Play and Child Development

The Role of Genetic and Environmental Influences on Young Children's Play
A Working Paper and Problem Analysis

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Abstract

Questions about how play develops continues to be an enigma to play researchers. Studies of the mechanisms and specific trajectories by which early years play come to impact aspects of child development are also limited. Behavioural genetics is a potentially useful research method which can be used to unpack questions about the origins of play. Despite being widely used to address aetiological questions about varying aspects of development; there are few attempts to apply behavioural genetics research to the study of play. This project will addresss this gap by using variables related to children, their parents, and the genetic propensities of both to explore linkages or interactions between play, children's outcomes and their environment. Existing cohort datasets from longitudinal studies (e.g. TEDS, ALSPAC, and MOBA) will be used to test hypotheses and validate findings by comparing results across data sets. The goal is to explore individual differences in children's play, the interaction between them, and determine whether associations between play and developmental outcomes are mediated by shared genetic or environmental factors. This work will make an important contribution to discussions about the nature and origin of play.

1 Introduction

That play is an integral aspect of child development is uncontested. For instance, evidence from the play literature shows critical links between play and important social, cognitive, and language outcomes in early childhood for different types of play (Lai, Ang, Por, & Liew, 2018; Weisberg, Zosh, Hirsh-Pasek, & Golinkoff, 2013). Yet play remains an enigma to researchers, specifically to those interested in questions about how play develops and whether play is causally linked to outcomes in child development (Weisberg & Gopnik, 2013). Criticisms of play research point out that studies of play primarily report behavioural associations that do not support strong causal claims about the contribution of play to specific aspects of child development (Lai et al., 2018; Lillard, 2013). In response, there is a call for better research, as well as different types of research that can clarify the possible roles of [pretend] play on development (Lillard et al., 2013). A likely means to achieve this goal is to explore alternative methodological approaches that differ from the typical behavioural research approaches traditionally used to study children's play. For instance, in contrast to correlational studies there should be more high-quality RCTs, longitudinal studies, as well as employing advance statistical models like Structural Equation Modeling in developmental work.

Towards this end, a promising yet unexplored alternative that can be applied to studying play is behavioural genetics research. According to Plomin (2001) behavioural genetics research has a long history of being instrumental in demonstrating the importance of genetics throughout psychology. He argues that behavioural genetics research is distinguished from psychology in that it asks questions about why individuals within a species differ in behaviour, the extent to which individual differences in behaviour are attributed to environmental and genetic influences, and the identification of specific genes responsible for the genetic influences on psychological traits or disorders; whereas, psychology addresses species-typical behaviour, e.g. the average age when pretend play emerges. Importantly, research in behavioural genetics have made significant inroads in studying complex psychological traits. It is, therefore, plausible to use behavioural genetics methodologies to investigate aetiological questions about why and how play develops.

In this research project, we will use a behavioural genetics approach to investigate the extent to which genetic and environmental influences predict individual differences in children's play, the interaction between genetic and specific environment influences, and whether associations between play and developmental outcomes like social skills, cognitive ability, language, and psychopathology are mediated by shared genetic or environmental factors including parents' genetics. This research project presents an innovative approach to better understanding the function of play, its origin, and purpose in child development. The goal is to advance understanding on how children's playful behaviours come to be and the pathways via which they exert their influence.

To further these aims, this problem analysis report is structured to include a discussion of an operational definition of play. We then present perspectives on the link between play and developmental outcomes and make a case for using behavioural genetics to study play. The subsequent sections in the paper maps out the phases of the project year by year and how the success of the project will be evaluated.

2 Operationalisation of Play

In order to tackle questions about genetic influence, we first need to operationalise the concept of play for this project. Historically, play is challenging to define owing to its multidimensional characteristic. To capture the multifaceted nature of play, we use a five criteria definition proposed by Burghardt (2010) who states that play: [1] is incompletely functional in the context in which it appears (e.g., it is not serious, of immediate use, or necessary for survival.);[2] is spontaneous, pleasurable, rewarding, or voluntary;[3] differs from other more serious behaviours in form (e.g., exaggerated) or timing (e.g., occurring early in life before the more serious version is needed); [4] is repeated, but not in abnormal and unvarying stereotypic form (e.g. distressed rocking, pacing); and [5] is initiated in the absence of acute or chronic stress (e.g., is uncoerced, appears voluntary, and engages the interest of the agent).

