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Prepulse Inhibition and Genetic Mouse Models of Schizophrenia

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Abstract

Mutant mouse models related to schizophrenia have been based primarily on the pathophysiology of schizophrenia, the known effects of antipsychotic drugs, and candidate genes for schizophrenia. Sensorimotor gating deficits in schizophrenia patients, as indexed by measures of prepulse inhibition of startle (PPI), have been well characterized and suggested to meet the criteria as a useful endophenotype in human genetic studies. PPI refers to the ability of a non-startling “prepulse” to inhibit responding to the subsequent startling stimulus or “pulse.” Because of the cross-species nature of PPI, it has been used primarily in pharmacological animal models to screen putative antipsychotic medications. As techniques in molecular genetics have progressed over the past 15 years, PPI has emerged as a phenotype used in assessing genetic mouse models of relevance to schizophrenia. In this review, we provide a selected overview of the use of PPI in mouse models of schizophrenia and discuss the contribution and usefulness of PPI as a phenotype in the context of genetic mouse models. To that end, we discuss mutant mice generated to address hypotheses regarding the pathophysiology of schizophrenia and candidate genes (i.e., hypothesis-driven). We also briefly discuss the usefulness of PPI in phenotype-driven approaches in which a PPI phenotype could lead to “bottom up” approaches of identifying novel genes of relevance to PPI (i.e., hypothesis-generating).

Keywords

Prepulse inhibition; startle; schizophrenia; mouse models

I. Introduction

Prepulse inhibition (PPI) of startle is a cross-species measure that refers to the ability of a non-startling “prestimulus” to inhibit the response to a startling stimulus ([96]; neurobiological reviews [64,190]). There have been numerous reports of PPI deficits in schizophrenia patients (for review see [19,197]), their unaffected first degree relatives [29], and patients with schizotypal personality disorder [28]. In addition to decreased PPI observed in schizophrenia patients, several other neuropsychiatric disorders are associated with decreased PPI, including Obsessive-Compulsive Disorder [189], Tourette’s syndrome [192], Huntington’s disease [195], manic bipolar patients [153], Panic Disorder [129], and adults with autism [154]. Thus, while there are several neuropsychiatric disorders that display decreased PPI compared to normal controls, PPI deficits in schizophrenia patients are the best characterized and the most widely replicated [19,114,128,130,197].

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While the meaning of deficient or reduced PPI for an organism has been debated, Swerdlow et al. (2008) have argued persuasively that it is a useful psychophysiological process for basic studies in humans and animals to probe neural circuitry and as a pharmacological screen. Additionally, PPI of startle has been suggested as a potentially useful endophenotype with which to understand the genetics of schizophrenia [18], meeting the criteria outlined for a viable endophenotype by Turetsky and colleagues [205]. Specifically, the endophenotype should be heritable, present in unaffected relatives, associated with a disorder with good test re-test reliability, able to be measured rapidly and easily, and have a discrete neurobiological basis that is related to the pathophysiology and genetics of a disease [205]. Hence, many in the field of schizophrenia genetics have focused primarily on neurophysiological measures such as PPI, P50 auditory evoked suppression, antisaccade eye movement, mismatch negativity, and P300 event related potential [205]. The assertion that PPI may be a useful endophenotype in genetic studies of schizophrenia, combined with the observation that PPI has a strong genetic component in mice [55], suggests that PPI may be a useful behavioral phenotype to consider in genetic mouse models related to schizophrenia. While there are certainly many other symptoms and deficits observed across the heterogeneous group of patients with schizophrenia, PPI appears to be a viable endophenotype for genetic studies and thus a reasonable approach to investigate in animal models of the genetics of schizophrenia. Mutant mouse models related to schizophrenia have been based primarily on the pathophysiology of schizophrenia, the known effects of antipsychotic drugs, and candidate genes for schizophrenia. In this review, we provide a selected overview of PPI in mouse models of schizophrenia and discuss the contribution and usefulness of PPI as a phenotype in the context of genetic mouse models. In a 2002 review of genetic mouse models of PPI, Geyer et al. [66] summarize studies of strain differences in PPI, genetic mutants, and the pharmacology of PPI in mice. More recently, there have been two particularly relevant reviews on mouse models of susceptibility genes for schizophrenia [143] and mouse models of altered PPI [197]. Hence, in order to avoid redundancy with these previous reviews, in the current review we highlight a few of the approaches to genetic mouse models of schizophrenia and discuss some of the important caveats to these approaches. To that end, we discuss mutant mice generated to address hypotheses regarding the pathophysiology of schizophrenia and candidate genes (i.e., hypothesis driven). We also discuss the usefulness of PPI in phenotype-driven approaches in which a PPI phenotype could lead to “bottom up” approaches of identifying novel genes of relevance to PPI (i.e., hypothesis-generating).

How does prepulse inhibition relate to symptoms of schizophrenia?

Many reports in the literature argue that PPI in animals models the positive symptoms of schizophrenia. This conceptualization stems primarily from the observation that drug-induced deficits in PPI are produced by psychotomimetic drugs such as amphetamine and PCP, and that drug-induced PPI deficits are reversed by first generation antipsychotics, which are all dopamine D₂ receptor antagonists. In a recent review, Jones et al. [103] nicely outline the animal models that map onto the clinical symptoms of schizophrenia and accurately point out that there are no suitable animal analogs of hallucinations or delusions. Jones et al. [103] do suggest that two other “positive symptoms”, psychomotor agitation and grossly disorganized behavior, may be assessed in animals through measures of locomotor response to novelty and patterns of motor activity, respectively. The misconception that PPI is a measure of the positive symptoms of schizophrenia most likely stems from the fact that models of PPI deficits (e.g., pharmacological disruptions) have been relatively successful in predicting antipsychotic medications, which are fairly effective at treating the positive symptoms of schizophrenia and less effective, if at all, at treating the negative symptoms and cognitive deficits in schizophrenia. Historically, of course, most drug development efforts have focused on the identification of antipsychotic treatments for the positive symptoms of schizophrenia, given that only these criteria were used to evaluate potential treatments for use in patients with schizophrenia.

