intracellular

domain is required for the trafficking of Dystroglycan through the endoplasmic reticulum

and/or Golgi apparatus, where Dystroglycan undergoes glycosylation, however

additional work is needed to verify this. As expected, β-Dag1 immunoblotting was

significantly reduced in *Emx^{Cre};Dag1^{cKOs}* and absent in *Dag1$^{cyto/-}$* mice but normal in the

glycosylation mutants (**Fig. 1D**). The residual β-Dag1 in *Emx1^{Cre};Dag1^{cKO}* brain is likely

due to *Dag1* expression in unrecombined cells, such as blood vessels, as well as

unrecombined tissue that remained after the forebrain dissection.

We next examined Dag1 protein levels during synaptogenesis using WGA-

enriched lysate from P21-P30 hippocampus. As expected, Dag1 glycosylation assessed

by IIH6 immunoblotting was severely reduced in *Emx1^{Cre};Dag1^{cKOs}* and

Emx1^{Cre};Pomt2^{cKOs} but normal in *Dag1$^{cyto/-}$* mice (**Fig. 1 Supp. 2B-C**). Immunoblotting

for β-Dag1 showed a significant reduction in *Emx1^{Cre};Dag1^{cKOs}* and *Dag1$^{cyto/-}$* mutants

but normal levels in *Emx1^{Cre};Pomt2^{cKOs}* (**Fig. 1 Supp. 2B, D**). Although localization of

Dag1 was not punctate in *Emx1^{Cre};Pomt2^{cKOs}* (**Fig. 1 Supp. 2A**), the overall level of β-

Dag1 was normal by WGA-enrichment, which enriches for proteins in the plasma

membrane (**Fig. 1 Supp. 2B, D**). It therefore remains possible that Dag1 still trafficks to

the cell surface in *Emx1^{Cre};Pomt2^{cKOs}* but fails to contact presynaptic axons and

therefore does not permit synaptogenesis.

Dystroglycan is required for cortical neuron migration in a glycosylation-

dependent manner

In neocortex, *Dag1* expression in radial glia is required for proper migration of

neurons, with *Dag1* conditional deletion from neuroepithelial cells or radial glia resulting

in Type II lissencephaly (S. A. Moore et al., 2002; Pawlisz & Feng, 2011; Satz et al.,

2008, 2010). This requires proper Dystroglycan glycosylation, but not its expression in

neurons (Chan et al., 2010; Holzfeind et al., 2002; Hu et al., 2011; Wright et al., 2012).

To compare cortical migration across our five models of dystroglycanopathy, we

performed immunostaining for the upper layer marker Cux1 (layers II/III-IV) and the

deep layer marker Tbr1 (layers III, VI) in P30 somatosensory cortex (**Fig. 2A-B**).

Emx1^{Cre};Dag1^{cKOs} and *Emx1^{Cre};Pomt2^{cKOs}* showed complete cortical dyslamination with

100% penetrance, whereas the cytoplasmic (*Dag1$^{cyto/-}$*) deletion mutants appeared

normal (**Fig. 2C-D**). *B4gat1$^{M155T/M155T}$* missense mutants showed a migration phenotype

only at the cortical midline, while $Fkrp^{P448L/P448L}$ missense mutants did not show any

cortical migration phenotype (**Fig. 2 C-D, Fig. 2 Supp. 1A**). These results indicate that

cortical migration depends on Dystroglycan glycosylation but does not require its

cytoplasmic domain. Furthermore, taken with the data in **Fig. 1B-D**, they illustrate that

the severity of the cortical migration phenotype scales with the degree of Dystroglycan

hypoglycosylation; $Emx1^{Cre};Dag1^{cKOs}$ and $Emx1^{Cre};Pomt2^{cKOs}$ model a severe form of

dystroglycanopathy (Walker-Warburg Syndrome, Muscle-Eye-Brain disease) and

$B4gat1^{M155T/M155T}$ and $Fkrp^{P448L/P448L}$ mutants modeling a milder form of the disease.

To further assess the impact of our functional domain mutations, we assessed

Laminin localization, the canonical interacting partner of Dystroglycan in the

extracellular matrix (ECM), in adult neocortex (Ibraghimov-Beskrovnaya et al., 1992).

Under WT conditions, Laminin immunoreactivity was evident at the pial surface where

Laminin and Dystroglycan interact at the interface between radial glial endfeet and the

cortical basement membrane (Satz et al., 2010). Laminin was also present in blood

vessels, where Dystroglycan-expressing perivascular astrocytes contribute to the

maintenance of water homeostasis (Menezes et al., 2014). In $Emx1^{Cre};Dag1^{cKO}$ cortex,

Laminin immunoreactivity at the pial surface was patchy and vascular Laminin showed

evidence of the neuronal migration phenotype described in **Fig. 2** (**Fig. 2 Supp. 2A**).

Laminin immunoreactivity in $Emx1^{Cre};Pomt2^{cKO}$ cortex similarly showed a patchy

appearance, albeit less severe than $Emx1^{Cre};Dag1^{cKOs}$, along with the evident cortical

migration phenotype (**Fig. 2 Supp. 2B**). $Dag1^{cyto/-}$ mutants, on the other hand, exhibited

normal Laminin immunoreactivity both at the pial surface and with regards to vascular

organization (**Fig. 2 Supp. 2C**).

Perisomatic CCK⁺/CB₁R⁺ interneuron targeting requires Dystroglycan in a non-

cell autonomous manner

CCK^+/CB_1R^+ IN innervation is largely absent from the cortex and hippocampus

when *Dag1* is deleted selectively from pyramidal neurons using *NEX^{Cre}* (Früh et al.,

2016; Miller & Wright, 2021). However, the development and function of CCK^+/CB_1R^+

INs has not been examined in mouse models that more broadly lack *Dag1* throughout

the central nervous system (CNS) and thus more accurately reflect the neuropathology

of dystroglycanopathy. We focused our analysis on region CA1 of the hippocampus, as

its overall architecture is grossly unaffected in each of our mouse models. Both

Emx1^{Cre};Dag1^{cKO} and *Emx1^{Cre};Pomt2^{cKO}* mice exhibited a mild granule cell migration

phenotype in dentate gyrus (**Fig. 3A**, yellow arrows), however CA1-CA3 showed normal

pyramidal neuron organization.

In WT control mice, CCK^+/CB_1R^+ IN axon terminals were abundant throughout

the hippocampus, with their highest innervation density in the CA1 pyramidal cell body

layer (*stratum pyramidale*, SP) where they form characteristic basket synapses onto

pyramidal neurons (**Fig. 3A-C**, **Fig. 3 Supp. 1A**). In *Emx1^{Cre};Dag1^{cKO}* mice,

CCK^+/CB_1R^+ axons were present but failed to target the pyramidal cell layer (**Fig. 3A-C**,

Fig. 3 Supp. 1A), a surprising difference from the phenotype observed in

NEX^{Cre};Dag1^{cKO} mice which lack $CCK^+/CB1R^+$ IN innervation entirely (Früh et al., 2016;

Miller & Wright, 2021) (**Fig. 3 Supp. 1C**). To confirm the $CCK^+/CB1R^+$ IN innervation

pattern in the context of widespread *Dag1* deletion, we generated *Nestin^{Cre};Dag1^{cKO}*

mice. *Nestin^{Cre}*, similar to *Emx1^{Cre}*, drives *Cre* recombination in forebrain progenitors,

however *Emx1^Cre* recombination begins around E10.5 and *Nestin^Cre* recombination

begins around E11.5 (Liang et al., 2012; Tronche et al., 1999). *Nestin^Cre;Dag1^cKOs*

showed the same CCK$^+$/CB1R$^+$ axon targeting phenotype as *Emx1^Cre;Dag1^cKOs* (**Fig. 3**

Supp. 1B), further suggesting that the observed *Emx1^Cre;Dag1^cKO* phenotype faithfully

models dystroglycanopathy neuropathology.

It was previously reported that the lack of CCK$^+$/CB1R$^+$ IN innervation of CA1

pyramidal neurons observed in *NEX^Cre;Dag1^cKOs* was accompanied by reduced

numbers of CCK$^+$/CB1R$^+$ INs (Miller & Wright, 2021). We therefore sought to quantify

CCK$^+$/CB1R$^+$ IN cell density in *Emx1^Cre;Dag1^cKOs* using both NECAB1 and NECAB2

antibodies (Miczán et al., 2021). As NECAB1 is expressed by both CCK$^+$/CB$_1$R$^+$ INs and

PV$^+$ INs, we performed immunolabeling for both NECAB1 and PV and quantified the

density of NECAB1$^+$;PV$^-$ cell bodies in CA1, finding no difference between

Emx1^Cre;Dag1^Ctrls and *Emx1^Cre;Dag1^cKOs* (**Fig. 3 Supp. 2A-B**). To confirm this, we also

quantified the density of NECAB2$^+$ cell bodies in CA1, again finding no difference

between genotypes (**Fig. 3 Supp. 2C, E**). Thus, the observed change in CCK$^+$/CB$_1$R$^+$ IN

axon targeting of CA1 pyramidal cells is not due to a reduction in cell numbers, but

rather a failure to innervate the appropriate compartment.

Emx1^Cre;Pomt2^cKO mice fully phenocopied the aberrant *Emx1^Cre;Dag1^cKO* CB$_1$R$^+$

immunoreactivity pattern (**Fig. 3A-C**), demonstrating that proper CCK$^+$/CB$_1$R$^+$ IN basket

axon targeting requires Dystroglycan glycosylation. Both the *B4gat1* and *Fkrp* mutants

showed a normal distribution of CB$_1$R$^+$ axon targeting to the somatodendritic

compartment of CA1 neurons, but with reduced CB$_1$R intensity in SP (**Fig. 3A-C**). The

cytoplasmic domain of Dystroglycan also plays a role in the appropriate targeting of

CB$_1$R immunoreactive axons, as the distribution of axons was perturbed in the *Dag1$^{cyto/-}$*

mutants, though with an intermediate phenotype in which the upper portion of SP

appeared normal while the lower portion of SP showed loss of selective CB$_1$R$^+$ axon

targeting (**Fig. 3A-C**).