For an activity to be considered playful all five criteria must be met in some respect (Burghardt,

2010). We think this conceptualisation is appropriate because it broadly accounts for play across species - in humans and animals [1]. For children, these may be exemplified as engagement in physical play, play with objects, symbolic play, pretence, socio-dramatic play, and games with rules - the five broad types of playful activities categorised by (Whitebread, Basilio, Kuvalja, & Verma, 2012). We will use this conceptualisation of play to capture the naturalistic and diverse ways that play is typically measured in large-scale longitudinal cohort studies which will be the source of data used for this research. Cohort studies typically measure children's engagement in playful activities by recording the different types and frequency of play that children participate in.

3 Play and Development

For nuero-typical children, play is purported to positively impact development. Evidence from observational and experimental research links play to language, emotional development, executive functions, social skills, problem solving, and creativity (Lillard et al., 2013). For instance, play is argued as critical for language learning and adult scaffolding through guided play is found to be influential in supporting learning (Hà, 2022; Weisberg & Gopnik, 2013). Early symbolic play abilities are closely related to long-term language development and pretend play has been linked to narrative development (Zhao & Gibson, 2022; Nicolopoulou & Ilgaz, 2013). Peer play or social play mediated by mother's support is found to be associated with reduced levels of anxiety in children and fathers engagement in playful interactions with children can have a positive influence on the children's socio-emotional development (Metin Aslan & Altinisik, 2022; Amodia-Bidakowska, Laverty, & Ramchandani, 2020). Playful activities like games and pretend play reportedly have positive psychomotor effects and contribute to significantly improving children's motor skills (Lai et al., 2018; Stagnitti & Unsworth, 2000). Additionally, role-playing is found to significantly bolster executive functions as well as general cognitive ability (Veraksa et al., 2021). Essentially, studies researching different types of play and how play links to development are ubiquitous in

[1] Although this work focuses on playful interactions in human, contrasts of inter-species can help clarify why play is ubiquitous.

psychology and for the most part have been beneficial in depicting how play develops and changes across the lifespan.

Theories of play underpin hypothesis generation in play research in psychology. According to Pellegrini, Dupuis, and Smith (2007), it is likely that early-years play is a low-risk strategy for developing traits that will be adaptive to an individuals' current and subsequent environments. From this perspective, play is construed as an adaptation which evolved to develop specific skills or developmental outcomes. This notion of play aligns with the idea that play serves an evolutionary function, a view that is widely argued in development psychology which suggests that play affords opportunities for the generation of new, and possibly adaptive, responses to novel environments (Pellegrini et al., 2007; Sgro & Mychasiuk, 2020). Evolutionary theory suggests that play behaviours persist when the benefits exceed its cost suggesting that the energy, time, and associated risks from playing results in some form of benefit and the costs of play may vary in different environments as available resources may modulate the costs and benefits of play (Jensen, 2021). The crux of the evolutionary argument is that the long period of childhood that mammal juveniles experience and the ubiquity of play during that period likely serves a functional purpose in their development (Buchsbaum, Bridgers, Skolnick Weisberg, & Gopnik, 2012).

However, another perspective proposed by Smith (2002) considers three competing views: (1) that play is simply a by product of development with no important developmental impact; (2) that play facilitates development in that it can help bring out important developmental outcomes but other developmental pathways can also generate similar consequences, and; (3) play is indeed necessary for specific important aspects of development and in its absence developmental outcomes will be significantly held back. These three hypotheses move beyond the functional evolutionary perspective and invites play researchers to critically consider other feasible explanations of why children play. Additionally, even when associations between play and development are identified the research does not necessarily distinguish whether the experiential effects of play are immediate or if the impact is long-term and only beneficial as children grow and become adults. Evaluating the impact of play from these three perspectives can be useful as Pellis, Burghardt, Palagi, and Mangel

(2015) cautions about treating the "why" - in studying why children play - as solely in terms of a function outcome because even if a particular function is served by play, it is unlikely to be served in the same manner for all species and environmental contexts. For instance, links between play and development may not be consistent when we begin to account for factors like individual and cultural differences in children's play, as well as variations in types of playful activities.