Attempts to correlate PPI deficits with positive and negative symptoms have yielded mixed results [200]. Some studies have reported negative correlations between PPI and thought disorder [139,151,152] or distractibility [109] in schizophrenia. In a recent study comparing cognitive function with PPI in over 300 subjects, there were no correlations between PPI and cognition as measured by traditional “pen and paper” tests (i.e., Wisconsin Card Sorting Task [WCST], California Verbal Learning Task, etc.), however, there was a positive relationship between PPI and Global Assessment of Function (GAF) and Independent Living scales [193]. Nevertheless, studies assessing behavioral measures reflecting cognitive constructs have demonstrated relationships to PPI performance. For example, converging evidence indicates that PPI is correlated with strategy formation and execution time in the Cambridge Neuropsychological Test Automated Battery (CANTAB) in healthy controls [12,43,68], a finding which should be further examined in patients with schizophrenia. Further work is needed to specify the aspect of cognitive function that might be best related to gating processes such as PPI [215]. For example, the CNTRICS (Cognitive Neuroscience measures of Treatment Response of Impaired Cognition in Schizophrenia) program funded by the National Institute of Mental Health considered PPI to provide a measure of the cognitive construct of “gain control” as a specific aspect of the perceptual abnormalities seen in patients with schizophrenia [83]. The series of CNTRICS workshops concluded that PPI may have utility as a biomarker for use in proof of concept studies of potential treatments for the cognitive deficits in schizophrenia that are not ameliorated by existing antipsychotic drugs.

Utility of prepulse inhibition measures in genetic models of schizophrenia

For the purpose of evaluating a genetic mouse model of schizophrenia, the more useful comparison to make is not between PPI and specific symptoms of schizophrenia but rather the relationship between a gene and the observable dependent measure, i.e., PPI. As mentioned above, PPI has been suggested to meet the criteria as an endophenotype for genetic studies of schizophrenia [205]. The approach of using endophenotypes in schizophrenia in genetic studies has greatly strengthened the ability to conduct cross-species translational studies by providing specific observables or endophenotypes for study in experimental animals (reviewed in [65], [80]). Useful endophenotypes in this context are measures that are observed in humans and can be measured in mice.

Hints to the role a gene may play in neural circuitry of PPI—Genetic manipulations have the potential to increase our understanding of the neural circuitry of neuropsychiatric disorders. A PPI deficit could indicate that the gene may be involved in the neural circuitry known to modulate PPI (e.g., cortical, limbic, striatal [190]); in other words it could function as a “surrogate measure for neural processes” as Swerdlow et al. [197] argue. For example, if a mouse is developed for a schizophrenia candidate gene with a relatively unknown function (or at least not an obvious relationship to schizophrenia pathology) and this mouse exhibits a PPI deficit, this may be an indication that limbic or striatal circuitry is altered. While a PPI deficit per se is not indicative of altered striatal or limbic circuitry, the presence of the deficit may suggest that these brain regions are affected by the genetic manipulation and provide a reasonable starting place for further hypothesis testing regarding the neurobiological implications of the genetic manipulation. Of course any evaluation of a PPI phenotype should be considered in the context of a thorough assessment of physical and sensory abnormalities (e.g., hearing loss), as pointed out in [66].

A pharmacological screen—Mutant mouse models offer the opportunity to screen putative antipsychotics that may involve a novel target. Most pharmacological studies of PPI are based primarily on the ability of a drug (e.g., dopamine D₂ antagonist) to reverse a drug-induced deficit in PPI (e.g., D₂ agonist; [64]). This approach can lead to what some have called “receptor tautology,” meaning that a model based on the disruptive effects of a dopamine D₂

agonist may only be able to predict drugs that act as D₂ receptor antagonists. Using mutant mice to screen for putative antipsychotics may provide a means to develop novel drug targets. Several important examples of mutant mice being used to test putative antipsychotics are reviewed in subsequent sections.

A tool to study gene-environment interactions—Based on the diathesis-stress model of schizophrenia, which postulates that a genetic susceptibility coupled with environmental factors may be required for the full manifestation of the disease [79], studies of gene-environment interactions may be particularly informative for schizophrenia. Three ways in which genetics and environmental manipulations have been utilized in genetic mouse models are: (1) using a mutant (e.g., knockout, KO) to delineate the mechanism of an environmental manipulation; (2) rescuing a phenotype in a mutant with an environmental manipulation; or (3) potentiating or unmasking a phenotype in a genetic mutant with an environmental manipulation (i.e., addressing the two-hit model of schizophrenia). There are a few examples in which PPI has been a useful endpoint with which to assess gene-environment interactions in mouse models of schizophrenia. For example, maternal immune activation (MIA) with PolyI:C during mid-gestation typically leads to deficits in PPI in adult offspring [140,178]. Interleukin (IL)-6 KO dams exposed to MIA during mid-gestation are insensitive to the effects of MIA (i.e., exposed offspring do not show deficits in PPI; [181]). Hence, PPI in a genetic mutant (IL-6 KO mice) was used to determine the mechanism for the effects of immune activation on brain development. An example of a PPI phenotype being “rescued” in a KO mouse comes from studies in Phospholipase C β 1 KO mice, in which PPI deficits and locomotor hyperactivity were attenuated in KO mice by environmental enrichment or clozapine [137]. While these are examples in which a genetic manipulation and an environmental manipulation interact, not all of these are true examples of gene-environment interactions in the sense of a “two-hit” hypothesis for schizophrenia. A good example of the “two-hit” approach are nuclear receptor null *Nurr1* heterozygous mice, which display reduced mesocortical and mesolimbic dopamine [50] and reduced PPI following postnatal isolation rearing, an effect not observed with either isolation rearing or genotype alone [51]. This study provides a good example of the utility of PPI in gene-environment models relevant to schizophrenia, specifically those designed to test the “two-hit” hypothesis for the etiology of schizophrenia. It should be kept in mind, however, that many studies assessing gene-environment effects are evaluating additive effects of two manipulations and must be interpreted with caution.

Evaluating the role of a susceptibility gene in schizophrenia pathology—When evaluating the role of a susceptibility gene implicated in the pathophysiology of schizophrenia, it is important to consider what criteria should be placed on a genetic/etiological model. In the present context, it is relevant to consider whether or not deficient PPI is a necessary phenotype with which to evaluate the usefulness of a targeted gene deletion of potential relevance to schizophrenia. Failure to see a PPI deficit in a mouse model may indicate a “false negative” particularly if other key behaviors relevant to schizophrenia are observed. For example, if a genetic mouse model shows deficits in social interaction and disturbances in performance on cognitive tasks such as attentional set shifting, but no differences in PPI, this does not indicate that the genetic model is not of relevance to schizophrenia. In other words, lack of a PPI phenotype should not “kill” a putative genetic model of schizophrenia. The likelihood of being able to represent all aspects of a heterogeneous disease in another species with a genetic mutation (most often a single gene deletion) is very rare if not impossible. In a recent review, Jones et al. [103] quote George Box, an industrial statistician, who said that “all models are wrong, some are useful” [16] and suggest that support for a model should be based on the convergence of data from multiple sources (e.g., many animal models, human genetic studies, etc.). Thus, no one phenotype should be considered as being neither necessary nor sufficient

to support a model for schizophrenia. Along these same lines, Swerdlow et al. [197] point out that schizophrenia patients with functional impairments may have PPI in the normal range because of the overlapping PPI distributions between healthy volunteers and schizophrenia patients, and thus an animal model should not be rejected based on “normal” PPI.