Due to the axonal targeting defect in the CCK$^+$/CB$_1$R$^+$ IN population, we next

examined the parvalbumin (PV) population of interneurons in the hippocampus, as

these cells also form perisomatic basket cell synapses on to CA1 pyramidal cells. There

was no significant difference in the number of PV$^+$ INs in CA1 of *Emx1^{Cre};Dag1^{cKO}* mice

and littermate controls (**Fig. 3 Supp. 2D, F**). Furthermore, the distribution of PV$^+$ IN

axons showed normal targeting to SP in all mouse models (**Fig. 3 Supp. 3A-B**),

indicating that the axon targeting phenotype is specific to the CCK$^+$/CB$_1$R$^+$ IN

population. Interestingly, *Emx1^{Cre};Dag1^{cKO}* mice exhibited a slight increase in PV

intensity in SP, perhaps indicating that there is a degree of compensation (**Fig. 3 Supp.**

3A-B).

Notably, CB$_1$R expression was also abnormal in brain regions outside of the

hippocampus. In somatosensory cortex, CB$_1$R immunostaining reflected the

dyslamination phenotype in both the *Emx1^{Cre};Dag1^{cKO}* and *Emx1^{Cre};Pomt2^{cKO}* mice

throughout neocortex and the *B4gat1$^{M155T/M155T}$* mice at midline, while it appeared

normal in cortex of *Dag1$^{cyto/-}$* and *Fkrp$^{P448L/P448L}$* mice (**Fig. 3 Supp. 4A**). CB$_1$R staining

was also reduced and disorganized in the basolateral amygdala (BLA) in

Emx1^{Cre};Dag1^{cKO} and *Emx1^{Cre};Pomt2^{cKO}* mice (**Fig. 3 Supp. 4B**). Interestingly, CB$_1$R

immunostaining in the inner molecular layer (IML) of dentate gyrus appears normal in all

mutants (**Fig. 3A**). In the IML, CB$_1$R is present in excitatory mossy cell axons targeting

dentate granule cells whereas in both cortex and amygdala CB_1R expression is

restricted to GABAergic interneurons (Földy et al., 2006; Katona et al., 2001; Monory et

al., 2015). Therefore, glycosylated Dystroglycan instructs the development of inhibitory

CB_1R^+ interneuron populations in multiple brain regions.

Dystroglycan is required for CCK^+/CB_1R^+ interneuron axon targeting during early

postnatal development

During early postnatal development, CCK^+/CB_1R^+ IN axons undergo a dramatic

laminar rearrangement, progressing from more distal localization amongst pyramidal

cell dendrites, to eventually target pyramidal neuron cell bodies in the hippocampus

(Miller & Wright, 2021; Morozov et al., 2009; Morozov & Freund, 2003a, 2003b). We

examined the developmental time course of CCK^+/CB_1R^+ IN axon targeting in our

$Emx1^{Cre}$;$Dag1^{cKO}$ mice beginning at P5, when the axons are first readily identifiable

(Berghuis et al., 2007; Eggan et al., 2010; Mulder et al., 2008; Vitalis et al., 2008). At P5

in control *$Emx1^{Cre}$;$Dag1^{Ctrl}$* mice, CCK^+/CB_1R^+ axons were initially concentrated in the

stratum radiatum (SR) of the hippocampus (**Fig. 4A-C**). Between P10 and P30, the

CCK^+/CB_1R^+ axons underwent developmental reorganization, with reduced innervation

of SR coinciding with a progressive increase in innervation of SP. In contrast, overall

CCK^+/CB_1R^+ innervation was initially reduced in the hippocampus of mutant

$Emx1^{Cre}$;$Dag1^{cKO}$ mice at P5, and these axons failed to undergo laminar reorganization

as they developed (**Fig. 4A-C**). By P30, after IN synapse formation and targeting are

largely complete in control mice, the density of CCK^+/CB_1R^+ axons in *$Emx1^{Cre}$;$Dag1^{cKO}$*

mice was uniform across all hippocampal lamina (**Fig. 4A-C**). Therefore, Dystroglycan

plays a critical developmental role during the first two postnatal weeks, for the proper

laminar distribution and perisomatic targeting of CCK$^+$/CB$_1$R$^+$ IN axons in the

hippocampus.

CCK$^+$/CB$_1$R$^+$ IN synapse formation requires postsynaptic glycosylated

Dystroglycan

Given the perturbed distribution of CCK$^+$/CB$_1$R$^+$ IN axons in the hippocampus,

we next wanted to determine whether the remaining CCK$^+$/CB$_1$R$^+$ IN axons were

capable of forming synapses in dystroglycanopathy models. Using VGAT as a marker of

inhibitory presynaptic terminals, we saw no difference in total VGAT puncta density in

SP in any of the mouse models, indicating that the total number of inhibitory synapses is

normal (**Fig. 5B-D**). Immunostaining for CB$_1$R showed a significant decrease in CB$_1$R in

SP of *Emx1^{Cre};Dag1^{cKO}*, *Emx1^{Cre};Pomt2^{cKO}*, *B4gat1$^{M155T/M155T}$*, and *Fkrp$^{P448L/P448L}$*

mutants, but not *Dag1$^{cyto/-}$* mutants (**Fig. 5E**). This suggests that the difference in CB$_1$R$^+$

axon distribution described in SP of *Dag1$^{cyto/-}$* mutants in **Fig. 3A-C** likely reflects a

change in CCK$^+$/CB$_1$R$^+$ IN axon targeting but not synapse formation, whereas

Emx1^{Cre};Dag1^{cKO} and all three glycosylation mutants exhibit a reduction in CCK$^+$/CB$_1$R$^+$

IN axon targeting and synapse number in SP. It should be noted that the data in **Fig.

3A-C** reflects axonal CB$_1$R intensity across all hippocampal layers, whereas the

quantification in **Fig. 5E** reflects the density of axonal swellings within SP. These data

therefore suggest that there is an overall reduction in CB$_1$R intensity in SP of *Dag1$^{cyto/-}$*

mutants that does not influence the number of CB$_1$R$^+$ axonal swellings. In contrast to

CCK$^+$/CB$_1$R$^+$ INs, the PV$^+$ population of basket interneurons showed no change in

puncta density in SP in any of the models (**Fig. 5 Supp. 2A-E**; analysis of VGAT, CB$_1$R,

and PV densities in SO and SR included in **Fig. 5 Supp. 1A-B** and **Fig. 5 Supp. 3A**.)

To better approximate the extent of basket synapse formation, we quantified the

co-localization between VGAT and CB$_1$R or PV. In SP, the percent of CB$_1$R puncta co-

localized with VGAT was reduced in the same models that showed a reduction in CB$_1$R

density (*Emx1^{Cre};Dag1^{cKO}*, *Emx1^{Cre};Pomt2^{cKO}*, *B4gat1$^{M155T/M155T}$*, and *Fkrp$^{P448L/P448L}$*

mutants) but not *Dag1$^{cyto/-}$* mutants (**Fig. 5C, F**), suggesting that CCK$^+$/CB$_1$R$^+$ INs

require postsynaptic glycosylated Dystroglycan in order to form synapses whereas the

cytoplasmic domain is required for axon targeting but not synapse formation.

Interestingly, the percent of PV co-localized with VGAT increased in the SP of

Emx1^{Cre};Dag1^{cKOs} and *Emx1^{Cre};Pomt2^{cKOs}* mice, with no change in any of the other

models (**Fig. 5 Supp. 2C, E**; analysis of co-localization in SO and SR included in **Fig. 5**

Supp. 1C, **Fig. 5 Supp. 3B**). It is possible that the reduction in inhibitory CCK$^+$/CB1R$^+$

synapses prompts homeostatic compensation through an increase in PV$^+$ synapses.

Alternatively, this may reflect competition between CCK$^+$/CB$_1$R$^+$ and PV$^+$ INs for

physical space on the perisomatic region of pyramidal cells, with the decrease in

CCK$^+$/CB$_1$R$^+$ synapses in *Emx1^{Cre};Dag1^{cKOs}* and *Emx1^{Cre};Pomt2^{cKOs}* allowing additional

PV$^+$ IN synapses to form.

CCK$^+$/CB$_1$R$^+$ interneuron basket synapse function is dependent on Dystroglycan

function

Perisomatic inhibitory basket cell synapses powerfully control activity in the

hippocampal circuit (Freund & Katona, 2007). Previous studies in *NEX^{Cre};Dag1^{cKO}* mice,

in which CCK⁺/CB₁R⁺ INs are absent, demonstrated reduced inhibitory synaptic function

(Früh et al., 2016). In the current study, however, CCK⁺/CB₁R⁺ INs are present but

mistargeted. Thus, we wanted to determine whether with the changes in CCK⁺/CB₁R⁺

basket synapse localization in our mouse models were associated with altered inhibitory

synaptic function. CCK⁺/CB₁R⁺ IN basket cells can be selectively activated by

muscarinic receptor activation, which increases the rate of spontaneous inhibitory post-

synaptic currents (sIPSCs) in nearby pyramidal cells (Früh et al., 2016; Nagode et al.,

2014). Thus, to assay function at CCK⁺/CB₁R⁺ IN synapses, we performed whole cell

patch clamp electrophysiology from CA1 pyramidal neurons in slices from control and

mutant mice. After recording 5 minutes of baseline sIPSCs, the cholinergic receptor

agonist Carbachol (CCh) was added to the bath and an additional 5 minutes of sIPSCs

were recorded. While both *Emx1^Cre^;Dag1^Ctrl^* and *Emx1^Cre^;Dag1^cKO^* cells displayed a