Guided by the significant contributions of genetic research to understanding complex human traits on topics like cognition, social interactions, and neurodivergent traits. (Polderman et al., 2015); we anticipate that learning about the influence of genetic and environmental effects on play including understanding the extent to which DNA explains individual differences can influence our understanding of existing theories of play. It is likely that we could also draw new knowledge and glean important conclusions from the study of play and genetics. The findings could potentially refine our understanding of how play develops, its impact on development, as well as our thinking on existing and potentially new theories of play.

4 Play and Behavioural Genetics

To understand how we can use behavioural genetics to study play requires a good understanding of the tenets of behavioural genetics research. There are some core principles of behavioural genetics that underpin the field and facilitate the interpretation of work in this space. This section will provide an overview of behavioural genetics research and suggest how behavioural genetics methods can be applied to the study of play.

Behavioural genetics is the study of genetic and environmental influences on behaviors or phenotypic traits (DiLalla, 2017; Nuffield, 2002). Genetics are the entire complement of an individual's DNA genotype. Phenotypes are all measurable or observable characteristics aside from an individual's genes. Environment refers to everything that influences an individual's phenotype e.g. biological factors, siblings, home setting, etc., apart from an individual's genotype. Research in behavioural genetics study individual differences for a trait at the level of the population not the in-

dividual. Some key assumptions of behavioural genetics research assert that the manifestation of a trait (or phenotype) can be explained by both genetic as well as non-genetic (or environmental) factors; more than one genetic factor usually contributes to a trait; and multiple genetic factors may interact with each other and have different effects depending on which other factors are present in the individual's genotype. Associations between genes and the environment may manifest in different forms of gene-environment interplays, e.g. gene-enviroment correlations whereby genetic and environmental influences on a trait may be correlated [2] or gene-environment interactions whereby genetic influences on a trait or behaviour are moderated by specific environmental exposures (Nuffield, 2002). The expectation is that by examining genetic influences more information can be gleaned about how the environment operates to affect behavior.

Behavioural geneticists use varied research designs to study the contribution that genetic factors make to human behaviour. These include the use of family studies that use observational research designs to assess and compare similarities between relatives - twins, siblings, and adopted children versus biological children. Family studies apply quantitative genetic methods [3] to examine the extent to which variations in traits are influenced by genetic factors in the population without focusing on particularly genes. A caveat, however, is that findings may be confounded by environmental influences which make family members similar. The study of twins is one type of family design and is perhaps one of the most common behavioural genetic research designs (Ayorech et al., 2016; McGue, 2010). Therefore, it could be usefully applied to study children's play.

The classical twin design compares the resemblance within pairs of reared-together identical twins who are genetically identical (monozygotic twins who share one hundred percent of their

[2]There are three types of gene-environment correlations:(1) Passive gene–environment correlation: where children inherit both genetic and environmental factors from their parents – for example, the children of musicians would inherit genetic factors that are associated with higher musical ability and would also be exposed to an environment with lots of activities related to music. (2) Active gene–environment correlation: where children actively create their environmental experiences based on their genetic propensities – for example, a musical child seeking out opportunities to learn instruments or join a choir. (3) Evocative gene–environment correlation: where children evoke environmental experiences that are correlated with their genetic propensities – for example, a musical child would be more likely to be noticed by the music teacher at school, who in turn would provide enhanced opportunities to that child (Asbury, McBride, & Rimfeld, 2021).

[3]Quantitative Genetics: A theory of multiple-gene influences that together with environmental variation, result in quantitative distributions of phenotypes. Quantitative genetic methods estimate genetic and environmental contributions to phenotypic variance and convariance in a population (Knopik, Neiderhiser, DeFries, & Plomin, 2017)

DNA) to the resemblance of within pairs of fraternal twins (dizygotic twins who are fifty percent similar genetically; same as non-twin siblings) (Knopik et al., 2017). The assumption of the classical twin design is that if genetic factors are important, then monozygotic twins (same-sex twins) should be more similar than dizygotic twins. From twin designs, a heritability statistic is estimated by comparing the correlation between identical twins with the correlation between fraternal twins for a specific trait (McGue, 2010). Heritability is interpreted as the proportion of the total phenotypic variance of a trait that is explained by genetic factors and environmental factors [4]. (Asbury et al., 2021). As a population statistic, heritability addresses genetic contributions to individual differences within a population. For example, if the heritability of height is ninety percent this means that ninety percent of the individual differences in height is due to genetic influences. Similarly, the heritability of play can tell us if children's propensity to be playful in a given context is primarily due to genetic influences. An understanding of the heritability of play can illuminate whether individual differences in children's play are attributed to genetic or environment factors or unmeasured shared and/non-shared environmental components. Such information can further justify the appropriateness of approaches like play-based interventions on different aspects of developmental delay. Although a caveat is that environment, genetic, or heritability estimates could differ in different populations at different times; hence interpretations are context bound (Knopik et al., 2017).