Alpha-7 ($\alpha 7$) nicotinic acetylcholine receptor (nAChR) KO mice provide a good example of a schizophrenia susceptibility gene in which mutant KO mice display some phenotypes of relevance to schizophrenia in the absence of a PPI phenotype. Based on a genetic association between the $\alpha 7$ nicotinic receptor and schizophrenia, decreased expression of $\alpha 7$ nicotinic receptors in brain regions associated with schizophrenia, and the high prevalence of smoking in schizophrenia patients, $\alpha 7$ nAChR KO mice have gained importance in our understanding of the pathophysiology of schizophrenia [56,134]. In fact, genetic studies have implicated the $\alpha 7$ nAChR gene (CHRNA7) in auditory P50 gating [57,119,135]. In an attempt to understand the relationship between auditory P50 gating and PPI, several groups have examined the relationship between the two forms of “gating” through correlational analysis in humans and rats (summarized in [145]). While P50 gating deficits and PPI deficits are reported in schizophrenia patients, often in the same group of patients, data from these studies suggest that there is a divergence of PPI and P50 gating measures in schizophrenia patients and healthy controls [20,145]. PPI and N40 gating, the rodent analog of P50 gating, also appear to diverge from each other when measured contemporaneously in rats [191]. Hence, the divergence of gating measures within schizophrenia patients and the overlapping distributions of PPI between schizophrenia patients and controls, suggests that PPI in animal models should not be used as the sole indicator of a schizophrenia-relevant phenotype. For example, $\alpha 7$ nAChR KO mice do not exhibit deficits in PPI [150]. They do, however, show impaired performance in delayed non-matching to sample tasks [52] and deficits in attention as measured by the 5-choice serial reaction time task [214]. Thus, the lack of a PPI phenotype in $\alpha 7$ nAChR KO mice should be evaluated in the context of other behaviors relevant to schizophrenia in these mice, the strong association between $\alpha 7$ nAChR and auditory gating, and the divergence of gating measures in schizophrenia.

Along the same lines, there is the possibility that a PPI deficit in a mutant mouse model could represent a “false positive”, in which a PPI phenotype may be suggestive of an association between that gene or pathway and schizophrenia and no such association is found. We would argue that the PPI phenotype should be interpreted as meaning that the given genetic manipulation may be involved in the regulation of PPI expression and caution that PPI phenotypes should not be automatically associated with schizophrenia. One example of a way to test for a “false positive” would be to examine whether or not the PPI deficit could be reversed with existing antipsychotic drugs.

II. Models of pathophysiology

Mutant mouse models of the pathophysiology of a disorder can be considered to reflect hypothesis-driven approaches. These models are based either on a known or a hypothesized neuropathology. The main approaches that will be reviewed here are based primarily on the pharmacology of psychotomimetic drugs, namely the glutamate and dopamine hypotheses of schizophrenia, and on evidence of GABA dysfunction in schizophrenia brains. Other approaches to modeling the pathophysiology of schizophrenia include mutants of specific proteins involved in neurodevelopment (e.g., Reelin, Synapsin II, STOP). While these approaches are extremely useful to our understanding of schizophrenia, they will not be reviewed here.

Glutamate

The glutamate hypothesis of schizophrenia is derived from evidence that acute administration of phencyclidine (PCP), a non-competitive N-methyl-D-aspartate (NMDA) antagonist, produces schizophrenia-like symptoms in healthy humans [98,101]. Extending such observations, several experimental studies have utilized another NMDA antagonist, ketamine, to induce a model psychosis in normal volunteers [1,113,146,207] and to exacerbate symptoms in patients with schizophrenia [132,133]. In rodents, extensive studies have examined the behavioral effects of NMDA antagonists and the ability of antipsychotic drugs to attenuate these effects. Of note, the PPI-disruptive effects of NMDA antagonists in rats appear to be largely insensitive to first generation antipsychotics but reduced by some second generation antipsychotics, mimicking the interactions observed in patients with schizophrenia (for review, see [63]). More recently, several different mutant mouse models have been created focusing on both NMDA and metabotropic glutamate receptors (mGluRs) as manipulations having specific relevance to the glutamate hypothesis of schizophrenia.

NMDA mutants—The NMDA receptor is composed of various conformations of multiple subunits (including NR1, NR2A-D, and NR3A-B). The most notable example of genetic mouse models of NMDA receptors is the NMDA receptor hypomorph mouse, in which the NR1 subunit of the NMDA receptor is markedly reduced. These mice exhibit substantial deficits in PPI compared to wildtype (WT) controls, which can be reduced by typical and atypical antipsychotic drugs [48,49,142]. Furthermore, these mice are more sensitive to the PPI-disruptive effects of amphetamine [142]. In another example, the NR3A subunit is transiently expressed during development and exists in low levels in adulthood. Although adult mice that overexpress the NR3A subunit exhibit normal PPI, male NR3A KO mice exhibit a transient increase in PPI during prepubertal development (i.e. 3–4 weeks postnatal), which may relate to developmental theories of glutamatergic involvement in schizophrenia [25]. Additionally, while NR2A KO mice do not display a PPI phenotype [17,183,199], NR2B KO mice show increased PPI [199].

Metabotropic glutamate receptor mutants—As a result of the model psychoses induced by antagonists of ionotropic NMDA glutamate receptors, interest has evolved in potential of pharmacological manipulations of glutamatergic synapses by targeting the metabotropic glutamate receptors. In one of the first such explorations, we identified a possible role of the type 5 metabotropic glutamate receptors (mGluR5) in PPI by using WT and mGluR5 KO mice backcrossed to two different background strains, 129SvPasIco and C57BL/6. In both strains, PPI was disrupted dramatically in the mGluR5 KO mice throughout a range of interstimulus intervals and sensory modalities [23]. Additional experiments in mGluR5 KO indicated that the PPI deficit in mGluR5 KO mice was independent of changes in baseline startle, mothering behavior, or breeding strategy and was not mimicked by acute administration of the mGluR5 antagonist MPEP [24]. Although the antipsychotic drugs raclopride and clozapine and the selective 5-HT_{2A} antagonist M100907 failed to attenuate PPI deficits in mGluR5 KO mice [22], subsequent research has shown that subchronic treatment with clozapine attenuates the PPI deficits in mGluR5 KO mice [82]. Additionally, PPI deficits, as well as latent inhibition deficits, in mGluR5 KO mice are reversed with the ampakine CX546 [123], suggesting the efficacy of a novel therapeutic target for schizophrenia. Another mutant of the metabotropic glutamate receptor I family, mGluR1 KO mice, also display decreased PPI compared to WT littermates, which was reversed with the mood stabilizer lamotrigine but not the dopamine antagonist raclopride [21]. Thus, the PPI deficits in mGluR5 and mGluR1 KO mice appear to be insensitive to traditional antipsychotics, but more responsive to chronic clozapine. Thus, the metabotropic glutamate receptor I family may offer a novel target for antipsychotic drugs acting upon the glutamate system.