CCh-mediated change in sIPSC frequency, this response was dramatically attenuated

in *Emx1^Cre^;Dag1^cKOs^* mice compared to *Emx1^Cre^;Dag1^Ctrl^* mice (**Fig. 6A-C**). Furthermore,

in *Emx1^Cre^;Dag1^Ctrls^*, 19/21 cells (90.5%) responded to CCh application (defined as a

>20% increase in sIPSC frequency), whereas only 13/22 cells (59.1%) responded in

*Emx1^Cre^;Dag1^cKOs^* (**Fig. 6 Supp. 1B**). Proper Dystroglycan glycosylation was also

required for CCK⁺/CB₁R⁺ IN synapse function, as *Emx1^Cre^;Pomt2^cKO^* mice exhibited the

same phenotype as *Emx1^Cre^;Dag1^cKOs^*: a reduced response to CCh overall, and a

reduced proportion of responsive cells (**Fig. 6A-C**, **Fig. 6 Supp. 1B**). CCh also

increased the mean sIPSC amplitude in each of the controls (**Fig. 6 Supp. 1A**), which

may reflect an increased contribution of larger-amplitude action potential-mediated

perisomatic events elicited by CCh (Früh et al., 2016; Nagode et al., 2014). Consistent

with the decreased function of CCK^+/CB_1R^+ IN synapses, a CCh-mediated change in

sIPSC amplitude was also absent in each of these models (**Fig. 6 Supp. 1A**). Together,

these data indicate that the altered perisomatic CCK^+/CB_1R^+ IN synaptic localization in

CA1 is associated with a functional deficit in synaptic signaling.

Dag1$^{cyto/-}$ mutants also had a dramatically attenuated sIPSC response to CCh

compared to WT controls (**Fig. 6C**). Notably, even baseline sIPSC frequency was

reduced in *Dag1$^{cyto/-}$* mutants (2.27±1.70 Hz) compared to WT controls (4.46±2.04 Hz, *p*

= 0.002), whereas baseline sIPSC frequencies appeared normal in all other mutants

when compared to their respective controls. Together with the finding that these

mutants contain a normal number of CCK^+/CB_1R^+ basket synapses (as measured using

immunohistochemistry; **Fig. 5A-D**), these results indicate that the cytoplasmic domain of

Dystroglycan may play a critical role in mediating the assembly of functional

postsynaptic signaling/receptor complexes at these synapses.

Neither of the more mildly hypoglycosylated mutants (*B4gat1$^{M155T/M155T}$*,

Fkrp$^{P448L/P448L}$) were different from their respective littermate controls in terms of the

magnitude of the CCh effect on sIPSC frequency (**Fig. 6C**), although the *B4gat1^{WT}* mice

appeared to possess a reduced effect of CCh compared to other control conditions (**Fig.**

6A-C). The *B4gat1* line is of a mixed genetic background, which could possibly explain

the difference in CCh response. This finding is of unclear significance and may have

obscured potential differences. Importantly, however, the marked functional synaptic

differences observed between the *Emx1^{Cre};Pomt2^{cKO}*, *Emx1^{Cre};Dag1^{cKO}* and *Dag1$^{cyto/-}$*

mice when compared with each of their respective controls described above was not

seen in either of these phenotypically milder mutants.

Together, these results suggest that Dystroglycan is required for the function of

CCK^+/CB_1R^+ IN perisomatic basket synapses in a glycosylation-dependent manner, as

evidenced by the $Emx1^{Cre};Dag1^{cKO}$ and $Emx1^{Cre};Pomt2^{cKO}$ synaptic phenotypes, and

that the intracellular domain of Dystroglycan is also required for normal CCK^+/CB_1R^+ IN

basket synapse function. However, we cannot rule out the possibility that CCK^+/CB_1R^+

INs are simply less responsive to CCh in the mutants, as we lack the tools to identify

$CCK^+/CB1R^+$ INs in live tissue for targeted recordings. In contrast, $B4gat1^{M155T/M155T}$ and

$Fkrp^{P448L/P448L}$ hypomorphic mutants both appear to retain sufficient Dystroglycan

glycosylation to maintain normal synapse function.

Increased seizure susceptibility in models of dystroglycanopathy

Human patients with dystroglycanopathy have an increased risk of seizures and

epilepsy (Dhaibani et al., 2018; Di Rosa et al., 2011; Raphael et al., 2014; Yang et al.,

2022), however the underlying cause has yet to be determined. The observed defects in

inhibitory basket synapse function suggest that alterations in neuronal circuit inhibition

could potentially predispose mutant mice to seizures. To test whether mouse models of

dystroglycanopathy exhibit a reduced seizure threshold, we exposed mice to the volatile

chemoconvulsant flurothyl and measured the latency to generalized tonic-clonic seizure

(TCS) (Egawa et al., 2021).

The latency to TCS was significantly faster in $Emx1^{Cre};Dag1^{cKO}$ mice than their

littermate controls (a 40.9% reduction on average, **Fig. 7A**), with no difference in

seizure latency between sexes in either group (**Fig. 7 Supp. 1C**). $Emx1^{Cre};Pomt2^{cKOs}$

and $Dag1^{cyto/-}$ mutants also had a significantly shorter latency to TCS than littermate

controls (42.9% and 33.6% reductions, respectively; **Fig. 7A**), indicating that the

mechanism underlying Dystroglycan's role in seizure susceptibility requires both

extracellular glycosylation and intracellular interactions. $B4gat1^{M155T/M155T}$ mutants

showed a small but significant reduction (16%) in seizure latency, despite exhibiting no

detectable functional deficit by electrophysiology (**Fig. 6A-C**, **Fig. 7A**). Finally,

$Fkrp^{P448L/P448L}$ mutants showed no significant change in seizure susceptibility (**Fig. 7A**).

Thus, the reduction in seizure latency reflects the severity of the synaptic phenotypes

across the various models of dystroglycanopathy. These results demonstrate that

disruptions in Dystroglycan function, including both its extracellular glycosylation and

intracellular interactions, increase sensitivity to seizures.

DISCUSSION

Recent work identified a key role for neuronal Dystroglycan in the establishment

and function of CCK^+/CB_1R^+ inhibitory synapses in the forebrain (Früh et al., 2016;

Miller & Wright, 2021). Deletion of *Dag1* selectively from pyramidal neurons

($NEX^{Cre};Dag1^{cKO}$) led to a near complete loss of CCK^+/CB_1R^+ INs during the first few

postnatal weeks. In this study, we sought to better understand how CCK^+/CB_1R^+ IN

synapse formation is affected in mouse models that more accurately reflect

dystroglycanopathy, in which Dystroglycan function is more broadly affected throughout

the CNS (**Figs. 1**, **2**). Using a model that deletes *Dag1* throughout the developing

forebrain ($Emx1^{Cre};Dag1^{cKO}$) we found that CCK^+/CB_1R^+ INs were present, but the

laminar organization of their axon terminals and their ability to form functional basket

synapses onto pyramidal neuron cell bodies in the hippocampus was impaired (**Figs. 3-**

6). The inability of CCK$^+$/CB$_1$R$^+$axon terminals to concentrate in the CA1-3 cell body

layer began to manifest during the first postnatal week, when dynamic changes in

laminar innervation by CCK$^+$/CB$_1$R$^+$ axons normally occur (**Fig. 4**). Furthermore, these

mice were found to exhibit a reduced seizure threshold compared to controls, showing

for the first time that mouse models of dystroglycanopathy are vulnerable to seizures

(**Fig. 7**). Because *Emx1^{Cre}* (and *Nestin^{Cre}*) conditional deletion of *Dag1* or *Pomt2* leads

to widespread loss of functional Dystroglycan in the forebrain in contrast with the

previously studied *NEX^{Cre}* conditional deletion, which targets pyramidal neurons, these

models more accurately model dystroglycanopathy.

We found that CCK$^+$/CB$_1$R$^+$ IN synapse formation and function are dependent on

proper Dystroglycan glycosylation and appear to correlate with the degree of

hypoglycosylation in different mutants. Complete reduction of glycosylation in

Emx1^{Cre};Pomt2^{cKO} mutants caused the same phenotypes seen in Dystroglycan

conditional knockouts (*Emx1^{Cre};Dag1^{cKO}*) (**Figs. 1-3, 5-6**), possibly due to the

mislocalization of Dystroglycan. The finding that glycosylation is required for

Dystroglycan synaptic localization in hippocampal pyramidal cells is similar to a

previous finding in retinal photoreceptors in the context of *Pomt1* conditional deletion

(Rubio-Fernández et al., 2018). In contrast, when *Fktn* deletion is induced in myotubes

β-Dystroglycan localization is unchanged, suggesting that this phenomenon is unique to

synaptic Dystroglycan (Beedle et al., 2012). One interpretation is that without

matriglycan present to mediate interaction with presynaptic cells, Dystroglycan is no

longer concentrated at synaptic sites, implicating it as a synaptic organizer. However,

the miswiring of the CCK$^+$/CB$_1$R$^+$ axons could also reduce the likelihood of postsynaptic

Dystroglycan encountering a presynaptic axon, discouraging synaptic localization.

Conversely, it is possible that glycosylation is required for trafficking to the surface in the

first place, however this is less likely given that the levels of β-Dystroglycan were normal

in membrane-enriched lysate (**Fig. 1, Fig. 1 Supp. 2**).

