

Origins of ASD and its methods of maintenance throughout evolution

Ivo van Haastert

Supervisor: Lysanne Jorna

25-06-2024

Behavioral neuroscience department

Summary

Autism spectrum disorder (ASD) includes a selection of neurodevelopmental disorders that are seen to be highly heritable. Core symptoms of ASD are repetitive obsessive behavior as well as deficits in communication and social interaction. Besides these characteristics, there are many comorbidities observed, including many of the psychiatric disorders. ASD presents itself as a heritable disorder with many negative consequences, its steady prevalence is therefore paradoxical. To find out why ASD still exists, the origin of ASD as well as exposure to evolutionary forces on ASD will be assessed in this thesis.

Explanations for the origin of ASD alleles were found in imbalances of genomic imprinting in genes involved with ASD. Another finding indicated codependence of ASD alleles with intelligence genes to be of importance in ASD origin. Concerning the evolutionary theories hypothesizing why ASD is still around, intertwinement with intelligence and adaptive strategies were discussed. Intelligence was seen to possibly indirectly provide benefits to ASD, while behavioral patterns seen in ASD might have directly led to benefits via specific strategies. These theories provide insightful perspectives on ASD, even in our current society. nevertheless, can they explain only part of the research question. Because of the multifactorial nature of ASD, further research is needed to better understand this complex disorder.

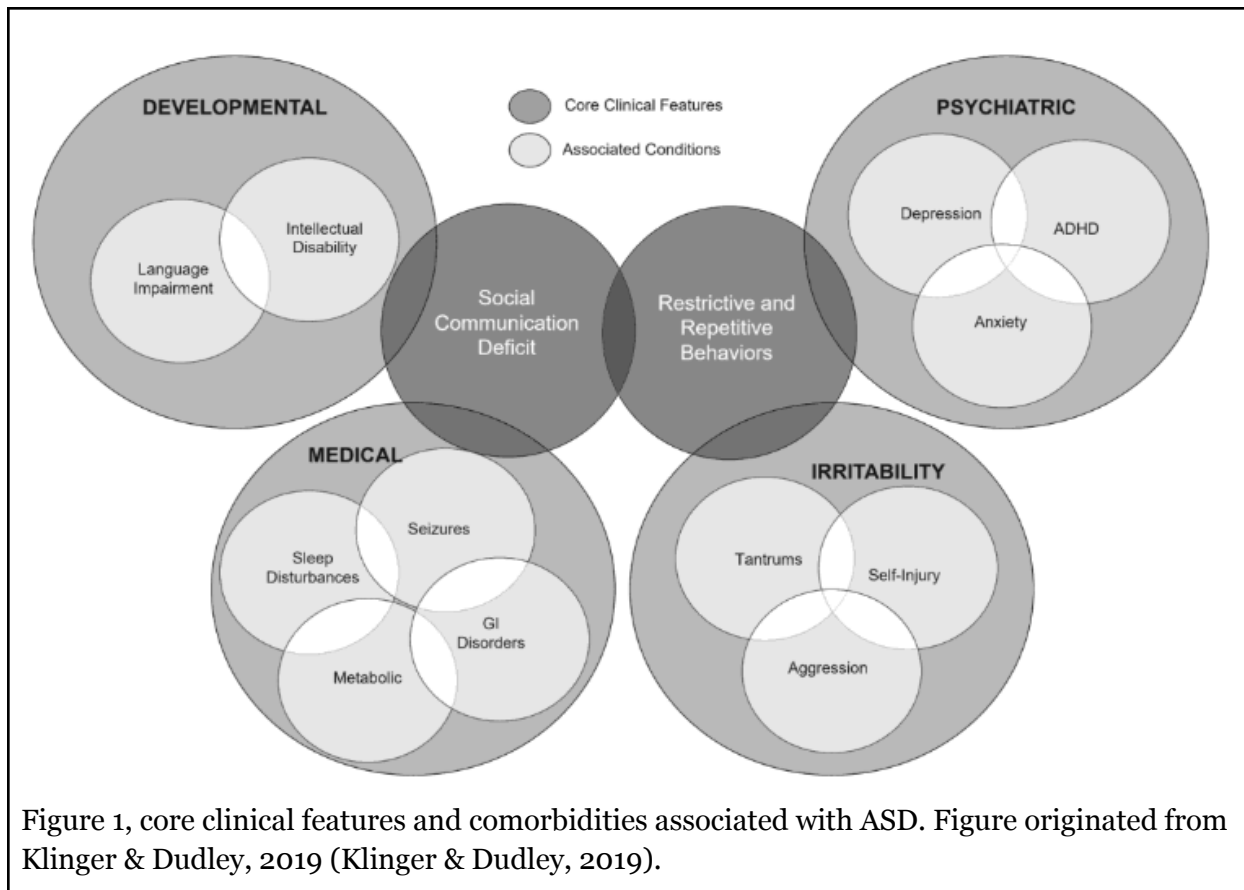
Table of contents

Introduction	2
Chapter 0, ASD genetics background	4
Heterogeneity	4
Polygenicity	5
Epistasis	5
Chapter 1, Where do the ASD alleles come from	6
Imbalanced imprinting	7
Interactions with intelligence	8
Chapter 2, Why did the ASD alleles persist in our society	9
Intelligence	10
Strategy-related fitness benefits	10
Chapter 3, Integration	12
Summary	12
Integration of intelligence theories	12
Integration of genetic and evolutionary theories	12
Timeline	13
The current society	14
Discussion	14
Conclusion	15
Acknowledgements	16
References	16