Homer mutants—Homer proteins are scaffolding proteins that are part of the postsynaptic density and are involved in synaptogenesis and receptor trafficking [53,209]. Homer proteins play important roles in glutamate synapses, in particular the clustering of mGluRs at dendritic synapses by linking mGluR proteins together [3,38]. In addition to alterations in memory, anxiety, and reward function, Homer1 KO mice display deficits in PPI that can be reversed by haloperidol [198] and “rescued” with adeno-associated virus delivery of the Homer 1c isoform to the prefrontal cortex [125]. Homer1 KO mice also show elevations in prefrontal cortical glutamate levels [198], which are also reversed by the Homer 1c isoform [125]. Subsequent studies on Homer1 KO mice tested at a later age than those in the Szumlinski et al. (2005) study, however, reported no differences in PPI [97].

Glycine mutants—The NMDA receptor complex is a ligand-gated ion channel, which contains several distinct modulatory sites [136]. PCP binds to a site located within the ion channel and acts as a non-competitive antagonist. Glycine binds to a site on the NMDA receptor complex and serves as a co-agonist at NMDA receptors [102]. Synaptic concentrations of glycine are regulated by glycine type 1 transporters (GLYT1), which are co-localized with NMDA receptors in forebrain and hippocampus (reviewed in [99]). The observation that glycine serves as a co-agonist and regulates NMDA receptor function has stimulated research on the therapeutic potential of targets for the glycine site on the NMDA receptor complex. In preclinical studies, glycine agonists and GLYT1 inhibitors have been shown to reverse both behavioral and neurochemical effects of PCP [99,100]. Specific to PPI, glycine transporter inhibitors reverse PPI deficits in adult rats sustaining neonatal ventral hippocampal lesions in [118] and dizocilpine-induced PPI deficits in mice [122]. Glycine site agonists have shown inconsistent effects on PPI, with glycine and D-serine but not D-cycloserine reversing dizocilpine-induced PPI deficits in mice in one study [106], and D-serine failing to block dizocilpine-induced PPI deficits in mice in another study [122]. Several clinical trials have investigated the efficacy of glycine agonists (e.g., glycine, D-serine, D-cycloserine) as adjuncts to antipsychotic treatment. D-serine has demonstrated efficacy in reducing positive, negative, and cognitive symptoms when added to ongoing antipsychotic treatment in schizophrenic patients [203]. D-cycloserine has been shown to improve negative symptoms when added to antipsychotic therapy in some clinical trials [72,73], but failed to show improvement in other trials [71,206].

Based on these pharmacological studies in animals and humans, several glycine receptor mutant mice have been created for behavioral and neurochemical studies. Mice with point mutations of the glycine site on the NMDA receptor, heterozygous *Grin1*(D481N/K483Q) mice, show decreased LTP, increased dopamine and serotonin function, deficient learning in the Morris water maze, and non-habituating hyperactivity [4]. Although their acoustic startle response is higher than WT controls, they display no difference in PPI. Interestingly, hyperactivity in the *Grin1* mutants was not significantly attenuated with clozapine at doses that reduced activity in WT mice, suggesting that the mice were less sensitive to clozapine.

Glycine transporter 1 (GlyT1) KO mice display improved performance on hippocampal-dependent memory tasks and no difference in baseline PPI [202]. Interestingly, GlyT1 KO mice are less sensitive to PPI reductions induced by amphetamine but not dizocilpine, contrary to the reports of GlyT1 inhibitors blocking dizocilpine-induced reductions in PPI. D-amino acid oxidase (DAO) degrades D-serine and has been implicated as a candidate gene for schizophrenia by genetic association studies. Mice with a naturally occurring mutation (*ddY/DAO-*) lack DAO and have increased extracellular levels of D-serine [2]. These mice display slightly higher acoustic startle but no differences in PPI. In locomotor tests, however, *ddY/DAO-* mice were resistant to the locomotor-stimulating effects of PCP [2]. Thus, mutations or gene deletions that result in increased extracellular levels of glycine or D-serine have at least

partially corroborated the studies of the efficacy of glycine agonists in pharmacological and developmental disruptions of PPI.

Dopamine

The dopamine hypothesis of schizophrenia was formulated close to 50 years ago and is based on the observation that dopamine agonists such as amphetamine can produce psychotic symptoms and that all clinically effective antipsychotics are dopamine D₂ receptor antagonists [41,60,169,174].

DAT KO mice—Mice lacking the dopamine transporter (DAT) gene display markedly increased levels of dopamine [70], deficits in sensorimotor gating [5,160,164], and hyperactivity relative to WT mice [58,70,164,182]. PPI deficits in DAT KO mice can be reversed with either D₁ or D₂ dopamine antagonists [164], the 5-HT_{2A} antagonist M100,907 [5], the atypical antipsychotics clozapine and quetiapine [160], as well as antidepressant drugs such as serotonin- or norepinephrine-selective reuptake inhibitors and monoamine transporter inhibitors such as cocaine [210]. Thus, DAT KO mice may provide a useful animal model for predicting the efficacy of novel drugs in treating psychiatric illnesses characterized by a dysregulated DA system. On the other hand, since general monoamine transporter inhibition appears to attenuate PPI deficits in DAT KO mice, this model may produce false positives when using it as a screen for antipsychotic medications.

GABA

GABA dysfunction in schizophrenia—Recent research has identified subtle neuronal abnormalities of GABAergic systems in schizophrenia brains. There is a decrease in the number of non-pyramidal cells in prefrontal cortex, anterior cingulate, and hippocampus (reviewed in [8]). These cells are typically GABAergic cells, which could lead to a loss of inhibitory modulation in these brain regions (reviewed in [8]). Indeed, GABAergic interneurons are dysfunctional in a number of brain regions in schizophrenia [120,9]. Deficits in γ -aminobutyric acid (GABA)-containing neurons are consistently reported, particularly in the frontal cortex [6], [7] and hippocampus [216,10]. Benes et al. [10] reported significantly reduced density of interneurons in CA2 and CA3 of brains of schizophrenia patients, including drug-free patients, suggesting that deficits in interneurons may play a contributory role in the pathophysiology of schizophrenia. Consistent with this interpretation, neurochemical studies demonstrated a deficit of GABAergic uptake sites in the hippocampus [167], while other reports showed a widespread compensatory up-regulation of post-synaptic specific GABA_A receptor binding activity throughout most sub-fields of the hippocampal formation [11] of schizophrenia patients. Therefore, there is substantial evidence for a functional impairment of GABAergic inhibitory interneurons in the hippocampus in schizophrenia [9,166]. These GABAergic deficits in schizophrenia could well be an initial deficit, perhaps of neurodevelopmental origin, that subsequently results in further progressive neuronal dysfunction and the development of schizophrenia in the second or third decade of life. These GABAergic deficits are unrelated to antipsychotic drug treatment, age, or duration of illness. We have shown a similar structural abnormality in rats that were reared in isolation and exhibit deficient PPI [88], providing further evidence that early environment plays an important role in normal neuronal development.

