Research report

Dopamine transporter genotype predicts implicit sequence learning

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ABSTRACT

Implicit learning, the non-conscious acquisition of sequential and spatial environmental regularities, underlies skills such as language, social intuition, or detecting a target in a complex scene. We examined relationships between a variation of the dopamine transporter (DAT1) gene (SLC6A3), which influences dopamine transporter expression in the striatum, and two forms of implicit learning that differ in the regularity to be learned and in striatal involvement. Participants, grouped as 9-repeat carriers or 10/10 homozygotes, completed the triplets learning task (TLT) and the spatial contextual cueing task (SCCT). The TLT assesses sequence learning, recruiting the striatal system, particularly as training continues. In contrast, the SCCT assesses spatial context learning, recruiting medial temporal brain networks. For both tasks, participants demonstrated learning in faster and/or more accurate responses to repeating patterns or spatial arrays. As predicted, TLT learning was greater for the 9-repeat carriers than the 10/10 group (despite equal overall accuracy and response speed) whereas there were no significant group differences in SCCT. Thus, presence of the DAT1 9-repeat allele was beneficial only for implicit sequence learning, indicating the influence of DAT1 genotype on one form of implicit learning and supporting evidence that implicit learning of sequential dependencies and spatial layouts recruit different neural systems.

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1. Introduction

Contemporary cognitive neuroscience increasingly incorporates genetics data to understand cognition [1]. However, our current understanding of genetic influences is limited because most research has focused on conscious, deliberate cognitive control (e.g., [2]), while the genetics of non-conscious, implicit phenomena has been understudied. Implicit learning refers to the acquisition of information about environmental regularities without intending to learn or becoming aware of what has been learned [3]. Here, we investigated the effects of a polymorphism in the gene (SLC6A3) coding for the dopamine transporter (DAT1) on two different forms of implicit learning, namely sequence learning and spatial context learning.

Implicit sequence learning involves learning sequential dependencies among events, which is necessary for skills such as language [4] and social intuition [5]. To investigate sequence learning, we used the triplets learning task (TLT; [6]). On each trial, participants encounter three sequentially presented stimuli, two red cues followed by a green target, each appearing in one of four spatial locations. Participants watch the red cues but respond only to the third, green target. Participants are unaware that certain series of events or "triplets" occur with greater frequency (high probability, HP) than others (low probability, LP). Nonetheless, with practice, they reveal sequence learning in the form of greater improvement in speed and/or accuracy for HP than LP triplets. Studies of Parkinson's and Huntington's disease patients with dopamine depletion and striatal pathology, respectively, have shown sequence learning deficits (e.g., [7,8]), indicating the involvement of the striatum and striatal dopamine system in this form of learning. Moreover, neuroimaging studies of implicit sequence learning in healthy young adults reveal striatal involvement that increases as practice continues [9–12].

Distinct from sequence learning, implicit spatial context learning refers to learning of regularities in spatial layouts, such as how context predicts where a target is likely to occur. For example, spatial context learning can help people anticipate where the stoplight is likely to be at an intersection. The spatial contextual cueing task (SCCT; [13]) measures this type of learning. Participants search for a target among distractors in displays with spatial con-

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figurations that either repeat across trials or are novel. Repeated configurations provide contextual guidance for locating the target. Implicit spatial context learning is revealed by faster and/or more accurate responding to repeated vs. novel configurations without explicit awareness. Functional imaging of healthy subjects has shown medial temporal lobe (MTL) involvement during spatial context learning in the SCCT [14,15]. In addition, impaired contextual learning has been observed in amnesics with MTL damage [16,17].

Sensitive recognition tasks and post-experimental interviews with participants have reliably demonstrated that both the TLT and SCCT measure implicit learning (e.g., [6,13,16,18]). Even after being told that regularities were present, participants cannot accurately describe their nature, nor can they discriminate between triplets that occur with HP vs. LP in the TLT and/or arrays that repeated vs. those that were novel in the SCCT.