Introduction

Autism spectrum disorder (ASD) is a collection of neurodevelopmental disorders that are established as highly heritable (Tick et. al., 2015). The prevalence of ASD seems to be increasing, with the Swedish study by *Idring et. al.* concluding an increase of almost 250% from 2001 to 2011 (Idring et. al., 2014). Remarkable statistics arise when subdividing the increase in diagnosis per intelligence quotient (IQ) category. Where cases of ASD with an intellectual disability only increased by approximately 20%, ASD cases with functional or even elevated IQ increased in prevalence by an impactful 700% (Idring et. al., 2014). This IQ-dependent increase can likely be attributed to the enhanced detection of current healthcare, resulting in the identification of milder and better-hidden cases as well. This leads to the conception that the actual prevalence of ASD is still underrepresented. Another factor in the steady increase in the prevalence of diagnosis likely concerns changes in diagnostic criteria (Chiarotti & Venerosi, 2020). The Diagnostic and Statistical Manual (DSM) V states multiple required symptoms for ASD in each of the following categories: Social interaction deficits, impaired communication, and restricted repetitive behavioral patterns (APA, 2013). These criteria are more inclusive than the criteria described in the previous version, the DSM IV (Kim et. al., 2014). There is a highly variable landscape of phenotypes associated with ASD, with a wide array of possible symptoms (Stevens et. al., 2019). These different ways ASD can show itself are debated to be either caused by distinct sub-variants or as a consequence of a severity gradient (Syriopoulou-Delli & Papaefstathiou, 2018). Current literature cannot decisively state which of the two is true. Studies investigating ASD phenotypes do make it clear that the effects and impact of ASD on an individual are dependent on the severity of the disorder (Matson et. al., 2008). Whether this severity is the result of a more or less severe subvariant or a severity gradient is not of importance. The conclusive message resides in the fact that ASD can show very differently according to its severity, therefore it is important to take the severity of ASD into account when theorizing.

The behavioral characteristics, as described in the DSM V criteria, often result in a serious impact on the life of ASD-diagnosed individuals. Reported are both reduced survival rate and quality of life (Mouridsen et. al., 2008; Woolfenden et. al., 2012; DaWalt et. al., 2019; Lin & Huang, 2017). Furthermore, the extensive network of comorbidities is also becoming more evident, due to the improvement of analysis methods. Common comorbidities of ASD include intellectual disability, sleep disturbances, and epilepsy (Kohane et. al., 2012). Comorbid psychological conditions include, but are not limited to: anxiety, attention deficit hyperactivity disorder (ADHD), obsessive-compulsive disorder (OCD), and depression (Khachadourian et. al., 2023). An overview of the comorbidities, including the ties with core morbidities, can be found in Figure 1.



The etiology of ASD is identified to a limited extent, due to its extremely complicated and intricate interplay with various processes. It is known that besides its hereditary side, there are also environmental, developmental, and epigenetic influences (Sealey et al., 2016; Willsey & State, 2015; Kubota & Mochizuki, 2016). Irrespective of this multifactorial cause, twin studies consistently elucidate the strong hereditary characteristics of ASD (Tick et al., 2015). A meta-analysis by *Tick et al.* estimated the role of heritability in explaining causal factors of ASD between 64-91% (Tick et al., 2015). The numbers provided by this meta-analysis clearly show the high heritability seen in the disorder.

Thus, ASD presents itself as a disorder with serious morbidity, including vast comorbidities, while also conveying high heritability. The combination of heritability and morbidity exposes the disorder to evolutionary forces acting through natural selection and adaptation (*Philosophy of Biology*, 2010). These forces rarefy the prevalence of said disorder over time, if not eradicate it, as a consequence of its reduced fitness. According to these evolutionary principles, ASD should decline in prevalence over time. ASD unexpectedly shows to be steadily prevalent. Research shows that ASD alleles have been exposed to strong and complex evolutionary forces, and thereby strong selection (Tsur et al., 2016). Hence, this observed prevalence cannot be explained by a

lack of evolutionary pressure. There must be a reason why ASD can escape the consequences of these evolutionary forces. With the aforementioned higher-than-expected prevalence, some forms of ASD may even indicate to be selected for by evolution. So regardless of the negative effects of ASD alleles, there must be a reason why the genes are still prevalent in our current society.