Just as twin studies estimate the effects of unmeasured genes and environmental influences on traits, there are behavioural genetic designs that can test the effects of measured genes directly rather than indirectly - as done with twin studies (Posthuma et al., 2003; Knopik et al., 2017). A genome-wide association study (GWAS) is one such design used to assesses the association between individual differences in a phenotype and DNA variations using thousands of individuals who have been genotyped on hundreds of thousands of DNA markers. The DNA markers are a catalog of common genetic variants or usually single nueclotide polymorphisms (SNPs) that

[4]Heritability in the context of twin studies constitute genetic factors - an indirect inference of DNA and environmental factors comprising of the shared environment - factors which make family members similar to one another and non-shared environments - factors which make family members different from one another (taking into account measurement error).

occur on the human genome (Stranger, Stahl, & Raj, 2011) [5]. Derived from the integration of quantitative genetics and molecuar genetics [6], GWAS directly test the effect of measured genetic variants in an attempt to identify specific genes responsible for genetic influence on behaviour, particularly complex traits; although, the joint variance explained by identified genetic variants is typically smaller than the heritability estimates from twin studies. SNP heritability measures the proportion of phenotypic variance explained by all measured SNPs (Zhu & Zhou, 2020). Previous GWAS have found significant gene variants associated with phenotypes like cognitive function, cognitive flexibility, educational attainment and childhood intelligence (Davies et al., 2016; Zhang et al., 2018). Similarly, A GWAS study could be useful for identifying genome-wide significant genetic loci associated with a trait - in this context play; which can then be further investigated to determine the functional relevance.

As with all GWAS of complex traits, interpretation of findings will involve navigating issues like pleiotropy, small gene effects, and limitations relating to ancestry in cohort studies. Pleiotropy is the phenomenon in which a single gene simultaneously influences a number of seemingly unrelated phenotypes. Small gene effects refers to cases where thousands of variants each have a small effect on a trait. Limitations of ancestry in cohort studies minimises study generalisability - an observation previously highlighted about twin studies (Nuffield, 2002). Notwithstanding, when carefully implemented and appropriately interpreted, GWAS produce robust results about complex relationships from studying genetic and phenotypic variations of traits - of which very little is known about children's play (Uffelmann et al., 2021).

One of the ways researchers use the results from GWAS is by using genome-wide significant SNPs to calculate polygenic scores (PS) (Choi, Mak, & O'Reilly, 2020). A large number of genetic variants or PS have been found to be associated with a wide range of complex traits. Therefore, we aim to estimate genetic correlations between traits by testing PS for play against other specific developmental phenotypes. This will indicate the degree of genetic correlation between play and

[5]Polymorphism is a locus with two or more alleles and a SNP is the most common type of DNA polymorphism which involves a mutation in a single nucleotide (Knopik et al., 2017).

[6]Molecular genetic methods involve studying genes at the level of the nucleotide sequence (Nuffield, 2002).

the developmental outcome. Equally, if the findings from GWAS studies prove inconclusive; an alternatively approach is to consider whether play moderates known genetic correlations reported in the literature, for example, genetic variants of language development and psycho-social outcomes ((Newbury et al., 2019)), genetic variants of cognitive functions/intelligence and achievement ((Davies et al., 2016)), etc. Armstrong-Carter, Wertz, and Domingue (2021) point out that polygenic scores for GWAs of a specific outcome (e.g., educational attainment) are relevant not just to researchers interested in that outcome (e.g., education) per se but also researchers studying children's development in other related domains.

At this point, there is little research on gene environment interactions in relation to children's play with the exception of experimental work in non-humans species that report independent effects of early experience and genetically influenced traits on social play (Gray, 2019; Herman, et al., 2010; Sgro, 2020). Consequently, it remains unclear whether play can be attributed to being heritable nor do we know the extent to which children and parents genetic propensities interact with and create environments that are conducive to playful behaviours. It could be that genetic and environmental influences either interact over time to produce diverse behavioural responses or acquired behaviour influences one's genotype (Pellegrini et al., 2007; Sgro & Mychasiuk, 2020). A comprehensive behavioural genetics approach like this study can allow us to begin to unpack genetic and environmental influences on children's play, if they exist.