Several lines of evidence indicate that GABA_A receptors (specifically, the alpha3 and alpha5 subunit-containing GABA_A receptors) may be useful targets in the treatment of schizophrenia [141]. As noted above, markers for GABAergic interneurons are reduced in schizophrenia and in the hippocampus of isolation-reared rats. The alpha5 subunit of the GABA_A receptor is specifically expressed in hippocampal and cortical neurons. Receptors containing the alpha5 subunit make up 15–20% of the GABA_A receptors in the hippocampus, are extrasynaptic, and modulate temporal and spatial memory functions (reviewed in [141]). Several different alpha5

GABA_A receptor inverse agonists have recently been shown to be cognitive enhancers in the delayed matching to position version of the water maze [34,44,186]. Mice with a partial deficit of alpha5 GABA_A receptor in hippocampus (alpha5(H105R) point-mutation) showed improved performance in trace fear conditioning, a hippocampal-mediated task [42] and a resistance to extinction of conditioned fear [212]. These mice also show reductions in PPI and locomotor hyperactivity [89] and decreased latent inhibition [61]. Alpha3 containing GABA_A receptor KO mice display deficits in PPI, which are normalized by haloperidol [213]. Additional GABAergic mutants include GABA transporter 1 and GAD65 KO mice. GAT1 KO mice exhibit decreased PPI in addition to reductions in open field activity [37]. Glutamic acid decarboxylase 65 (GAD65) KO mice lack the GABA synthesizing enzyme GAD65 and show decreased PPI [92].

This review of mutant mouse models of the pathophysiology of schizophrenia is not meant to be exhaustive. Many other mouse mutants of relevance to schizophrenia such as second messenger systems (e.g., CaMKIV, PLCB1) and neuropeptides (e.g., neurotensin, CRF) have been created and evaluated for alterations in PPI. The readers are referred to the recent review by Swerdlow et al. [197] for a description of these mutants.

III. Genetic mouse models as pharmacological tools

Historically, animal models of relevance to schizophrenia have been driven primarily by studies combining pharmacological inducing conditions (e.g., PCP) paired with relevant dependent measure(s) (e.g., PPI, locomotor hyperactivity; latent inhibition). Most of that literature is based on studies in rats and is reviewed extensively elsewhere [67]. These pharmacological models have been instrumental in establishing three of the most prominent theories of schizophrenia, the dopamine hypothesis [40,175], the serotonin (or serotonin-dopamine) hypothesis [15,81], and the glutamate hypothesis [81,113]. More recent attempts to develop models of relevance to schizophrenia involve genetic mouse models (reviewed in [66,143,197]). As noted below, in translating what we have learned about the pharmacology of rat PPI to that of genetic mouse models we must keep in mind several important differences between the pharmacology of mouse vs. rat PPI, since the models themselves have been built on rat pharmacology.

While none of the dopamine receptor KO mice (e.g., D₁, D₂, D₃, D₄, D₅) show PPI phenotypes per se, dopamine receptor mutant mice have proven useful to dissect the pharmacological profile of dopamine agonists in the disruption of PPI. The pharmacology of dopamine effects on PPI in mice is complex. For example, mice are less sensitive to the PPI-disruptive effect of dopamine D₂ receptor agonists than are rats [162,163]. Strain comparisons of dopamine agonists suggest that many strains, including one of the most commonly studied background strains C57BL/6 mice, are not sensitive to the PPI-disruptive effects of dopamine D₂ agonists [163]. Data from our laboratory suggest that the D₁ receptor plays a more important role in the modulation of PPI in mice compared to rats. For example, direct acting dopamine agonists such as apomorphine [162] and indirect dopamine agonists such as cocaine disrupt PPI primarily via D₁ receptors [45]; whereas D₂ receptors appear to modulate amphetamine-induced PPI deficits [165] and only partially mediate PPI disruptions induced by cocaine [45]. In contrast, both apomorphine- and amphetamine-induced PPI disruptions in rats are blocked by dopamine D₂ antagonists [64]. Thus, dopamine receptor KO mice have aided in our understanding of the pharmacological effects of dopamine agonists on PPI. Additionally, selective D₂ agonists such as quinpirole reduce PPI in rats (with differing sensitivities to the PPI disruptive effects depending on the strain and the prepulse to pulse interval [194,196, 208]), whereas selective D₁ agonists do not disrupt PPI in rats on their own (or do so only weakly) [64,163,194]. Thus, while dopamine agonist-induced disruptions of PPI in rats vary

depending on the interstimulus intervals and the strain, there does appear to be a species difference in the relative D1 vs D2 contribution to PPI disruption with dopamine agonists.

As with the dopamine system, some serotonergic drugs have been found to produce different and even opposite effects on PPI in rats and mice. Specifically, while 5-HT_{1A} agonists decrease PPI in rats [180], the same 5-HT_{1A} agonists (e.g., 8-OH-DPAT) increase PPI in mice [47]. Furthermore, indoleamine hallucinogens such as psilocin and 5-MeO-DMT increase PPI in mice [159] while decreasing PPI in rats [112]. Mutant mouse lines lacking specific serotonin receptor subtypes have been particularly useful in delineating the respective contributions of specific serotonin receptors to the effects of serotonin agonists on PPI (reviewed in [47,66]). Similarly, mutants of specific subunits of the GABA_A receptor have been extremely useful in dissecting the effects of drugs acting at each of these subunits [171]. For example, studies using mice with a point mutation in the alpha1-containing subunit demonstrated that the sedative properties, but not the anxiolytic properties, of benzodiazepines were mediated by the alpha1 subunit [171]. A similar approach could be taken with known or putative antipsychotics. Overall, pharmacological disruptions of PPI and their reversal with antipsychotics have been better characterized in rats than in mice, although the literature on PPI pharmacology in mice is rapidly increasing [197]. In order to use mutant mouse models to examine the receptor mechanisms for alterations in PPI, more complete dose response studies are warranted in mice.