A milder reduction in glycosylation ($B4gat1^{M155T/M155T}$) resulted in a cortical

migration phenotype that was restricted to midline (**Fig. 3 Supp. 4**) and a small

reduction in CCK^+/CB_1R^+ axon terminals and synaptic puncta density in CA1 which did

not appear to affect synapse function (**Figs. 3, 5-6**). The mildest reduction in

glycosylation amongst our models was observed in $Fkrp^{P448L/P448L}$ mutants, which

exhibited normal cortical migration but the same mild defect in CCK^+/CB_1R^+ IN axon

targeting and synaptic puncta density observed in $B4gat1^{M155T/M155T}$ mutants (**Figs. 3, 5-**

6). Together, these three glycosylation mutants illustrate the degree of

hypoglycosylation required for neurodevelopmental processes and show that defects in

synaptic function only arise in the context of severely reduced glycosylation; the residual

Dystroglycan function present in $B4gat1^{M155T/M155T}$ and $Fkrp^{P448L/P448L}$ mutants is

sufficient for most aspects of brain development. Finally, using $Dag1^{cyto/-}$ mutants that

lack the intracellular domain of Dystroglycan, we found that the intracellular domain

plays a role in some, but not all, neurodevelopmental processes. The intracellular

domain is not required for neuronal migration in neocortex or synapse formation in CA1

(**Figs. 2 and 5**) but is required for the proper targeting of CCK^+/CB_1R^+ IN axons in CA1-

3 (**Fig. 3**) and for subsequent CCK^+/CB_1R^+ IN basket synapse function (**Fig. 6**).

Dystroglycan is an essential transsynaptic organizing molecule for CCK⁺/CB₁R⁺

basket synapses

Synaptogenesis requires multiple distinct steps: (1) synaptic partner recognition,

(2) recruitment and assembly of core pre- and post-synaptic machinery, (3)

differentiation and maturation of synaptic identity, and (4) synaptic maintenance

(Südhof, 2018). Based on data from this study (**Fig. 4**) and previous work from our

group and others, mice lacking *Dystroglycan* exhibit defects in CCK⁺/CB₁R⁺ IN

development at the earliest time point they can be reliably identified (P0-P5), before the

peak phase of inhibitory synapse formation (P9), suggesting that Dystroglycan functions

at the earliest stages of synaptogenesis such as synaptic partner recognition (Favuzzi

et al., 2019). Determining the precise onset of synapse targeting and formation for most

IN subtypes, including CCK⁺/CB₁R⁺INs, is limited by a lack of genetic tools for

visualizing and manipulating IN subtypes during developmental stages.

The impairment in CCK⁺/CB₁R⁺ IN development throughout the forebrain

suggests a trans-synaptic role for Dystroglycan (**Fig. 3, Fig. 3 Supp. 4**). The identity of

the trans-synaptic binding partner between Dystroglycan-expressing cells and

CCK⁺/CB₁R⁺ INs remains unknown. Our data in *Emx1^{Cre};Pomt2^{cKO}* mice point to a

critical role for the glycan chains on Dystroglycan mediating this binding. All proteins

that bind to the glycan chains on Dystroglycan do so through at least one Laminin G

(LG) domain. There are over 25 LG-domain containing extracellular or transmembrane

proteins expressed in the hippocampus. Neurexins, a family of highly alternatively

spliced synaptic cell-adhesion molecules (*NRXN1-3*) which each contain multiple LG

domains, bind Dystroglycan in a glycosylation-dependent manner (Boucard et al., 2005;

Fuccillo et al., 2015; Reissner et al., 2014; Sugita et al., 2001). The specific splice

isoforms of *Nrxns* that bind Dystroglycan are expressed by CCK$^+$/CB$_1$R$^+$ INs (Fuccillo et

al., 2015; Ullrich et al., 1995). *Neurexin-3* conditional knockout (targeting all *Nrxn3*

isoforms) and CRISPR-mediated *Dag1* knockout both result in similar synaptic deficits

in olfactory bulb and prefrontal cortex (Trotter et al., 2023). While a Dystroglycan knock-

in mouse with reduced glycosylation that impairs Neurexin binding (*Dag1^{T190M}*) shows

normal CCK$^+$/CB$_1$R$^+$ synapse formation by immunohistochemistry, the functionality of

these synapses was not assessed by electrophysiology (Früh et al., 2016). Similar to

B4gat1$^{M155T/M155T}$ and *Fkrp$^{P448L/P448L}$* mutants, the *Dag1^{T190M}* mutation does not fully

eliminate Dystroglycan glycosylation, and therefore does not rule out the possibility that

Neurexins play a role at CCK$^+$/CB$_1$R$^+$ synapses. It is also possible that a yet

undescribed Dystroglycan interacting protein is required for initial synapse recognition,

and Nrxn-Dag1 interactions are required for subsequent synapse maturation and

maintenance only. Indeed, the majority of studies indicate that Neurexins are not

required for the initial formation of synapses, but rather regulate the maturation and

structural maintenance of synapses after they have formed (Chen et al., 2017;

Dudanova et al., 2007; Lin et al., 2023; Missler et al., 2003; Trotter et al., 2023).

Interestingly, while Dystroglycan localizes to both PV$^+$ and CCK$^+$/CB$_1$R$^+$ inhibitory

basket synapses in CA1, only the CCK$^+$/CB$_1$R$^+$ IN population was affected in the

dystroglycanopathy models (Früh et al., 2016). Presumably, PV$^+$ INs have a distinct

developmental program independent of Dystroglycan and likely require a different

postsynaptic recognition partner.

A role for the Dystrophin-Glycoprotein Complex in CCK$^+$/CB$_1$R$^+$ interneuron

development

In brain and muscle tissue, Dystroglycan forms a complex with Dystrophin and

several other proteins, collectively known as the Dystrophin Glycoprotein Complex

(DGC). Like Dystroglycan, Dystrophin is also expressed throughout the forebrain and is

associated with inhibitory synapses in multiple brain regions (Knuesel et al., 1999).

Patients with mutations in *Dystrophin* develop Duchenne Muscular Dystrophy (DMD),

and frequently exhibit cognitive impairments in the absence of brain malformations,

suggesting a general role for the DGC in synapse development and function (Jagadha

& Becker, 1988; Moizard et al., 2000; Naidoo & Anthony, 2020). A mouse model of

DMD lacking all neuronal Dystrophin isoforms (*mdx*) exhibits defects in CCK$^+$/CB$_1$R$^+$ IN

synapse development and abnormal innervation in the hippocampus, resembling the

innervation pattern we observed in *Emx1^{Cre};Dag1^{cKO}* and *Emx1^{Cre};Pomt2^{cKO}* mice in this

study (Krasowska et al., 2014). Since Dystroglycan interacts with Dystrophin through its

intracellular domain, we expected to observe similar phenotypes in mice lacking the

intracellular domain of Dystroglycan (*Dag1$^{cyto/-}$*). However, *Dag1$^{cyto/-}$* showed a milder

axon targeting defect than *Emx1^{Cre};Dag1^{cKO}* or *mdx* mice. In addition, IIH6 puncta were

normally localized to the somatodendritic compartment in *Dag1$^{cyto/-}$* mutants, suggesting

that Dystroglycan does not require interactions with Dystrophin for is localization to

somatodendritic synapses. However, Dystroglycan's synaptic localization has not been

examined in the *mdx* mutants. Clearly, additional work is required to better understand

the relationship between Dystroglycan and Dystrophin at synapses in the brain.

While the density of CCK$^+$/CB$_1$R$^+$ IN synaptic puncta was normal in *Dag1$^{cyto/-}$*

mice, synaptic function was impaired to the same level as *Emx1^{Cre};Dag^{cKO}* and

Emx1^{Cre};Pomt2^{cKO} mice, and seizure latency was reduced. Given that *Dag1$^{cyto/-}$* and

B4gat1$^{M155T/M155T}$ mutants show a similar reduction in Dystroglycan glycosylation (**Fig.**

1B-C), our observation that the functional synaptic phenotype is restricted to the

Dag1$^{cyto/-}$ mutant reinforces the notion that the intracellular domain of Dystroglycan

plays an active role in organizing essential postsynaptic signaling elements. One

possibility is that the intracellular domain of Dystroglycan is required to recruit additional

postsynaptic scaffolding elements and receptors necessary for CCK$^+$/CB$_1$R$^+$ basket

synapse function (Uezu et al., 2019). Importantly, *Dag1$^{cyto/-}$* mice did not show a cortical

migration phenotype (**Fig. 2A-D**), indicating that the functional synaptic deficits and

reduced seizure latency occurred independent of cortical malformation.

Altered inhibitory synapse development and function may contribute to

neurological symptoms in dystroglycanopathy

In addition to muscular atrophy and hypotonia, dystroglycanopathy patients often

present with central nervous system symptoms. Patients with the most severe forms of

dystroglycanopathy (FCMD, Muscle-Eye-Brain disease, and Walker-Warburg

Syndrome) exhibit structural changes including hypoplasia of the retina, brainstem and

spinal cord, cerebellar cysts, hydrocephalus, Type II lissencephaly, and microcephaly,

associated with seizures and cognitive disability (Meilleur et al., 2014; Mercuri et al.,

2009). Patients with milder forms of dystroglycanopathy may show cognitive disability

and/or seizures without gross brain malformations, suggesting that there may be

synaptic deficits independent of early neurodevelopmental processes (e.g. neuronal

migration, axon guidance) (Mercuri et al., 2009; Yang et al., 2022). The mouse models

used in this study recapitulate the full spectrum of brain malformations seen in human

patients. $Emx1^{Cre};Dag^{cKO}$ and $Emx1^{Cre};Pomt2^{cKO}$ mice show Type II lissencephaly

consistent with severe dystroglycanopathy, whereas $B4gat1^{M155T/M155T}$ and

$Fkrp^{P448L/P448L}$ mutants have relatively normal cortical development consistent with mild

dystroglycanopathy. Mutations in any of the genes involved in the glycosylation of

Dystroglycan can result in dystroglycanopathy with seizures, but the incidence and

severity of seizures is higher in patients with brain malformations (Mercuri et al., 2009;

Wang et al., 2017; Yang et al., 2022).

Mice have been used to model dystroglycanopathy for decades, however to our

knowledge the present study is the first to investigate seizure susceptibility in mouse

models of dystroglycanopathy. It is probable that the CCK^+/CB_1R^+ interneuron axon

targeting and synapse phenotypes in the mouse models described in the present study

contribute to their seizure susceptibility and open the possibility that defective inhibitory

synaptic signaling mechanisms may underlie seizures in dystroglycanopathy patients.