Previous work has demonstrated double dissociations between implicit sequence learning and implicit spatial context learning by differentiating the brain regions involved. Specifically, reduced sequence learning but not spatial contextual learning was revealed in healthy older compared to younger adults [19], consistent with findings that healthy aging is associated with greater volume declines in the striatum than in the MTL [20]. This result was supported by Negash et al. [21] who found that spatial contextual learning, but not sequence learning, was reduced in older adults with mild cognitive impairment, a condition associated with MTL pathology, compared to age-matched controls. In addition, Negash showed that healthy older individuals carrying the ApoE-e4 allele, which is also associated with MTL atrophy [22], showed reduced spatial contextual learning, but not sequence learning, compared to non-e4 carriers. Thus, implicit sequence learning and implicit spatial context learning are dissociable and appear to be differentially influenced by individuals' genetic profiles.

The present study examined relationships between these two forms of implicit learning and a polymorphism in DAT1, which influences DAT expression levels [23]. Although DAT1 is present throughout the brain [23,24], it is expressed most abundantly in the striatum and plays a key role in striatal dopamine transmission, in that it is the primary means of clearing extracellular dopamine from the synaptic cleft [25], thereby regulating synaptic dopamine concentrations [26]. DAT1 displays a polymorphic 40 base pair variable number of tandem repeats in the 3′ untranslated region. The most common variations, the 9- and 10-repeat alleles, result in individual differences in DAT availability in the brain [27]. Most studies have found that the 10-repeat allele is associated with more DAT availability [28–32]. It has been suggested that individuals who carry two copies of this allele (i.e., 10/10 homozygotes) have higher DAT density and therefore less dopamine in the synapse than 9-repeat carriers [33]. However, other studies have reported greater DAT density in 9-repeat carriers [34–36], and no DAT density differences between genotypes [37,38].

If, indeed, 10/10 homozygotes have more DAT expression and less dopamine, we would expect to see decreased learning in tasks facilitated by higher levels of striatal dopamine. Thus, we sought to determine the functional influence of DAT1 genotype on striatal-based implicit sequence learning vs. MTL-based implicit spatial context learning. Based on evidence that DAT1 expression is higher in the striatum than the MTL [23], we expected that DAT1 genotype would influence sequence learning but not spatial context learning. Specifically, we hypothesized that 9-repeat carriers would show greater sequence learning than 10/10 homozygotes in the later stages of sequence learning, given evidence that striatal involvement increases with training (e.g., [11]). In contrast, we expected that DAT1 genotype would be unrelated to spatial contextual learning, which relies on the integrity of the MTL.

2. Methods

2.1. Participants

Participants were 37 Georgetown University students who received either monetary compensation or course credit for their participation. Participants were grouped according to their DAT1 genotype. Participants in the 9-repeat/9-repeat homozygous group ($n = 7$) and the 9-repeat/10-repeat heterozygous group ($n = 11$) were combined, henceforth called 9-repeat carriers, and compared to 10/10 homozygotes ($n = 19$). The genotype groups did not differ in age (9-repeat carriers: $M = 20.2 \pm 1.2$; 10/10 homozygotes: $M = 20.2 \pm 1.2$), years of education (9-repeat carriers: $M = 14.1 \pm 1.0$; 10/10 homozygotes: $M = 14.4 \pm 1.0$) or gender (9-repeat carriers: 15 females; 10/10 homozygotes: 12 females) (p's > .17). Based on self-report, participants were without psychiatric disorder (e.g., ADHD) and did not use drugs known to influence cognitive functioning (e.g., dopaminergic medications). The Georgetown University Institutional Review Board approved all experimental procedures, and all participants gave informed consent.

2.2. Genotyping for DAT1

DNA was extracted from Oragene saliva kits (DNA Genotek Inc., Ottawa, Ontario, Canada). The 40 base pair VNTR polymorphism in the 3′ UTR of DAT1 was genotyped by PCR as previously described [39] using the following primers; forward: 5′-TGTGGTGTAGGGAACGGCCTGAG-3′ reverse: 5′-CTTCCTGGAGGTCACGGCTCAAGG-3′. PCR was performed using the AccuprimeTM Taq DNA polymerase system (Invitrogen) with the following PCR program: 94 °C for 2 min, followed by 35 cycles of 94 °C for 30 s, 60 °C for 30 s, and 68 °C for 1 min. The PCR products were then run out on a 2% agarose gel stained with ethidium bromide. A 100 bp DNA ladder was then used to identify the various repeat alleles by size: 7-repeat (360 bp), 8-repeat (400 bp), 9-repeat (440 bp), 10-repeat (480 bp), and 11-repeat (520 bp).