IV. Candidate gene approach: “Top-Down” Approach

Heritability estimates for schizophrenia range from 24–80% depending on whether the studies used diagnosis or endophenotypes in the estimations [32,84,188]. Linkage studies have identified several chromosomal regions and candidate genes thought to be involved in the pathogenesis of the disease (reviewed in [86,87,187]). As the field of schizophrenia genetics has developed, several gene targets have been identified consistently and have thus been modified in mouse models through gene deletion or the addition of a transgene. When evaluating candidate genes for mouse models, one should consider that many single nucleotide polymorphisms (SNPs) identified in genetic screens for schizophrenia involve mutations in introns of genes. Thus, it is very important to consider (1) whether or not functional mutations in the gene have been identified before embarking on mutant mouse models, and (2) the impact of species-specific alterations in gene function in the mutant mouse [126]. For the purposes of this review, our discussion is limited to a few of the candidate genes that have been associated with schizophrenia, namely neuregulin, COMT, and DISC-1.

Neuregulin

Neuregulin is a family of peptides related to an epidermal growth factor that is coded for by four different genes (NRG1-4). Genetic association studies have identified NRG1 as a susceptibility gene for schizophrenia [85,185]. NRG1 binds to the tyrosine kinase receptor ErbB4 [26]. The neuregulin family of peptides is expressed widely during development and plays an important role in neuronal migration, axon guidance, glial cell development, and synapse formation [138]. Neuregulins are also expressed in the adult brain, where they play a role in adult neurogenesis and can affect neuronal activity [138]. Neuregulin is conceptualized as a crucial player in a family of interacting genes that contribute to the development of neuronal systems involving NMDA, GABAergic, $\alpha 7$ nAChR, and other receptors in brain. NRG1 is a large peptide and thus several different mutant mouse models have been created for NRG1 as well as its receptor target ErbB4, with varying effects on brain development and behavior [62,77,143,168]. While the NRG1 gene deletion is lethal, behavioral and neuroanatomical studies have been conducted on NRG1 heterozygotes. For example, NRG1 and ErbB4 heterozygotes show reduced NMDA receptor expression and abnormal behavior [36,185]. Specifically, type III NRG1 heterozygotes (NRG1(tm1.1Lwr+/-)) show PPI deficits that are accompanied by enlarged lateral ventricles, prefrontal cortex hypofunction, and deficits in

delayed alternation memory tasks [36]. Thus the type III NRG1 heterozygotes represent a mouse model of a candidate gene for schizophrenia that shows several phenotypes of relevance to schizophrenia. Neuregulin interacts with the $\alpha 7$ nAChR, which has long been implicated in gating mechanisms [56]. The deficits in PPI in type III NRG1 heterozygous mice are reversed by subchronic administration of nicotine [36], mimicking the nicotine-induced improvement in PPI we have reported in healthy and schizophrenic humans [158].

Initial reports indicated that mice heterozygous for gene deletion of the Nrg1 transmembrane domain displayed PPI deficits [185]. These initial studies also reported that there were no differences in PPI between WT and KO ErbB4 mice [185]. Subsequent studies, however, reported some baseline behavioral differences in mice heterozygous for gene deletion of the NRG1 transmembrane domain, such as increased locomotor activity and investigatory behavior, and decreased anxiety-like behavior, but no baseline difference in PPI [14]. When challenged with tetrahydrocannabinol, however, NRG1 heterozygotes were slightly more sensitive to the PPI-enhancing effects of tetrahydrocannabinol [14]. Similar mice heterozygous for the NRG1 transmembrane domain show hyperactivity and some evidence of increased anxiety-like behavior [108] and decreased social novelty behavior [144]. Mice heterozygous for a mutation in the immunoglobulin (Ig) -like domain (Ig-nrg-1) show impaired latent inhibition and an increased sensitivity to the locomotor-decreasing effects of clozapine, but showed no differences in locomotor activity [168]. Based on previous unpublished reports of no PPI phenotype in similar mice with mutations of the NRG1 Ig domain, the authors did not test the mice in an acoustic startle/PPI paradigm [168]. Mice heterozygous for the NRG1 EGF-like domain are hyperactive in a novel environment and showed a potential increased sensitivity to the PPI-disruptive effects of dizocilpine, which was not supported by a statistically significant interaction between genotype and drug [46]. An interesting related mutant is the BACE1 (β -site APP-cleaving enzyme 1) KO mouse. Because of the role BACE1 plays in the "proteolytic processing" of NRG1, BACE-1 KO mice have been examined for neuroanatomical and behavioral differences relevant to schizophrenia. BACE-1 KO mice with impaired NRG1 show deficits in PPI, locomotor hyperactivity, increased sensitivity to dizocilpine, and reduced dendritic spine density in hippocampal pyramidal neurons [172].

Taken together, it appears that NRG1 heterozygotes have a varied phenotype depending on the targeted domain of the gene with the most consistent behavioral abnormality being locomotor hyperactivity. For more extensive reviews of the different NRG1 mutants that have been created and their resultant phenotypes see [46,143]. Overall, the PPI phenotype in NRG1 mutants has been inconsistent. Perhaps the most promising model that has shown abnormalities in multiple neuroanatomical and behavioral endpoints relevant to schizophrenia is the Type III NRG1 heterozygote mouse [36]. Based on the improvement in PPI with chronic nicotine in the mice, the Type III NRG1 heterozygotes may prove to be an interesting model against which to test novel therapeutic targets.

Catechol-O-Methyltransferase (COMT)

Chromosome 22q11 has been implicated in the genetics of schizophrenia based on the evidence that humans with 22q11.2 deletion have an increased risk for schizophrenia and that three of the genes implicated in schizophrenia, COMT, PRODH, and Gnb1L, lie within this chromosomal region [78,87,107]. In fact, microdeletions of 22q11.2 are among the most commonly known genetic risk factors for schizophrenia [124]. Some mouse models have been generated as potential models of the 22q11 gene deletion. For example, the Df1/+ mice display deficits in PPI and learning and memory [105]. While the approach of modeling the entire chromosomal deletion may be informative, another approach has been to target the specific susceptibility genes in that chromosomal region.

The COMT gene is one of the more robust genetic “hits” for schizophrenia [204]. COMT is involved in the catabolism of dopamine and norepinephrine at the synapse and heavily localized in the frontal cortex, where levels of DAT are low [176], and thus is the primary mode of dopamine metabolism in the frontal cortex. A SNP causing a missense mutation of codon 158 Valine (val) to Methionine (met) in the coding region was found in the human COMT gene [117,204]. The Val158Met polymorphism is a functional polymorphism, decreasing COMT enzymatic activity by 40% in the prefrontal cortex [35], increasing levels of dopamine in the prefrontal cortex and affecting many cognitive processes that are deficient in schizophrenia (e.g., working memory, attention, information processing, [204]; but see [184]). COMT may be a susceptibility gene for schizophrenia, as Val158Met conferred an increased risk for developing schizophrenia in those individuals that smoked cannabis [33]. Recent evidence suggests that the COMT Val allele is associated with reduced P300 and P50 ERPs [59,76, 127] and reduced PPI [161,170], presumably due to decreased dopamine function in the prefrontal cortex. The PPI decreases observed with the COMT Val allele are attenuated with the COMT inhibitor tolcapone [69]. Studies also support the involvement of prefrontal cortex dopamine transmission in PPI across humans [90,91,115] and rodents [190], with decreased dopamine in prefrontal cortex or the administration of dopamine antagonists being associated with reductions in PPI.