Although severe neuronal migration phenotypes In $Emx1^{Cre};Dag1^{cKO}$ and

$Emx1^{Cre};Pomt2^{cKO}$ mice may contribute to seizure activity, our observation that $Dag1^{cyto/-}$

mutants showed both abnormal CCK^+/CB_1R^+ synaptic function and reduced seizure

latency, with intact cortical migration, indicates that the seizure phenotype is likely

associated with synaptic defects. Supporting these results, CCK^+/CB_1R^+ interneurons in

the hippocampus are selectively lost in models of temporal lobe epilepsy with recurrent

seizures induced by pilocarpine. CCK^+/CB_1R^+ axons in CA1-3 begin to degenerate

within hours of status epilepticus, whereas PV$^+$ INs are unaffected in this model

(Whitebirch et al., 2023; Wyeth et al., 2010).

While our *B4gat1$^{M155T/M155T}$* mutants showed only a slightly reduced seizure

latency, the mutants experienced more severe seizures than the other mouse models,

resulting in death in 50% of cases (4/8 mutants compared to 0/6 fatalities among

littermate controls) (**Fig. 7 Supp. 1A**). Flurothyl-induced seizures are typically

generalized forebrain seizures; however in seizure-prone mouse models or in mice

exposed to higher concentrations of flurothyl, mice can experience a suppression of

brainstem oscillations followed by sudden death (Gu et al., 2022; Kadiyala et al., 2016).

The *B4gat1$^{M155T/M155T}$* mutation was originally identified based on a hindbrain axon

guidance phenotype, suggesting they may have currently unknown defects in brainstem

development or circuitry that could render them more susceptible to fatal brainstem

seizures (Wright et al., 2012). Because the *Dag1* and *Pomt2* mutants are forebrain-

specific conditional knockouts, (**Fig. 1 Supp. 1A**), we would not anticipate abnormal

axon guidance in the brainstem or hindbrain of these mutants. Further research on the

nature and progression of seizures observed in mouse models may have a profound

impact on our understanding of dystroglycanopathy and potential therapeutic

interventions.

Potential therapeutics for the restoration of synapse function in patients with

dystroglycanopathy

Most patients with dystroglycanopathy present with mutations in one of the 19

genes required for the glycosylation of Dystroglycan, resulting in hypoglycosylated

Dystroglycan. We have demonstrated that a mild reduction in the glycosylation of

Dystroglycan, as seen in $Fkrp^{P448L/P448L}$ and $B4gat1^{M155T/M155T}$ mutants, does not

significantly disrupt synapse function. This suggests that glycosylation may not need to

be restored to wild-type levels in order to achieve normal synapse function. Gene

replacement therapy may be well suited to treat certain forms of dystroglycanopathy by

rescuing glycosylation. AAV-mediated delivery of fully functional glycosyltransferases

has been shown to significantly improve muscle pathology and function in dystrophic

mice, however synaptic phenotypes have not been examined (Kanagawa, 2021).

Supplementation with (CDP)-ribitol, which is synthesized by *CRPPA* (previously known

as *ISPD*), can restore functional Dystroglycan glycosylation and improve muscle

function in mouse models with hypomorphic mutations in *CRPPA* or *Fkrp* (Cataldi et al.,

2018). In mice lacking functional *CRPPA* or *Fkrp* in skeletal muscle, (CDP)-ribitol can

further enhance the therapeutic impact of gene restoration (Cataldi et al., 2020).

However, whether (CDP)-ribitol treatment can improve Dystroglycan function in other

models of dystroglycanopathy, or is capable of restoring Dystroglycan glycosylation and

synaptic function in the nervous system, remains untested.

CONCLUSION

We demonstrate that Dystroglycan is critical for the postnatal development of

CCK^+/CB_1R^+ interneuron axon targeting and synapse formation/function in the

hippocampus of severe mouse models of dystroglycanopathy. Extracellular

glycosylation of Dystroglycan and intracellular interactions involving the cytoplasmic

domain are both essential for Dystroglycan's synaptic organizing role. Mice with a

partial reduction in glycosylation have relatively normal CCK^+/CB_1R^+ interneuron axon

targeting and synapse function, suggesting that even a partial restoration of

glycosylation may have some therapeutic benefit. These findings suggest that

CCK^+/CB_1R^+ interneuron axon targeting defects may contribute to cognitive

impairments and seizure susceptibility in dystroglycanopathy.

MATERIALS AND METHODS

Animal husbandry

All animals were housed and cared for by the Department of Comparative

Medicine (DCM) at Oregon Health and Science University (OHSU), an AAALAC-

accredited institution. Animal procedures were approved by OHSU Institutional Animal

Care and Use Committee (Protocol # IS00000539), adhered to the NIH *Guide for the*

care and use of laboratory animals, and provided with 24-hour veterinary care. Animal

facilities are regulated for temperature and humidity and maintained on a 12-hour light-

dark cycle and were provided food and water *ad libitum*. Animals older than postnatal

day 6 (P6) were euthanized by administration of CO_2, animals <P6 were euthanized by

rapid decapitation.

Mouse strains and genotyping

The day of birth was designated postnatal day 0 (P0). Ages of mice used for

each analysis are indicated in the figure and figure legends. Mouse strains used in this

study have been previously described and were obtained from Jackson Labs, unless

otherwise indicated (**Table 1**) (Chan et al., 2010; Cohn et al., 2002; Goebbels et al.,

2006; Gorski et al., 2002; Hu et al., 2011; Peron et al., 2015; Satz et al., 2009; Tronche

et al., 1999; Wright et al., 2012). Breeding schemas are as described in **Table 2**. Where

possible, mice were maintained on a C57BL/6 background. *Dag1$^{cyto/-}$* mice occurred at a

frequency lower than Mendelian, suggesting that a proportion of progeny die

embryonically. To increase viability of pups, the *Dag1^{cyto}* line was outcrossed to a CD-1

background for one generation. The *B4gat1* line has a mixed genetic background: it was

founded on a C3H/He background and then crossed on to C57BL/6 for future

generations. Genomic DNA extracted from toe or tail samples (Quanta BioSciences)

was used to genotype animals. Primers for genotyping can be found on the JAX

webpage or originating article. For each mouse strain, littermate controls were used for

comparison with mutant mice. For all experiments, unless otherwise noted, mice of both

sexes were used indiscriminately. See **Supplementary Table 1** for a summary of sexes

used in each experiment.

Table 1. Mouse strains

Common name	Strain name	Reference	Stock #
Dag1^{Flox}	*B6.129(Cg)-Dag1$^{tm2.1Kcam}$/J*	(Cohn et al., 2002)	009652
Dag1^{cyto}	N/A	(Satz et al., 2009)	N/A
Pomt2^{Flox}	*POMT2tm1.1Hhu/J*	(Hu et al., 2011)	017880
B4gat1^{M155T}	*B6(C3)-B4GAT1^{m1Ddg}/J*	(Wright et al., 2012)	022018
Fkrp^{P448L}	*C57BL/6NJ-Fkrp^{em1Lgmd}/J*	(Chan et al., 2010)	034659
R26$^{LSL-H2B-mCherry}$	*B6.Gt(ROSA)26Sor$^{tm1.1Ksvo}$*	(Peron et al., 2015)	023139
Emx1^{Cre}	*B6.129S2-Emx1$^{tm1(cre)Krj}$/J*	(Gorski et al., 2002)	005628
Nestin^{Cre}	*B6.Cg-Tg(Nes-cre)^{1Kln}/J*	(Tronche et al., 1999)	003771
NEX^{Cre}	*NeuroD6$^{tm1(cre)Kan}$*	(Goebbels et al., 2006)	MGI:4429523

680   **Table 2. Breeding schemes**

Breeding Scheme	Control Genotype	Mutant Genotype

Emx1$^{Cre/+}$;Dag1$^{+/-}$ x Dag1$^{Flox/Flox}$	*Emx1$^{Cre/+}$;Dag1$^{Flox/+}$*	*Emx1$^{Cre/+}$;Dag1$^{Flox/-}$*
Nestin$^{Cre/+}$;Dag1$^{+/-}$ x Dag1$^{Flox/Flox}$	*Nestin$^{Cre/+}$;Dag1$^{Flox/+}$*	*Nestin$^{Cre/+}$;Dag1$^{Flox/-}$*
NEX$^{Cre/+}$;Dag1$^{+/-}$ x Dag1$^{Flox/Flox}$	*NEX$^{Cre/+}$;Dag1$^{Flox/+}$*	*NEX$^{Cre/+}$;Dag1$^{Flox/-}$*
Emx1$^{Cre/+}$;Pomt2$^{Flox/+}$ x Pomt2$^{Flox/Flox}$	*Emx1$^{Cre/+}$;Pomt2$^{Flox/+}$*	*Emx1$^{Cre/+}$;Pomt2$^{Flox/Flox}$*
Dag1$^{cyto/+}$ x Dag1$^{+/-}$	*WT*	*Dag1$^{cyto/-}$*
B4gat1$^{M155T/+}$ x B4gat1$^{M155T/+}$	*WT*	*B4gat1$^{M155T/M155T}$*
Fkrp$^{P448L/+}$ x Fkrp$^{P448L/+}$	*WT*	*Fkrp$^{P448L/P448L}$*

Perfusions and tissue preparation

Brains from mice younger than P15 were dissected and drop fixed in 5 mLs of

4% paraformaldehyde (PFA) in phosphate buffered saline (PBS) overnight for 18-24

hours at 4°C. Mice P15 and older were deeply anesthetized using CO2 and

transcardially perfused with ice cold 0.1M PBS for two minutes to clear blood from the

brain, followed by 15 mLs of ice cold 4% PFA in PBS. After perfusion, brains were

dissected and post-fixed in 4% PFA for 30 minutes at room temperature. Brains were

rinsed with PBS, embedded in 4% low-melt agarose (Fisher cat. no. 16520100), and

sectioned at 50µm using a vibratome (VT1200S, Leica Microsystems Inc., Buffalo

Grove, IL) into 24-well plates containing 1 mL of 0.1M PBS with Sodium Azide.