2.3. Triplets learning task (TLT)

On a computer screen, participants viewed four open circles that filled in either red or green in discrete, sequentially ordered, three-event trials or "triplets" (see Fig. 1a). For description purposes below, the four stimulus locations are referred to as 1–4, with 1 as the leftmost position and 4 as the rightmost position, though these numbers never appeared on the screen. Participants were asked to observe the first two consecutive red events and then to respond only to the third, green target event location, by pressing one of four corresponding buttons with their dominant hand. Red events were displayed for 120 ms each, and the green target remained in view until participants made a correct response to its location, with 650 ms separating the correct response and the first cue on the following trial [6].

A randomly chosen set of 16 triplets occurred with high probability (HP) and the remaining possible 32 triplets occurred with low probability (LP). Repetitions (e.g., 111, 222) and trills (e.g., 141, 232) were not presented because studies have shown that they reflect pre-existing response tendencies, in addition to learning [40–42]. The frequency of HP to LP triplets was approximately nine to one. Each participant received the same set of HP and LP triplets, but their order of presentation was randomized within each block. Participants were not informed of any regularities; their only instruction was to respond as quickly and accurately as possible. Participants completed three testing sessions, each consisting of 5 blocks of 50 trials. During breaks after each block, participants viewed their mean reaction time and accuracy scores. These scores were presented in an attempt to maintain performance around 92% accuracy. Depending on their accuracy in the preceding block, participants were instructed in one of three ways via a message on the screen: "focus more on speed", "focus more on accuracy" or "speed and accuracy are about right".

2.4. Spatial contextual cueing task (SCCT)

Participants viewed 12 item stimulus arrays that each contained a single target, a horizontal letter T (rotated 90°) and 11 distractors, which were rotated letter L's (0°, 90°, 180°, or 270°) that were made to look more like the target by offsetting the point of intersection by 3 pixels ([16]; expt. 2) (see Fig. 1b). These visual arrays were presented in white against a gray background and were randomly generated by placing the 12 items into cells of an invisible grid (6 rows × 8 columns), with items repositioned by 63 pixels along each axis to avoid colinearity. Target location was balanced for distance from the screen's center and screen half (left/right); no target appeared in the four center or corner cells.

On each trial, a white fixation dot appeared for 1 s, followed by a visual array that remained on the screen for up to 10 s until a response was made. Participants were asked to locate the target and to respond to its orientation as quickly and as accurately as possible by pressing the "z" (if the tail of the T was facing left) or "/" (if the tail of the T was facing right) on the keyboard, making no more than 1 or 2 errors per block. Once a response was detected, participants received auditory feedback of a high-pitch tone for a correct response or a low-pitch tone for an incorrect response. If no response was made, a low-pitch tone sounded after 10 s.

A spatial contextual regularity is embedded in this task, such that half the visual arrays repeated across blocks. In these repeated arrays, the distractor array predicted
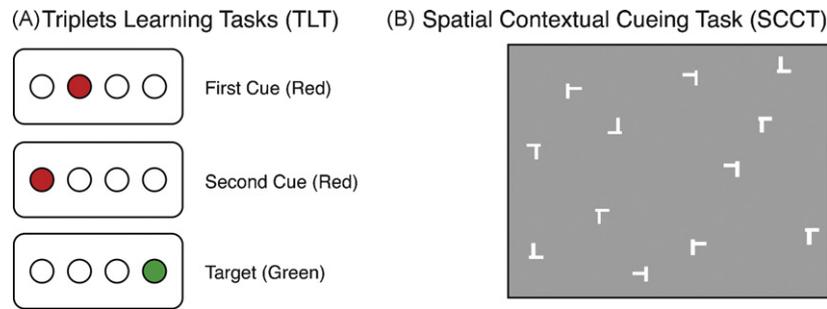
(A) Triplets Learning Tasks (TLT)

First Cue (Red)

Second Cue (Red)

Target (Green)

(B) Spatial Contextual Cueing Task (SCCT)

Fig. 1. Sample displays from the triplets learning task (A) and spatial contextual cueing task (B).

the location of the target, but not its orientation (i.e., the correct response). In other words, regularities in spatial arrays provided contextual guidance for the location of the target, but not whether the target was facing left or right. The remaining arrays for each block were randomly generated for each trial, creating a novel configuration that only appeared once throughout the experiment. Each participant received the same set of repeated and novel arrays, but their order was randomized within each block. Following 12 practice trials, participants completed 30 blocks of 12 trials each, with 6 repeated and 6 novel trials per block [43]. Participants were encouraged to take short breaks after each block.