To date, two approaches have been taken to model the genetic alterations in COMT observed in schizophrenia – both gene deletion [74,147,211] and a transgenic approach in which mice overexpress a human COMT-Val polymorphism [147]. COMT deficiency in mice increases dopamine signaling primarily in the prefrontal cortex but not in the dorsal striatum [74,211]. COMT KO mice do not display alterations in PPI [74,147], although startle magnitude was increased in COMT KO mice compared to COMT WT and heterozygous mice [147]. Similarly, COMT transgenic mice with the human COMT-Val polymorphism overexpressed do not show differences in PPI, although there is a trend for the mice to have decreased PPI [147]. In contrast, COMT-Tg mice do show disrupted attentional set shifting, working memory, and recognition memory [147]; whereas, COMT KO mice perform better on working memory tasks compared to their WT controls [147]. Thus, alterations in prefrontal cortex dopamine in these mice are associated with performance on cognitive tasks but not PPI. One issue to address, however, is that the human COMT-Val transgene was overexpressed in the presence of the mouse COMT gene. In these mice, the residual mouse COMT contributes to dopamine degradation, as does MAO. Compared to humans, MAO rather than COMT appears to play a major role in the degradation of dopamine in rodents [54,111]. Thus, while the data in COMT mutant mice clearly suggest that alterations in COMT gene can affect cognitive function, no clear relationship has been shown between COMT gene and PPI in mice.

Proline dehydrogenase (PRODH)

Another gene in the 22q11.2 region implicated in schizophrenia is proline dehydrogenase (PRODH). PRODH knockdown mice with reduced enzymatic activity of proline dehydrogenase have been shown to have reduced PPI [75]. In subsequent studies, PRODH knockdown mice backcrossed to a 129SvEv background exhibited an increase in glutamate release and alterations in COMT enzyme activity. The PRODH knockdown mice also displayed an increased sensitivity to the behavioral (increased locomotor activity) and neurochemical (increased dopamine release) effects of amphetamine, suggesting that there were functional interactions between the PRODH and COMT genes [148]. In these studies, PRODH knockdown mice showed no differences in baseline PPI, but did show PPI deficits when administered tolcapone, a COMT inhibitor, an effect not observed in WT mice [148].

Disrupted in Schizophrenia 1 (DISC1)

First identified in a Scottish pedigree, the Disrupted in Schizophrenia 1 (DISC1) gene has shown association with schizophrenia and behavioral and neuroanatomical biomarkers for schizophrenia (for review see [131,157]). The DISC1 gene was discovered through a cytogenetic approach, which identified a translocation between chromosome 1 and chromosome 11, a balanced t(1;11) (q42.1;q14.3) translocation, which was associated with schizophrenia and mood disorders (for review see [157]). DISC1 gene, encoding multiple isoforms of DISC1 protein [157] for review), was found to be disrupted by the breakpoint on chromosome 1. DISC1 isoforms appear to be cell-type-specific, are expressed throughout the brain (particularly regions implicated in schizophrenia such as the hippocampus), and are developmentally regulated [156]. Human imaging and behavioral studies have shown DISC1 to be functionally linked to schizophrenia. DISC1 is associated with abnormal P300 ERP [13], neurocognitive function (e.g., learning and memory; [27,31,93], and schizophrenia neuropathology such as reduced prefrontal gray matter [31] and reduced hippocampal size [30]. DISC1 protein interacts with several proteins that are important during neurodevelopment such as Ndel1, implicated in neuronal migration, and FEZ1, implicated in neurite extension [131]. DISC1 also interacts with phosphodiesterase 4B (PDE4B) to affect neuronal signaling via effects on cAMP levels [131].

Based on the strong genetic link between DISC1 and schizophrenia, several genetic mouse models have been created either via inducible transgenics or mutants with a missense mutation produced with by induced mutagenesis. For example, mice with a missense mutation in exon 2 of the DISC1 gene (L100P, and to a lesser extent Q31L, mutants) show decreased PPI and latent inhibition. PPI and latent inhibition phenotypes were reversed with antipsychotic drug treatment and rolipram, a PDE4 inhibitor, specifically in the L100P mutants [39]. These mice with missense mutations in the DISC1 gene also show evidence of overall decreased brain volume (9–13% reduction; [39]). Other DISC1 mutants have been generated by overexpressing a DISC1 transgene with temporal and/or regional specificity. For example, mice expressing a dominant negative form of the DISC1 gene under the α CaMKII promoter, which drives gene expression the forebrain, mainly pyramidal neurons of the cortex and hippocampus and granule cells of the dentate gyrus, display several phenotypes of relevance to schizophrenia [94]. Specifically, these mice have enlarged lateral ventricles, decreased parvalbumin immunoreactivity in the prefrontal cortex, locomotor hyperactivity, modest reductions in PPI, and increased immobility in the forced swim test [94]. The decreased PPI in the dominant negative DISC1 transgenic mice only occurs at one out of four prepulse intensities (74 dB). The use of relatively high prepulse intensities (74–90 dB), the lack of a strong intensity-dependent effect on PPI in control mice, and the high level of PPI (85% at the lowest prepulse intensity in control mice) make the PPI decrease difficult to interpret in these DISC1 transgenic mice. Further evaluation of the PPI phenotype would be needed to conclusively argue that these mice have reductions in PPI. Considering that these mice are slow to find a hidden food pellet [94], thought should be given to potential deficits in sensory detection and future tests of PPI should determine whether or not the putative PPI deficit is due to a hearing loss. Using a similar approach, Pletnikov et al. [155] generated a mouse with inducible expression of mutant human DISC1 under the control of the α CaMKII promoter. Consistent with previous studies, the mutant mice showed mild enlargement of lateral ventricles and decreased neurite outgrowth. Interesting sex-specific effects on behavior were observed. Male mutants showed increased locomotor activity and decreased social interaction; whereas females displayed decreased spatial memory in the probe test of the water maze. The mutant human DISC1 mice, however, did not display any alterations in PPI [155]. Mice with an inducible dominant negative DISC1 C-terminal fragment transiently expressed early in postnatal development (postnatal day 7) showed reduced hippocampal dendritic complexity and behavioral differences including impaired spatial working memory in a delayed nonmatch to place test, reduced social

interaction, and decreased time to immobility in the forced swim test [121]. These behavioral and neuronal phenotypes were apparent only after early postnatal induction of the DISC1 transgene and not when the DISC1 transgene was expressed in adulthood [121]. To our knowledge, PPI was not tested in these mice.