5 Project Aims

We propose a project that combines variables related to children's play, their development and the genetic propensities of children as well as their parents where possible. We use these variables to explore linkages between phenotypic traits related to children's play and development with environment and genetic influences. During each year of the project, we aim to undertake distinct goals.

Year One: We will investigate the heritability of play in early childhood using data of twin

pairs from the longitudinal Twins Development Study (TEDS).

Year Two: We will investigate whether children's play behaviours are linked to genetic indices by conducting a genome-wide association (GWAs) study of play using data from the Norwegian Mothers and Fathers Study (MOBA).

Year Three: We seek to determine whether polygenic scores associated with children's playful behaviours are also correlated with other aspects of their developmental using data either from the Avon Longitudinal Study of Parents and Children (ALSPAC).

6 Research Design

A secondary data analysis research design will be implemented using data from multiple cohort studies e.g. the Twins Early Development Study (TEDS), the Norwegian Mother Father and Child Cohort Study (MOBA), and the Avon Longitudinal Study of Parents and Children (ALSPAC) which contain good quality genetic and behavioural data on children and parents. The datasets have very large sample sizes (combined 45,000 families) thus have statistical power appropriate for addressing the proposed research questions. An anticipated challenge will be identifying high quality play variables from each dataset. Additionally, the extent to which the variables will be comparable may limit comparisons across studies. However, this study presents an opportunity to reflect on how play is measured in cohort studies by comparing measured dimensions of play across cohorts and checking whether there a commonalities in a construct level definition of play considering that play is multidimensional. The proposed project will combine cutting edge techniques from the fields of quantitative genetics and developmental psychology to study the routes via which play influences aspects of children's development in a genetically sensitive investigation.

7 Year One

7.1 Research Questions

1. Which child outcomes are most strongly associated with play across childhood?

2. Is play heritable?

7.2 Methods

This study uses twin data from TEDS to determine which child outcomes share the strongest associations with play. The purpose of RQ1 is to collect evidence of significant phenotypic associations between play and development (e.g. cognitive development, language, psychopathology) for children 2-5-years old. The purpose of RQ2 is to estimate the heritability of play and extent to which the phenotypic associations in RQ1 are influenced by overlapping genetic and environmental influences. The extent to which the correlations differ in monozygotic compared to dizygotic twin pairs that will indicate whether genetic/environmental influences are important in the correlations. This study is underway and is preregistered on OSF.

7.3 Training

- Statistical Genetic Methods for Human Complex Traits online session with University of Boulder Colorado, International Statistical Genetics Workshop, 6-16 June, 2022

- Genome-wide association analysis (GWAs) training in preparation for year two, Introduction to the statistical analysis of genome wide association studies, 27th June to 1st July 2022.

8 Year Two

8.1 Research Questions

1. Can we identify genetic predictors of playfulness in children from a genome-wide association study?

8.2 Methods

A genome wide association study (GWAS) will be conducted to examine whether genotype data and is related to phenotypic traits of play in children. For this study, one of the largest European databases of genotype data of children and their parents - the Norwegian Mother and Father and Child Study (MOBA) will be used given it is a larger dataset which will increased the statistical power of the study. The goal is to determine whether there are robust estimates of the SNP-based heritability of play variables and their genetic correlations. This study will be pre-registered on OSF.