2.5. Procedure

Participants first performed the TLT, followed by the SCCT within a single testing session. Including breaks, total testing time was approximately 1 h. On a separate testing day, typically the next day but no more than a week later, participants completed two other unrelated implicit learning tasks that are not reported here. At this time, the experiment concluded with an interview as a probe of participants' declarative knowledge in all the implicit learning tasks. Four increasingly specific questions were asked: (1) Did you notice anything about the tasks you have performed? (2) Did you notice any repeating patterns within the tasks? (3) Did you use any particular strategies? (4) There were, in fact, regularities in the tasks you just completed. Knowing this, could you describe any of these regularities? Both the TLT and SCCT have consistently yielded evidence of implicit learning on sensitive recognition tasks [6,43]; therefore, we did not include such measures after each task in the current study in order to keep learning implicit in all tasks completed.

3. Results

3.1. Implicit sequence learning (TLT)

Median reaction times (RTs) were determined for correct responses for each triplet type for each participant on each block. Overall accuracy was ∼93%, so few trials were omitted. These data were then averaged across blocks to obtain a single mean RT for each participant for HP and LP triplets for each of the 3 testing sessions. A similar procedure was used to calculate the mean accuracy for each participant for each triplet type.

To assess potential group differences in implicit sequence learning, genotype (9-repeat carriers, 10/10 homozygotes) × triplet type (HP, LP) × session (1–3) mixed-design ANOVAs were conducted separately for accuracy and reaction time measures. Genotype varied between-subjects, and triplet type and session varied within-subjects. For accuracy, sequence learning was revealed as a main effect of triplet type, $F(1, 35) = 8.54$, $p = .006$, $r_{effect} = .44$, with more accurate responses to HP vs. LP triplets. There was a main effect of session, $F(2, 70) = 4.87$, $p = .01$, $r_{effect} = .35$, demonstrating that the feedback provided after every block guided participants to overall performance levels of 92% accuracy, as intended. No interactions reached significance (p's > .26). The lack of a main effect or interaction with genotype showed that feedback served to successfully match the groups on overall accuracy, which aids interpretation of reaction time data, in that there are no speed-accuracy trade offs.

For reaction time, skill learning can be seen in Fig. 2, with overall RT (regardless of triplet type) decreasing across sessions, $F(2, 70) = 35.53$, $p < .0001$, $r_{effect} = .71$, reflecting overall skill and prac-

tice. Sequence learning was seen as a main effect of triplet type, $F(1, 35) = 98.85$, $p < .0001$, $r_{effect} = .86$, with faster responding to HP relative to LP triplets. This sequence learning effect (or separation of HP and LP trials) increased with practice, as indicated by the significant triplet type × session interaction, $F(2, 70) = 3.59$, $p = .03$, $r_{effect} = .31$. Finally, and most important, there was a genotype × triplet type × session interaction, $F(2, 70) = 5.19$, $p = .008$, $r_{effect} = .36$, indicating that there are group differences between genotypes which vary with practice. No other main effects or interactions reached significance (p's > .26).

To explore this interaction more fully, we calculated sequence-specific learning scores, i.e., mean difference RT scores (LP − HP), which are shown in Fig. 3a. Single sample t-tests indicated that these learning scores were significantly different from 0 for all three sessions (session 1: $t(37) = 4.93$, $p < .0001$, $r_{effect} = .41$; session 2: $t(37) = 7.99$, $p < .0001$, $r_{effect} = .65$; session 3: $t(37) = 7.55$, $p < .0001$, $r_{effect} = .62$), indicating sequence-specific learning. Most importantly, as predicted, when these scores were compared between the genotypes at each session, learning was significantly greater for the 9-repeat carriers than the 10/10 homozygotes in session 3 only, $t(35) = 2.25$, $p = .03$, $r_{effect} = .13$.

The same effect can be seen in Fig. 3b, which illustrates individual RT difference scores from session 3. Using a median split on these difference scores, we classified any subject with a difference score greater than or equal to 27.4 as being a high learner and any subject with a difference score less than 27.4 as being a low learner (see Fig. 3b). Of the 19 high learners, 13 were 9-repeat carriers and 6 were 10/10 homozygotes and of the 18 low learners, 5 were 9-repeat carriers and 13 were 10/10 homozygotes, $\chi^2(2) = 6.11$, $p = .01$. Thus, at the individual level, most 9-repeat carriers were high learners whereas most 10/10 homozygotes were low learners.