Immunohistochemistry

Single and multiple immunofluorescence detection of antigens was performed as

follows: free-floating vibratome sections (50µm) were briefly rinsed with PBS, then

blocked for 1 hour in PBS containing 0.2% Triton-X (PBST) plus 10% normal goat or

donkey serum. Sections were incubated with primary antibodies (**Table 3**) diluted in

blocking solution at 4°C for 48-72 hours. For staining of Dystroglycan synaptic puncta,

an antigen retrieval step was performed prior to incubation in primary antibody. Briefly,

sections were incubated in sodium citrate solution for 15 min at 95 degrees in a water

bath. Following incubation in primary antibody, sections were rinsed with PBS then

washed with PBST three times for 20 min each. Sections were then incubated with a

cocktail of secondary antibodies (1:500, Alexa Fluor 488, 546, 647) in blocking solution

overnight at room temperature. Sections were washed with PBS three times for 20 min

each and counterstained with Hoechst 33342 (1:10,000, Life Technologies, Cat#

H3570) for 20 min to visualize nuclei. Finally, sections were mounted on slides using

Fluoromount-G (SouthernBiotech) and sealed using nail polish.

Table 3. Primary antibodies used for immunohistochemistry

Target	Host	Dilution	Source	Catalog #	RRID
α-Dystroglycan (IIH6C4)	Mouse	1:250	Millipore	05-593	AB_309828
β-Dystroglycan	Mouse	1:50	Leica Biosystems	NCL-b-DG	AB_442043
CB1R	Guinea pig	1:1000	Synaptic Systems	258-104	AB_2661870
Cux1	Rabbit	1:500	Santa Cruz Biotech	sc-13024	AB_2261231
Laminin	Rabbit	1:1000	Sigma	L9393	AB_477163
NECAB1	Rabbit	1:500	Sigma	HPA023629	AB1848014
NECAB2	Rabbit	1:500	Proteintech	12257-1-AP	AB_2877841
NeuN	Mouse	1:250	Millipore	MAB377	AB_2298772
Parvalbumin	Rabbit	1:1000	Swant	PV27	AB_2631173
Parvalbumin	Mouse	1:50	Swant	235	AB_10000343
Somatostatin	Rabbit	1:2000	Peninsula Labs	T-4103	AB_518614
Tbr1	Rabbit	1:500	Millipore	AB10554	AB_10806888
VGAT	Rabbit	1:500	Synaptic Systems	131-003	AB_887869
VGAT	Guinea Pig	1:500	Synaptic Systems	131-005	AB_1106810
VGlut3	Rabbit	1:1000	Synaptic Systems	135-203	AB_887886
VIP	Rabbit	1:1000	ImmunoStar	20077	AB_572270

Microscopy

Imaging was performed on either a Zeiss Axio Imager M2 fluorescence upright

microscope equipped with an Apotome.2 module or a Zeiss LSM 980 laser scanning

confocal build around a motorized Zeiss Axio Observer Z1 inverted microscope with a

Piezo stage. The Axio Imager M2 uses a metal halide light source (HXP 200 C),

Axiocam 506 mono camera, and 10X/0.3 NA EC Plan-Neofluar, 20X/0.8 NA Plan-

Apochromat objectives. The LSM 980 confocal light path has two multi-alkali PMTs and

two GaAsP PMTs for four track imaging. Confocal images were acquired using a

63X/1.4 NA Plan-Apochromat Oil DIC M27 objective. Z-stack images were acquired and

analyzed offline in ImageJ/FIJI (Schindelin et al., 2012) or Imaris 9.8 (Oxford

Instruments). Images used for quantification between genotypes were acquired using

the same exposure times. Brightness and contrast were adjusted in FIJI to improve

visibility of images for publication. Figures were composed in Adobe Illustrator 2023

(Adobe Systems).

Image Quantification

For imaging experiments, 4-8 images were acquired from 2-4 coronal sections per

animal, and at least three animals per genotype were used for analysis.

Cortical Lamination

Images of somatosensory cortex were acquired using a 10X objective on a Zeiss Axio

Imager M2. 4µm z-stacks covering 16µm were acquired and multiple tiles were stitched

together. Maximum projections were used for analysis. In FIJI, the straight line tool with

a 300µm line width was used to measure the fluorescence profile from corpus callosum

to pial surface. Background fluorescence was determined as the average fluorescence

of the 20 darkest pixels; background was then subtracted from all points. The cortical

distance was broken into 10 bins and average fluorescence within each bin was

compared between genotypes.

Hippocampal CA1 CB$_1$R and PV Distribution

Images of dorsal hippocampal CA1 were acquired using a 20X objective on a Zeiss

Axio Imager M2. Maximum projection images of 0.6µm z-stacks covering 9µm were

analyzed in FIJI. The straight line tool with a 300µm line width was used to measure the

fluorescence profile within SO, SP, and SR of CA1, avoiding Parvalbumin[+] cell bodies.

Background fluorescence was determined as the average fluorescence of the 50

darkest pixels; background was then subtracted from all points. The thickness of SP

was determined using Hoechst fluorescence. Average fluorescence within SO/SP/SR

was compared between genotypes.

Interneuron Cell Counts in CA1

Images of dorsal hippocampal CA1 were acquired using a 10X objective on a Zeiss

Axio Imager M2. Maximum projection images of 4µm z-stacks covering 40µm were

analyzed in FIJI. Immunolabeled NECAB1/NECAB2/PV cell bodies were counted if they

were within 100µm of *stratum pyramidale*. The freehand line tool was used to measure

the length of *stratum pyramidale*. Cell number was normalized to the length of *stratum*

pyramidale present in the analyzed region.

Hippocampal CB$_1$R/PV/VGAT Density and Co-localization

Images of dorsal hippocampal CA1 were acquired using a 63X objective on a Zeiss

LSM 980. 0.2µm z-stacks covering 3µm were analyzed in Imaris. Hoechst fluorescence

was used to determine the bounds of SP. The Imaris Spots function was used to

determine the location of synaptic puncta in 3-dimensional space. Synaptic puncta were

deemed to be co-localized if they were within 1µm of each other.

Western Blot

Cortex or hippocampus was dissected and solubilized in 1 mL of lysis buffer containing

100mM NaCl, 50nM Tris, 2.5mM CaCl$_2$, 1% Triton X-100, 1% n-Octyl-β-D-

glucopyranoside, and protease inhibitors. Lysate was incubated at 4°C for 1 hour and

then spun at 12,500g for 25 minutes. Supernatant containing 3,000µg (cortex) or

2,000µg (hippocampus) of protein (as determined by Pierce BCA Protein Assay) was

applied to agarose-bound Wheat Germ Agglutinin (WGA) (Vector Labs) overnight at

4°C. Beads were washed 3X in TBS and boiled in 1X LDS sample buffer with 2-

Mercaptoethanol (1:100) for 5 minutes. Samples were run on a 4-15% gradient

polyacrylamide gel at 100V for 75 minutes and then transferred to a PVDF membrane

(100V for 100 minutes). For immunoblotting, membranes were blocked in 5% milk TBST

and then incubated overnight at 4°C in 5% milk TBST containing primary antibody.

Antibodies used: α-Dystroglycan (IIH6C4) (Millipore cat. no. 05-593, mouse IgM, 1:500),

MANDAG2 (DSHB cat. no. 7D11, mouse IgG1, 1:500), β3-tubulin (Cell Signaling

Technology cat. no. 5568, rabbit, 1:2000). Membranes were washed 3X in TBST and

incubated on fluorescent IRDye secondary antibody (1:10,000, LI-COR) in 5% milk

TBST for 1 hour at room temperature. Membranes were imaged using a LI-COR

Odyssey CLx 0918 imager and signal analyzed using LI-COR Image Studio Lite version

5.2.

Electrophysiology

For acute slice preparation, mice were deeply anesthetized in 4% isoflurane and

subsequently injected with a lethal dose of 2% 2, 2, 2-Tribromoethanol in sterile water

followed by transcardial perfusion with 10 mL ice cold cutting solution containing the

following (in mM): 93 NMDG, 2.5 KCl, 1.2 NaH_2PO_4, 30 $NaHCO_3$, 20 HEPES, 24

glucose, 5 Na Ascorbate, 2 Thiourea, 3 Na Pyruvate, 13 N-Acetyl Cysteine, 1 Kynurenic

acid, 10 $MgSO_4$, 0.5 $CaCl_2$; pH 7.3, 300-340mmol/kg. After rapid decapitation, the brain

was briefly submerged in ice cold cut solution bubbled with carbogen (95% oxygen, 5%

CO2) and then sectioned into 300µm sagittal sections (Leica VT1200S vibratome) in

bubbled ice-cold cut solution. Slices were recovered in 37°C cut solution, bubbled, for

15 minutes followed by 1 hour in room temperature recording ACSF (containing, in mM:

125 NaCl, 25 $NaHCO_3$, 1.25 NaH_2PO_4, 3 KCl, 25 D-Glucose, 2 $CaCl_2$, 1 $MgCl_2$) with an

osmolarity of 310-320mmol/kg and supplemented with 1.5mM Na Ascorbate, bubbled.