An alternative approach to unraveling the role of DISC1 in brain development is to conduct comparisons of the DISC1 gene across strains of mice. 129S6/SvEv mice carry a 25 bp deletion in exon 6 of the mouse DISC1 gene. C57BL6/J mice do not carry this deletion. Koike and colleagues [110] transferred the DISC1 mutated 129S6/SvEv allele to the C57BL6/J background. The resultant C57BL/6J mice with the DISC1 mutated allele showed altered neuronal morphology in hippocampus and prefrontal cortex [116] and impaired working memory as measured by a delayed non-match to place test [110,116]. The mutant DISC1 mice, however, did not differ from WT mice in locomotor activity, PPI, water maze performance, novel object recognition performance, or fear conditioning [110,116]. Yet another approach to modeling the DISC1 mutation has been to generate transgenic mice expressing two copies of a truncated form of DISC1 encoding the first 8 exons using a bacterial artificial chromosome (BAC) [177]. These mice display many of the phenotypes previously reported (e.g., enlarged lateral ventricles, reduced cerebral cortex, decreased parvalbumin in the prefrontal cortex, disrupted latent inhibition, increased immobility in the forced swim test) in addition to novel phenotypes including thinning of cortical layers II/III, decreased neuronal proliferation in developing cortex, reduced parvalbumin cells in the hippocampus, and reduced vocalizations in response to stress [177]. To our knowledge, PPI has not yet been assessed in these mice. Taken together, there is some limited evidence for the effects of altered DISC1 expression on PPI in mice. While some neuroanatomical and behavioral phenotypes appear to be somewhat consistent across the various DISC1 mutants, PPI does not appear to be a robust phenotype associated with alterations in DISC1 in mutant mouse models.

Making the appropriate mutant mouse for the DISC1 translocation has proven difficult, with many different strategies for modeling the genetic mutation in neuropsychiatric illness as described above. All of these models have been based on the hypothesis that the functional mutation in the human psychiatric conditions results from a truncated form of DISC1. However, the genetic mutation in the Scottish schizophrenia is not just the truncation of the DISC1 gene. A novel gene, termed Boymaw or DISC1FP1 (DISC1 Fusion Partner 1), was also found to be disrupted on chromosome 11. Two fusion transcripts are generated between DISC1 and Boymaw genes in the translocation carriers in the Scottish schizophrenia family [217]. Thus, expressing the two fusion transcripts would be a better strategy for creating mutant DISC1 mice for the study of neuropsychiatric disorders.

V. Hypothesis generating: “Bottom-Up” approach

What can a PPI phenotype tell us about novel genes for schizophrenia? The field of molecular genetics continues to produce new mutant mouse models with unknown effects on the central nervous system. Many of these mutants have behavioral abnormalities that have been observed anecdotally. One such example of the way a novel gene of relevance to psychiatric conditions can be discovered through the creation of a mutant mouse is the SP4 gene. SP4, a member of the Sp1 family of transcription factors, is expressed restrictively in the developing nervous system and most abundantly in adult hippocampus in mice. Hypomorphic Sp4 mice showed vacuolization in the hippocampus, age-dependent decrease in neurotrophin-3 expression in the dentate granule cells, and robust deficits in both PPI and contextual memory [218]. The restoration of Sp4 expression, via a Cre-dependent rescue strategy, completely rescued all the observed molecular, histological, and behavioral abnormalities [218]. These studies revealed a novel Sp4 pathway that is important for hippocampal development and essential to many behaviors, including PPI, relevant to schizophrenia [218]. Zhou and colleagues have gone on

to examine the role of the human SP4 gene in schizophrenia and bipolar disorder. Several SNPs from the human SP4 gene are found to associate with both bipolar disorder and schizophrenia in both Caucasian and Chinese samples [219]. This represents an example in which a PPI phenotype, in combination with other behavioral abnormalities, suggested the association of this gene with neuropsychiatric disorders. Similar “bottom-up” approaches have been taken through the use of inbred mouse strain comparisons [149], recombinant congenic mouse strains [104,201], selective breeding of mice and rats for high and low levels of PPI [95,173], and strain differences in the response to the pharmacological disruptions of PPI in rats [179,196].

While these types of “bottom-up” approaches would not directly implicate a given gene with schizophrenia, particularly since PPI deficits are not unique to schizophrenia, they may be useful in identifying genes or gene products relevant to the regulation of PPI expression. The phenotype, however, would suggest that the gene might be relevant to neuropsychiatric disorders in which PPI deficits have been observed.

VI. Discussion

Mutant mouse models of schizophrenia provide a unique way to assess the function of a susceptibility gene, test hypotheses about the pathophysiology of the disease, address treatment mechanisms of antipsychotic drugs, and generate hypotheses about the function of relatively unknown genes. In this review, we provided a brief overview of PPI deficits in some of these approaches and present specific examples where appropriate. As mentioned above, it is not likely that all aspects of a heterogeneous disease will be recapitulated in another species with a genetic mutation. Convergence of behavioral and neuroanatomical or neurochemical data in a given mutant mouse has been observed in several mutant mouse models (e.g., Type III NRG1 heterozygotes) and support clinical data on the link between the candidate gene and schizophrenia. As we point out throughout the review, no one phenotype such as PPI should be considered as being either necessary or sufficient to substantiate a model as having relevance to schizophrenia.

Future animal studies addressing schizophrenia would benefit greatly from more neurobiologically based biomarkers for schizophrenia. Such an approach has been taken in the CNTRICS initiative, in an explicit attempt to incorporate more cognitive neuroscience based testing into treatment trials of putative cognitive therapies for schizophrenia. Along the same lines, genetic studies of schizophrenia have focused on psychophysiological endophenotypes such as PPI instead of the broader, more heterogeneous diagnosis of schizophrenia. In fact, many laboratories are now using PPI as an endophenotype in genetic studies of schizophrenia [18,84]. Some of these genetic studies have generated further support for a genetic contribution to PPI [84], and other studies have suggested that genetic variants in COMT directly affect PPI levels (as reviewed above) [161,170]. Thus, as human studies materialize with more neurobiologically defined behavioral measures, the ability to translate these measures or “endophenotypes” to animal models should improve dramatically.

In this review, we assert that PPI in mutant mouse models related to schizophrenia offers a behavioral endpoint that has shown predictive validity in rat pharmacological models, cross species homology with the same measure in humans, and alterations in response to genetic manipulations implicated in the pathogenesis of schizophrenia. While these mutant mouse models are not without shortcomings, they offer some of the best attempts at etiological models that are possible in rodents. Merging the genetic etiological models with a second hit approach may strengthen some of the mutant mouse models. Hence, consideration for other factors, such as the importance of environmental risk factors (e.g., prenatal infection) and the role of epigenetics (e.g., DNA methylation) in the etiology of schizophrenia, should also be incorporated with genetic models.

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