3.2. Implicit spatial context learning (SCCT)

For each participant, median RT for correct trials and percentages of correct responses were calculated separately for each array
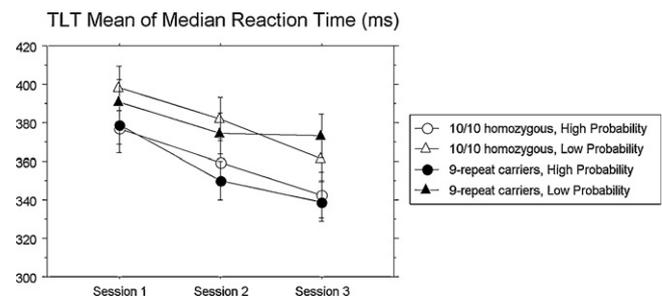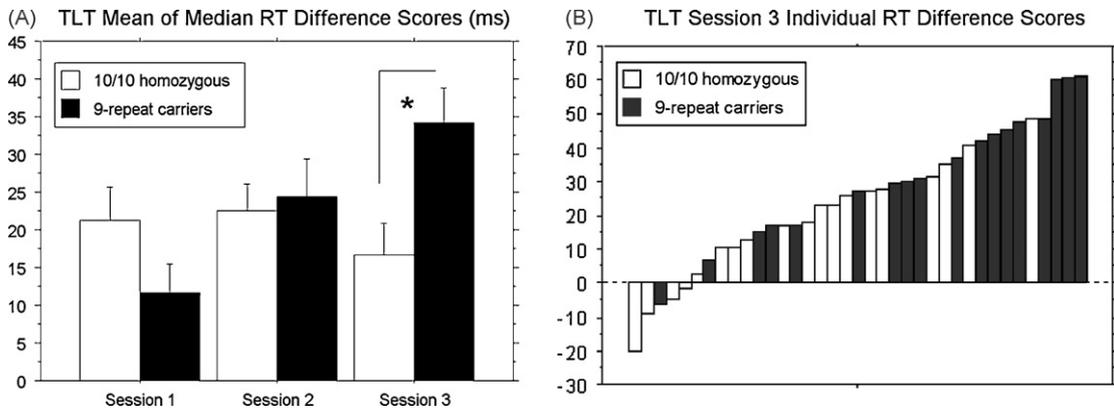

Fig. 2. Triplets learning task (TLT). Mean of median reaction time (ms) over sessions for high- and low-probability triplets for 9-repeat carriers and 10/10 homozygotes. Error bars represent the standard error of the mean.

Fig. 3. Triplets learning task (TLT). (A) Mean of median reaction time difference scores (ms) between triplet types (i.e., low probability minus high probability) across sessions for each genotype. Error bars represent standard error of the mean. (B) Mean of median reaction time difference scores (ms) for individual subjects for session 3, with subjects ordered by the magnitude of their difference score.

type for each block and averaged into three 10 block sessions. Similar to TLT, mean of median RTs (see Fig. 4) and mean accuracy were analyzed separately in genotype (9-repeat carriers, 10/10 homozygotes) × array (repeated, novel) × session (1–3) mixed ANOVAs, with genotype varied between-subjects, and array and session varied within-subjects. For accuracy, visual search skill learning was seen as a significant main effect of session, $F(2, 70) = 5.72$, $p = .005$, $r_{effect} = .38$, showing that accuracy improved with practice. No other main effects or interactions reached significance ($p > .12$). Overall, accuracy was high ($M = 94.9\%$, SD $= .05$).

For mean of median RT, shown in Fig. 4, visual search skill learning was revealed by a significant main effect of session, $F(2, 70) = 94.01$, $p < .0001$, $r_{effect} = .85$, demonstrating that responses became faster with practice. Spatial context learning was revealed by a significant main effect of array, $F(1, 35) = 18.00$, $p = .002$, $r_{effect} = .58$; participants responded faster to repeated vs. novel arrays. Finally, as predicted, no main effects or interactions with genotype approached significance, $p > .35$, indicating that contextual learning did not differ for 9-repeat carriers and 10/10 homozygotes.