CA1 pyramidal cells were patched in whole cell configuration using 3-5MΩ

borosilicate glass pipettes filled with high chloride internal solution containing the

following (in mM): 125 CsCl, 2.5 $MgCl_2$, 0.5 EGTA, 10 HEPES, 2 Mg-ATP, 0.3 Na-GTP,

5 QX-314; pH 7.2, 300mmol/kg. Pipettes were wrapped in parafilm to reduce capacitive

currents. Cells were voltage clamped at -70mV and continuously superfused with 2-3

mL/min bubbled recording ACSF (310-320mmol/kg) containing 10µM NBQX to block

excitatory transmission. Recordings were performed at 34°C. After 5 minutes of

spontaneous IPSC (sIPSC) recording, 10µM Carbachol was added to the perfusate and

another 5 minutes of sIPSC were recorded. Slices were discarded after exposure to

Carbachol. Signals were amplified with an AxoPatch 200B amplifier (Molecular

Devices), low-pass filtered at 5 kHz, and digitized and sampled at 10 kHz with a NIDAQ

analog-to-digital board (National Instruments). Data were acquired and analyzed using

a custom script in Igor Pro 8 (Wavemetrics). A hyperpolarizing step of -10mV was

applied before each sweep to monitor input resistance, series resistance, and measure

cell capacitance. Series resistance was not compensated and was maintained below

20MΩ. Cells were excluded if series resistance changed by more than 25%.

To calculate the proportion of cells that responded to Carbachol, cells were

sorted into "responsive" and "non-responsive" categories. Cells were categorized as

responsive if sIPSC frequency increased by 20% or more with the addition of

Carbachol. If sIPSC frequency in a cell changed by less than 20% or less than 0.5Hz it

was deemed non-responsive.

Flurothyl Seizure Induction

Mice aged P40-P55 were used for the flurothyl-induced seizure susceptibility assay to

determine seizure threshold. Briefly, mice were placed in an enclosed glass chamber

equipped with a vaporization chamber out of reach of the mouse. Volatile liquid 10% Bis

(2,2,2-Trifluorotheyl) Ether (Millipore Sigma cat. no 287571) in 95% EtOH was delivered

to the vaporization chamber at a rate of 6 mL/hour. Seizure latency was determined as

the amount of time until generalized tonic-clonic seizure (TCS). Upon exhibiting TCS,

animals were immediately removed from the chamber and returned to their home cage,

whereupon seizures ceased rapidly. Sample size was determined using power analysis

as described below. The *Emx1^{Cre};Dag1* experimental groups were powered sufficiently

to determine sex differences. Because no sex difference was found (**Fig. 7 Supp. 1C**),

sexes were pooled for the remaining experiments. For statistical tests, outliers were

excluded. Outliers were calculated as follows: first, the interquartile range (IQR) was

calculated and multiplied by 1.5. This 1.5*IQR value was subtracted from the 25%

quartile (Q1) and added to the 75% quartile (Q3). Points outside of the range Q1 -

1.5*IQR < x < Q3 + 1.5*IQR were categorized as outliers and indicated as such on all

graphs. This was done to remove bias from extreme outliers observed in this

experiment.

Statistical analysis

Phenotypic analyses were conducted using tissue collected from at least three

mice per genotype from at least two independent litters. The number of mice and

replicates used for each analysis ("N") are indicated in **Supplementary Table 1**. Power

analysis using pilot data was used to determine samples sizes with $\alpha = 0.05$ and $\beta =$

0.80. Phenotypes were indistinguishable between male and female mice and were

analyzed together. In many cases, highly penetrant phenotypes revealed the genotypes

of the mice and no blinding could be performed. For comparisons between two groups,

significance was determined using a two-tailed Students t-test. For comparisons

between more than two groups, significance was determined using a 2-way ANOVA

with Tukey HSD post-hoc analysis. Statistical significance was set at $\alpha = 0.05$ ($p < 0.05$)

and data presented as means ± SEM. Statistical analyses and data visualization were

performed in R (version 4.0.2).

DATA AVAILABILITY

The data that support the findings of this study are available from the corresponding

author upon reasonable request.

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Figure 1. Dystroglycan synaptic localization and glycosylation in mouse models of dystroglycanopathy. (A) Schematic depiction of Dystroglycan in different mouse models. The IIH6 antibody recognizes the matriglycan repeats on extracellular αDag1. Hippocampal CA1 of P30 mice immunostained for Dystroglycan glycosylation (IIH6, green) and nuclear marker Hoechst (blue) show puncta of glycosylated Dystroglycan localized to the perisomatic region of pyramidal cells and to blood vessels (magenta arrowheads); scale bar = 50μm. Lower panels show cell bodies in SP; scale bar = 25μm. CA1 layers: SO, *stratum oriens*; SP, *stratum pyramidale*; SR, *stratum radiatum*.

(B) WGA-enriched lysates from P0 forebrain were immunoblotted for IIH6, β-Dag1, and β-tubulin. **(C-D)** Quantification of immunoblot in **(B)**. Error bars show mean + SEM.

Figure 1 Supplement 1. *Emx1^{Cre}* **drives recombination in forebrain excitatory neurons and astrocytes, but not interneurons or microglia. (A)** Left; endogenous red fluorescence in the forebrain of P60 *Emx1^{Cre};R26$^{LSL-H2B-mCherry}$* reporter mice (scale bar = 1mm). Right; coronal section of the forebrain from *Emx1^{Cre};R26$^{LSL-H2B-mCherry}$* mice showing robust nuclear mCherry signal (magenta) in the cortex and hippocampus (scale bar = 500μm). **(B-E)** mCherry⁺ nuclei shown with markers of multiple cell types in the brain including astrocytes (GFAP, green) **(B)**, microglia (Iba1, green) **(C)**, and neurons (NeuN, green) **(D)** (scale bar = 100μm). Insets show enlarged images of mCherry⁺ nuclei with cell type markers (scale bar = 20μm). **(E)** mCherry⁺ nuclei with markers for different interneuron subtype markers (yellow arrowheads) (scale bar = 100μm) (VIP = Vasoactive intestinal peptide, NECAB = Neuronal calcium-binding protein 1, SOM = Somatostatin). *CA1 layers: SO, stratum oriens; SP, stratum pyramidale; SR, stratum radiatum.*

Figure 1 Supplement 2. Dystroglycan glycosylation is required for synaptic localization. (A) Immunostaining for matriglycan (IIH6, green) and β-Dag1 (magenta) in CA1 pyramidal cells of WT controls, *Emx1^Cre^;Dag1^cKOs^*, *Emx1^Cre^;Pomt2^cKOs^*, and *Dag1^cyto/-^* mutants. Scale bars = 25μm. **(B)** WGA-enriched lysates from P21-P30 hippocampus were immunoblotted for IIH6 and β-Dag1. **(C-D)** Quantification of immunoblot in **(B)**. Error bars show mean + SEM.

Figure 2. Dystroglycan is required for cortical neuron migration in a glycosylation-dependent manner and independent of intracellular interactions.
Immunostaining for cortical layer markers **(A)** Cux1 (layers 2-4) and **(B)** Tbr1 (layers 3 and 6) in P30 somatosensory cortex (scale bar = 200µm). Layer markers are shown in green. Nuclear marker Hoechst is shown in magenta. Quantification of fluorescence intensity of layer markers shown for **(C)** Cux1 and **(D)** Tbr1. Shaded regions of intensity profile illustrate ± SEM. See **Supplementary Table 1** for Ns. *Significance: * = p < 0.05, ** = p < 0.01, *** = p < 0.001, NS = p ≥ 0.05. Abbreviations: CC, corpus callosum; A.U., arbitrary units.*

Figure 2 Supplement 1. Cortical migration is disrupted at midline of _B4gat1$^{M155T/M155T}$_ but not _Fkrp$^{P448L/P448L}$_ mutants. (A) Immunostaining for cortical layer marker Cux1 (layers 2-4) in P30 somatosensory cortex (scale bar = 500μm). Cux1 is shown in green. Nuclear marker Hoechst is shown in magenta. Cortical migration is normal in both _B4gat1_ and _Fkrp_ point mutants except at midline, where the _B4gat1_ mutants show a migration phenotype not seen in the _Fkrp_ point mutants. This phenotype was observed with 100% penetrance in the _B4gat1_ mutants and 0% in the _Fkrp_ mutants.

Figure 2 Supplement 2. Laminin immunoreactivity in adult neocortex appears discontinuous in *Dag1* mutants. (A-C) Immunostaining for ECM protein Laminin (green). Nuclear marker Hoechst is shown in blue. Scale bar = 1000μm.

Figure 3. *Dag1* **is required for CCK$^+$/CB$_1$R$^+$ basket IN perisomatic axon targeting in** ***stratum pyramidale*** **of hippocampal CA1-3. (A)** Nuclear marker Hoechst (upper panels) shows hippocampal morphology. Granule cell migration is disrupted in dentate gyrus of *Emx1^{Cre};Dag1^{cKOs}* and *Emx1^{Cre};POMT2^{cKOs}* (yellow arrows). CA1-3 gross morphology is normal in all models. CB$_1$R immunostaining (lower panels) shows abnormal CCK$^+$/CB$_1$R$^+$ basket interneuron targeting in CA1-3 to varying degrees across models (scale bar = 400µm). **(B)** Higher magnification view of CB$_1$R immunostaining in CA1 (scale bar = 50µm). **(C)** Quantification of CA1 CB$_1$R fluorescence intensity profile. Shaded regions of intensity profile illustrate ± SEM. Gray region highlights SP. See **Supplementary Table 1** for Ns. *Significance: * = p < 0.05, ** = p < 0.01, *** = p < 0.001, NS = p ≥ 0.05. Abbreviations: A.U., arbitrary units; SO, stratum oriens; SP, stratum pyramidale; SR, stratum radiatum.*

Figure 3 Supplement 1. CCK⁺/CB₁R⁺ IN axon targeting phenotypes in hippocampal CA1 of various *Dag1^cKOs*. CB₁R immunostaining in hippocampal CA1 of control mice (left panels) and *Dag1^cKOs* (right panels) generated using *Emx1^Cre* (forebrain progenitors, E10.5) **(A)**, *Nestin^Cre* (neural stem cells in the central and peripheral nervous systems, E11.5) **(B)**, and *NEX^Cre* (forebrain postmitotic excitatory neurons, E12.5) **(C)**. Scale bar = 50μm. *Abbreviations: SO, stratum oriens; SP, stratum pyramidale; SR, stratum radiatum.*