9 Year Three

9.1 Research Questions

1. To what extent do genetic variants of play correlate with child development outcomes?

2. Do specific environmental variables (e.g. SES, number of siblings, etc.) moderate genetic influences on play.

3. Are there longitudinal pathways of gene-environment interplay on children's development through play?

9.2 Methods

In this study, first, play polygenic scores will be created which will then be used to test genetic variations between children's play and development. The play PS scores created will be based on the GWAS results from study 2 and as the GWAS was undertaken using MOBA data; PS scores will be created in using ALSPAC data. This is because PS scores are not created in the same sample that the GWAS was carried out. For RQ1, we will explore if genetic variants of play also influence aspects of child development e.g. language, cognitive development, psychopathology, etc. Additional outcome variables, unique to ALSPAC can also be considered for inclusion in the study. If play polygenic scores are significantly associated with the other variables, it will suggest that there some genetic overlap between play and the other variables which would suggest that some of the variants influencing play also influence the other variables. Although different, we will then be able to compare the findings to the results from study 1 which explored the heritability of play with similar variables; thus allowing us to better understanding genetic influences of play using indirect measures (twin study) and direct measures (a study using PS scores). Additionally, RQ2 investigates a moderation effect to determine whether environmental variables moderate the association between play polygenic scores and aspects of development. RQ3 checks associations at different time-points of development (early to middle childhood) to see whether or not they change. This study will also be pre-registered on OSF.

10 Extension of Work

10.1 Research Questions

1. To what extent are correlations between key genetic variants and phenotypic traits relevant to child development moderated by play?

2. Can we model the effect of gene-environment interplay on children's play behaviours using parents' genetics?

3. Is there an effect of genetic nurture on play?

10.2 Methods

In the literature review section, we discussed that it is plausible that the GWAS planned for study 2 could have non-significant results in identifying genetic variants of play. Were this to occur, other research questions could be explored. For instance, we can investigate whether play moderates genetic correlations based on reports of significant genetic influence on related variables. Armstrong-Carter et al. (2021) argue that to select a polygenic score to use in their own work, developmental psychologists may consider not only scores from GWAS of the particular trait they are interested in, but also from GWAS of traits that are related to their trait of interest. Given the ubiquity of play in early childhood, RQ1 proposes an exploratory approach that involves studying the moderating effect of play on observed genetic correlations between variables links to play. Another potentially interesting area of focus is a study of the influence of parents genetics on children's play phenotype. Additionally, an exploration of the phenomenon of genetic nurture whereby the child's phenotype is influenced not only by the transmitted parent alleles but also by the alleles that are were not transmitted could also be explored (Kong et al., 2018).

11 Planning for Impact

Given the novelty of this research, we intend to apply the principles of open science during the life-cycle of the project by sharing for each study pre-registrations, data analysis codes (R-Scripts) and preprint manuscripts on OSF. An overarching project profile linked to OSF will be maintained on Github. The goal is to have an open platform for sharing findings with other [play] researchers and stakeholders who may be interested in the contribution of behavioural genetics research to the study of play. Additionally, we intend to publish the findings from each study and take up opportunities to disseminate research outputs at conferences, seminars, etc. We hope to stimulate impact by sharing research findings with practitioners and policymakers through social and print

media, as well as through other dissemination mediums. For example, we conduct a workshop with practitioners and parents to share and discuss the implications o the work. Play is widely viewed as integral to child development and the findings could justify advocacy for play-based approaches and interventions that support early child development and learning.

12 Expert Panel Consultations

A cadre of experts with diverse backgrounds, e.g. play researchers, genetics researchers, individuals with experience working in policy linked to play or genetics research, practitioners working in early years play settings, etc. have agreed to share critical feedback on this work. The goal is to consult with experts through stimulating conversations that yield a high level of critical discussion and feedback at least once for each year of the project. We appreciate that experts are very busy so anticipate consultations to take approximately two hours or less, yearly. We would like to thank for the following persons for agreeing to be an expert panelist:

- Professor Kathryn Asbury - University of York
- Nicola Bulter - CEO OF Young K and C
- Professor Jenny Gibson - University of Cambridge
- Anita Grant - Islington Play Association
- Dr Olakunle Oginni - Kings College London
- Professor Paul Ramchandani - University of Cambridge
- Dr Deena Weisberg - Villanova University

We appreciate that experts may need to become familiar with the project proposal if they are to share their thoughts on the feasibility of the project and its potential to impact the field of play research. Hence, in the first year, we will share via email the working paper which sets out the

problem analysis and the proposal for the implementation of the research project to individual members of the panel. We will kindly ask experts to read and review the working paper and problem analysis and return oral and/or written feedback that includes their general thoughts and questions on the research ideas proposed. A follow-up meeting (using zoom) can then be scheduled to discuss, with the project lead, impressions of the project and feedback after reading the working paper and problem analysis. As the project is for three years, subsequent consultations (year two and year three) may be held either in the same one-to-one format or as online discussion joint session with members of the panel. We are keen to receive objective input from outside the project team that will add value to the project implementation.

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