Because there was no array × session interaction, we conducted an ANOVA across blocks (1–10) within the first session only, to ensure that the main effect of array was reflecting learning. This revealed a significant array × block interaction, $F(9, 324) = 2.04$, $p < .05$, $r_{effect} = .23$, with the array effect significant on block 10, $t(36) = 2.32$, $p < .05$, $r_{effect} = .13$, but not on block 1, $t(36) = 1.66$, $p > .05$, $r_{effect} = .07$. No main effects or interactions with genotype were significant (p's $> .12$). Thus, learning occurred within the first session for both groups.
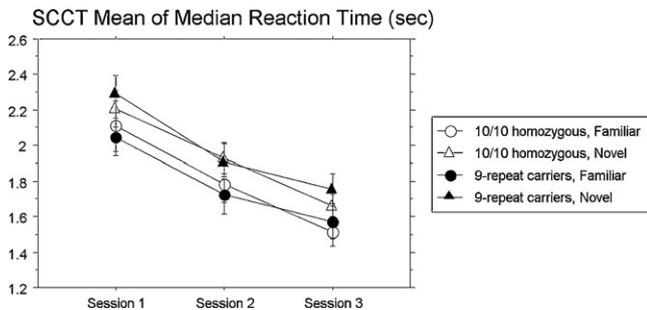
Fig. 4. Spatial contextual cueing task (SCCT). Mean of median reaction time (s) over sessions for new and repeated configurations for both 9-repeat carriers and 10/10 homozygotes. Error bars represent the standard error of the mean.

3.3. Implicitness

Comments from the post-experimental interviews were examined for insight into the regularities that may have been detected or the strategies people used. These revealed no evidence of declarative knowledge. No one could accurately describe the regularities from the TLT or the SCCT. In addition, no explicit strategies for these two learning tasks were reported.

4. Discussion

The present study investigated whether DAT1 genotype contributed to individual differences in implicit learning of sequential regularities and spatial contexts in healthy young adults. As predicted, DAT1 was related to sequence learning, with greater learning for the 9-repeat carriers than 10/10 homozygotes over time. In contrast, there were no significant group differences in spatial contextual learning. Because response speed and accuracy were nearly identical between the groups for both learning tasks, overall performance differences cannot account for the observed implicit sequence learning differences, suggesting specificity in how DAT1 contributes to neural and behavior functions. To our knowledge, this is the first study to reveal a relationship between DAT1 and implicit learning, indicating that some individual differences in implicit learning of sequential regularities are influenced by genotype.

Reduced sequence learning in 10/10 homozygotes likely reflects differences in striatal dopamine between DAT1 genotypes. Indeed, our results are consistent with the assumption that 10/10 homozygotes have greater levels of striatal DAT availability when compared to 9-repeat carriers [28–32] and that this higher gene expression leads to decreased levels of synaptic dopamine in that region [33]. Thus, our findings demonstrate the importance of dopamine for implicit sequence learning, even in healthy young adults. Reductions in striatal dopamine have previously been found to impair implicit sequence learning, as revealed by learning deficits in Parkinson's disease patients [44]. Similarly, children with ADHD, a disorder well characterized by dopamine dysfunction [45,46], have shown sequence learning impairments in comparison to healthy controls [47]. Moreover, older adults show reduced implicit sequence learning relative to young adults [6,48,49] that may result from age-related decreases in striatal dopamine [50–52]. In fact, when using the same version of the TLT used here, older adults performed similarly to the present study's young 10/10 homozygotes in that the learning deficit was revealed only in the third training session [53].

If 9-repeat carriers are indeed learning more than 10/10 homozygotes, then they would be predicted to respond faster on HP triplets and slower on LP triplets than 10/10 homozygotes. This is because as people learn the predictive relationships within the triplets, they increasingly anticipate the correct target on trials with HP triplets. In contrast, on trials with LP triplets, people come to anticipate a different target than actually occurs. Thus, to avoid making too many errors (participants were guided to 92% accuracy), participants must first inhibit the expected, incorrect response. The results shown in Fig. 2 are consistent with this, but with the group difference carried primarily by the LP trials. This pattern of results may be related to ceiling performance on the HP trials, in that participants were responding around 340 ms by session 3 (M: 339.46, SE: 7.8), which is faster than what has been reported previously for HP triplets in the TLT [6,18]. Thus, responses to the LP triplets may provide a more sensitive measure of triplet contingency learning in the present study. This interpretation is also consistent with reports that 9-repeat carriers have increased incidence of response inhibition when compared to 10/10 homozygotes [54,55].