Figure 3 Supplement 2. CCK⁺/CB₁R⁺ IN cell numbers are unchanged in
Emx1^{Cre};Dag1^{cKOs}. **(A)** Immunostaining in hippocampal CA1 for NECAB1 (left) and PV (right) in *Emx1^{Cre};Dag1^{Ctrl}* and *Emx1^{Cre};Dag1^{cKO}* mice. NECAB1 labeling is evident in PV⁺ cells (example shown in blue inset) and in an additional PV⁻ population that contains the CCK⁺/CB₁R⁺ population (example shown in magenta inset). The average number of NECAB1⁺;PV⁻ cells per 100μm of SP is quantified in **(B)**. Immunostaining for NECAB2 **(C)** and PV **(D)** with cell number quantification in **(E)** and **(F)**. Scale bar = 100μm. Error bars show mean + SEM. See **Supplementary Table 1** for Ns.
*Significance: * = p < 0.05, ** = p < 0.01, *** = p < 0.001, NS = p ≥ 0.05. Abbreviations: SP, stratum pyramidale; PV, parvalbumin.*

Figure 3 Supplement 3. Parvalbumin⁺ basket INs do not require *Dag1* for proper axon targeting in hippocampal CA1. (A) Parvalbumin (PV) immunostaining in P30 hippocampal CA1 shows that PV⁺ basket interneurons exhibit normal distribution in CA1 for all genetic models except for an increase in PV intensity within *stratum pyramidale* of *Emx1^Cre^;Dag1^cKOs^* (scale bar = 50μm). **(B)** Quantification of CA1 PV fluorescence intensity profile. Shaded regions of intensity profile illustrate ± SEM. Gray region highlights SP. See **Supplementary Table 1** for Ns. *Significance: * = p < 0.05, ** = p < 0.01, *** = p < 0.001, NS = p ≥ 0.05. Abbreviations: A.U., arbitrary units; SO, stratum oriens; SP, stratum pyramidale; SR, stratum radiatum.*

Figure 3 Supplement 4. Altered CB$_1$R expression in cortex and basolateral amygdala of *Dag1* and *POMT2* mutants. (A) CB$_1$R immunostaining in P30 coronal sections showing somatosensory cortex (Ctx) and CA1 of hippocampus (Hipp) (scale bar = 400µm). **(B)** CB$_1$R immunostaining (green) shown with nuclear marker Hoechst (magenta) in basolateral amygdala (BLA) (scale bar = 250µm).

Figure 4. *Dag1* is required for CCK⁺/CB₁R⁺ IN axon targeting during early postnatal development. (A) Immunostaining for CB₁R⁺ axon terminals (green) in the hippocampus of *Emx1^Cre^;Dag1* controls (left) and cKOs (right) at ages P5-P30. Nuclear marker Hoechst is shown in magenta. White arrowheads indicate migration errors in dentate granule cells *Emx1^Cre^;Dag1^cKO^* mice. Scale bar = 500μm. **(B)** Higher magnification images of CB₁R⁺ axon terminals in CA1 of *Emx1^Cre^;Dag1* controls (left) and cKOs (right) at ages P5-P30. Scale bar = 100μm. **(C)** Quantification of CB₁R fluorescence intensity profile in CA1. Shaded regions of intensity profile illustrate ± SEM. Gray region highlights SP. See **Supplementary Table 1** for Ns. *Significance: * = p < 0.05, ** = p < 0.01, *** = p < 0.001, NS = p ≥ 0.05. Abbreviations: A.U., arbitrary units; SO, stratum oriens; SP, stratum pyramidale; SR, stratum radiatum.*

Figure 5. *Dag1* and *Pomt2* cKOs exhibit impaired CB1R⁺ basket synapse formation in *stratum pyramidale* of hippocampal CA1. P30 coronal sections

immunostained for **(A)** CB_1R and **(B)** VGAT in hippocampal CA1; merged image in **(C)** shows CB_1R in magenta and VGAT in green. (A-C) Scale bar = 50µm. (Higher magnification view of SP in **(C')**; scale bar = 10µm.) **(D)** Quantification of VGAT puncta density in SP expressed as a percent of control. **(E)** Quantification of CB_1R puncta density in SP expressed as a percent of control. **(F)** Quantification of co-localization between VGAT and CB_1R in SP to estimate putative CB_1R^+ basket cell synapse formation. Error bars show mean + SEM. (For quantification of puncta densities and co-localization in SO and SR see **Fig. 5 Supp. 1**.) See **Supplementary Table 1** for Ns. *Significance: * = $p < 0.05$, ** = $p < 0.01$, *** = $p < 0.001$, NS = $p \geq 0.05$. Abbreviations: SO, stratum oriens; SP, stratum pyramidale; SR, stratum radiatum.*

Figure 5 Supplement 1. Extended quantification of images in Figure 5A-C.
Quantification within hippocampal CA1 SO and SR regions and all regions pooled
together. **(A)** Quantification of VGAT puncta density expressed as a percent of control.
(B) Quantification of CB_1R puncta density expressed as a percent of control. **(C)**
Quantification of co-localization between VGAT and CB_1R to estimate putative CB_1R^+
basket cell synapse formation. Error bars show mean + SEM. (To see quantification of
puncta densities and co-localization in SP see **Fig. 5D-F**.) See **Supplementary Table 1**

for Ns. *Significance: * = p < 0.05, ** = p < 0.01, *** = p < 0.001, NS = p ≥ 0.05.*
Abbreviations: SO, stratum oriens; SP, stratum pyramidale; SR, stratum radiatum.

Figure 5 Supplement 2. *Dag1* and *Pomt2* cKOs exhibit increased PV⁺ basket synapse formation in *stratum pyramidale* of hippocampal CA1. P30 coronal sections immunostained for **(A)** PV and **(B)** VGAT in hippocampal CA1; merged image

in **(C)** shows PV in magenta and VGAT in green. Yellow arrows indicate PV$^+$ interneuron cell bodies. (A-C) Scale bar = 50µm. (Higher magnification view of SP in **(C')**; scale bar = 10µm.) **(D)** Quantification of PV puncta density in SP expressed as a percent of control. **(E)** Quantification of co-localization between VGAT and PV in SP to estimate putative PV$^+$ basket synapse formation. Error bars show mean + SEM. (To see quantification of puncta densities and co-localization in SO and SR see **Fig. 5 Supp. 2**.) See **Supplementary Table 1** for Ns. *Significance: * = p < 0.05, ** = p < 0.01, *** = p < 0.001, NS = p ≥ 0.05. Abbreviations: PV, parvalbumin; SO, stratum oriens; SP, stratum pyramidale; SR, stratum radiatum.*

Figure 5 Supplement 3. Extended quantification of images in Fig. 5 Supp. 2A-C. Quantification within hippocampal CA1 SO and SR regions and all regions pooled together. **(A)** Quantification of PV puncta density expressed as a percent of control. **(B)** Quantification of co-localization between VGAT and PV to estimate putative PV⁺ basket cell synapse formation. Error bars show mean + SEM. (To see quantification of puncta densities and co-localization in SP see **Fig. 5 Supp. 2D-E**.) See **Supplementary Table 1** for Ns. *Significance: * = p < 0.05, ** = p < 0.01, *** = p < 0.001, NS = p ≥ 0.05. Abbreviations: PV, parvalbumin; SO, stratum oriens; SP, stratum pyramidale; SR, stratum radiatum.*

Figure 6. *Dag1* is required for CCK⁺/CB₁R⁺ IN synapse function in hippocampal CA1 in a manner dependent on both glycosylation and intracellular interactions. **(A)** Representative traces showing 15 seconds of sIPSC recordings at baseline (top) and after the addition of carbachol (bottom). **(B)** Quantification of average sIPSC frequency at baseline and after the addition of carbachol. **(C)** Quantification of the change in sIPSC frequency with the addition of carbachol. Error bars show mean + SEM. See **Supplementary Table 1** for Ns. *Significance: * = p < 0.05, ** = p < 0.01, *** = p < 0.001, NS = p ≥ 0.05. Abbreviations: sIPSC, spontaneous inhibitory postsynaptic current; CCh, carbachol.*

Figure 6 Supplement 1. Additional quantification of sIPSC recordings. (A) Quantification of average sIPSC amplitude at baseline and after the addition of carbachol. Error bars show mean + SEM. **(B)** Quantification of the proportion of carbachol-sensitive cells within each genotype. Non-responsive cells are shown in lighter color, responsive cells are shown in darker color. See **Supplementary Table 1** for Ns. *Significance: * = p < 0.05, ** = p < 0.01, *** = p < 0.001, NS = p ≥ 0.05. Abbreviations: sIPSC, spontaneous inhibitory postsynaptic current; CCh, carbachol.*

Figure 7. Reduced seizure induction threshold in models of dystroglycanopathy.
(A) Quantification of latency (in seconds) to generalized tonic clonic seizure upon exposure to 10% flurothyl delivered at a constant rate. Open points denote statistical outliers. See **Supplementary Table 1** for Ns. *Significance: * = p < 0.05, ** = p < 0.01, *** = p < 0.001, NS = p ≥ 0.05.*

Figure 7 Supplement 1. Extended seizure induction threshold data.
(A) Proportion of mice that died as a direct result of a flurothyl-induced seizure.
Survivors are depicted in darker colors, fatalities in lighter colors. **(B)** To minimize the
number of animals needed for this experiment, certain genotypes were pooled together.
Here we show that pooled genotypes are not different. Statistical tests were run where
Ns were sufficient to provide meaningful comparison. **(C)** Seizure latencies split by sex.
Note: only the *Emx1^{Cre};Dag1* group is powered sufficiently to statistically compare
sexes. Open points denote statistical outliers. Error bars show mean + SEM.