Though some studies of healthy young adults have revealed significant behavioral differences as a function of DAT1 genotype [56,57], most work has revealed minimal or non-existent behavioral differences between genotypes ([58,59], see also [60], for a review). Here, we demonstrated a significant difference in sequence learning between DAT1 genotype that was not driven by just one or two subjects. This indicates that the TLT may be among the more sensitive measures to reveal behavioral effects of DAT1 genotype, perhaps because the task recruits fewer regions outside the DAT-rich striatum than previously employed tasks.

To our knowledge, only one previous study has examined the relationship between genotype at a polymorphism relevant to the dopamine system and implicit learning. Keri et al. [61] used a weather prediction task that has been characterized by implicit striatal-based processes during early learning and explicit MTL-based processes later on [62]. Results revealed that a polymorphism of the dopamine D3 receptor (DRD3) gene, which is found in higher densities in the ventral striatum relative to the MTL [63], was associated with early, striatal-based learning, but not later, MTL-based learning. These findings, together with the present study, suggest that relationships between implicit learning and dopaminergic genes can provide additional insight into the neurochemical and neuroanatomical mechanisms of implicit learning. For example, our results provide evidence that contextual cueing and sequence learning involve different neural substrates [18,19,21,47]. Because DAT1 has greater expression in the striatum relative to the MTL [23], our findings add to a body of work showing that implicit sequence learning requires striatal brain networks as training progresses, whereas implicit spatial context learning does not, reflecting instead the integrity of the MTL (e.g., [16]).

Future research will be needed to overcome some limitations in the current study. First, the sample here is relatively small. Because the rate of false positive results is higher with smaller samples and less power [1], replication with a larger sample is in order.

Second, we included no measures of explicit knowledge of the presented spatial or temporal patterns, other than a brief post-experimental interview. Even so, extensive evidence, using similar participant populations and the same versions of the TLT and the SCCT as those used here, indicates that even when sensitive recognition tests are given, people are unable to discriminate between predictable and unpredictable items, thus showing no explicit knowledge [6,43]. Further, people do not report adopting conscious, deliberate strategies for stimulus selection [13,18,19]. This stands in contrast to other learning tasks, like weather prediction [62], in which participants often develop explicit knowledge with practice and use hypothesis-testing strategies that make it difficult to dissociate implicit from explicit learning [64].

Third, we did not counterbalance task order; participants always completed the TLT before the SCCT. As a result, participants may have been more fatigued for the second task. However, this is unlikely to explain our pattern of results. Both implicit learning paradigms were relatively short (∼30 min each), and thus, training was not significantly longer than typical testing sessions. Moreover, both groups demonstrated strong learning effects in both sequence and spatial context learning that are comparable to previous studies of similar populations (see [6,43]). Further, it seems unlikely that genotype would interact with fatigue to confound the results presented here.

The present study extends evidence for genetic influences on cognition beyond the domain of explicit processes to implicit forms of learning. Future studies should explore the contributions of multiple dopaminergic genes for possible gene–gene interactions on implicit learning. For example, if there is a dopamine dosage effect, alleles that decrease dopamine availability might combine to further impair implicit sequence learning. Alternatively, there may be specificity in how different dopamine genes influence different forms of implicit learning, depending on the regions of the brain where genes are preferentially expressed and protein expression patterns. Sequence learning may be more sensitive to DAT1 genotype, whereas other forms of learning (e.g., reward-based learning) may be more sensitive to polymorphisms in other genes relevant to dopaminergic function (e.g., DARPP-32, DRD2) [65].

5. Conclusions

In sum, our findings revealed an association between a polymorphism of DAT1 and striatal-based implicit sequence learning, such that the presence of at least one 9-repeat allele was beneficial for detecting sequential regularities over time. In contrast, no relationship was observed between DAT1 genotype and implicit spatial context learning, a form of learning associated with the MTL. How these implicit learning differences influence real-world behaviors should be a topic of future research. The continued study of genetic influence on cognitive functioning among healthy adults may provide more insight into the neurochemical and anatomical correlates of memory, including various forms of implicit learning and processing.

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