This thesis will discuss the current conceptions regarding the paradoxical prevalence of ASD, taking two perspectives into account. Firstly, the thesis focuses on the origin of ASD and assesses whether the involved alleles are inevitably incorporated into the population genetics. This could be accomplished via interactions with other mechanisms or even with other genes that are advantageous. Secondly, this thesis assesses the possible advantages of ASD throughout time, localizing any direct advantages the disorder may provide. For instance, a specific mating strategy. Here, the behavioral patterns seen in ASD can contribute to the success of the strategy, leading to an addition of fitness. This concludes the following research question: What could be the origin of ASD and why does ASD remain prevalent in human society throughout time?

Putting together theories answering the question is important, as it will expand the knowledge currently available about ASD, especially focusing on why this disorder is still around. This perspective is valuable, as it highlights the opportunities where ASD can be advantageous, or connected to advantageous traits. Furthermore, the origin of ASD will be assessed as to its interactions with and evolution of other biological processes. This provides a perspective of ASD as an essential component in the development of modern human society. Lastly, will the observation of ASD throughout time allow for illumination of its prospects in the future, i.e. will ASD persist in our society?

Chapter 0, ASD genetics background

This chapter provides an overview of the mechanisms that the genes involved in ASD are exposed to. It illustrates the complexity of the involved genetics, consequently leading to complex expression of its behavioral symptoms and varying severity. Three mechanisms seen to be present in ASD will be discussed: heterogeneity, polygenicity, and epistasis.

Heterogeneity

Heterogeneity refers to a characteristic where multiple variations are present. ASD comprises phenotypic as well as genetic heterogeneity. The phenotypic heterogeneity of ASD has been established in this thesis, by emphasizing the variation in symptoms as well as severity (Warrier et. al., 2022). Genetic heterogeneity is seen as a phenomenon where variation of genetic makeup can cause the same disorder (An & Cladianos, 2016). The number of genes that are found to be associated with ASD seems to be increasing.

This is, in part, a consequence of novel gene analysis techniques (Alonso-Gonzalez et al., 2019). Different research groups assess the number of genes involved in ASD according to their own parameters, so a consensus on the amount of ASD-involved genes is lacking (Schaaf et al., 2020). Nevertheless, multiple hundreds of involved genes are conventionally identified through all of these studies investigating ASD genetics. So the genetic makeup of ASD involves hundreds of specific alleles. A study by Wei et al., compared 31 meta-analyses that aimed to identify consistent ASD alleles (Wei et al., 2021). Only one allele was consistently seen throughout all studies, with four other alleles showing inconsistent but still significant presence. The remaining involved genes did not show consistent ASD allele presence throughout ASD-diagnosed individuals. This means that there are many different ASD genotypes that do not share a lot of similarities, as different studies did not report genotype consistency (Wei et al., 2021). Therefore, many variations of genetic makeup can all produce ASD. These results indicate an extremely high level of genetic heterogeneity. Variants in genetic architecture naturally lead to variation in phenotypes, and in the case of ASD, also severity.

Polygenicity

Polygenic disorders are classified according to the requirement of multiple genetic factors to be involved in their etiology. ASD is not only heterogeneous but also encompasses a polygenic architecture (Choi & An, 2021). Therefore, there are not only multiple genetic variants that can give rise to ASD, these variants also have to consist of multiple genes to be able to convey ASD. This means that the genes involved in ASD play a small role on their own, and only together make up the disorder. Disorders with a polygenic architecture are likely to comprise genes of which some are pleiotropic and contribute also to traits with beneficial effects (Ploeger & Galis, 2011). Pleiotropic genes are genes that affect more than one phenotypic trait. The many involved genes that are also frequently seen to be pleiotropic, can explain the great variety in phenotypes and severity of ASD. To conclude, ASD is a polygenic disorder, the manifestation of which occurs according to many involved genes.

Epistasis

Epistasis encompasses all types of gene x gene effects, commonly referred to as gene interactions. The genes associated with ASD are frequently suspected to interact with other genes in the form of epistatic interactions (Ploeger & Galis, 2011; Mitra et al., 2017). There are several lines of evidence supporting the presence of these interactions. Firstly, epistasis is a common and natural factor of polygenic and neuropsychiatric disorders (Lvovs et al., 2012; Webber, 2017). Then there are the many comorbidities and large variations in comorbidity associated with ASD. These can be explained by, and even traced to, epistatic interactions (Ploeger & Galis, 2011; Bishop, 2010). A study that reported language impairment as a consequence of gene x gene interaction between

ASD genes in a simulation serves as an example (Bishop, 2010). Lastly, many of the genes involved in ASD are reported to be tightly intertwined with other genetic clusters, in particular the makeup of IQ (Wang et. al., 2013). Epistasis is the proposed mechanism by which this intertwinement takes place (Ploeger & Galis, 2011). To elucidate the theory, genes involved in ASD interact epistatically with genes involved with intelligence, thereby affecting each other's functioning. This may contribute to a dependency, or intertwinement, between these interacting genes to maintain the functioning as is. These intricate interactions between IQ and ASD will be more elaborately discussed in the next chapter. The collective evidence for the presence of epistasis even introduces the notion that this principle has been an important factor in the evolutionary trajectory of ASD (Ploeger & Galis, 2011).

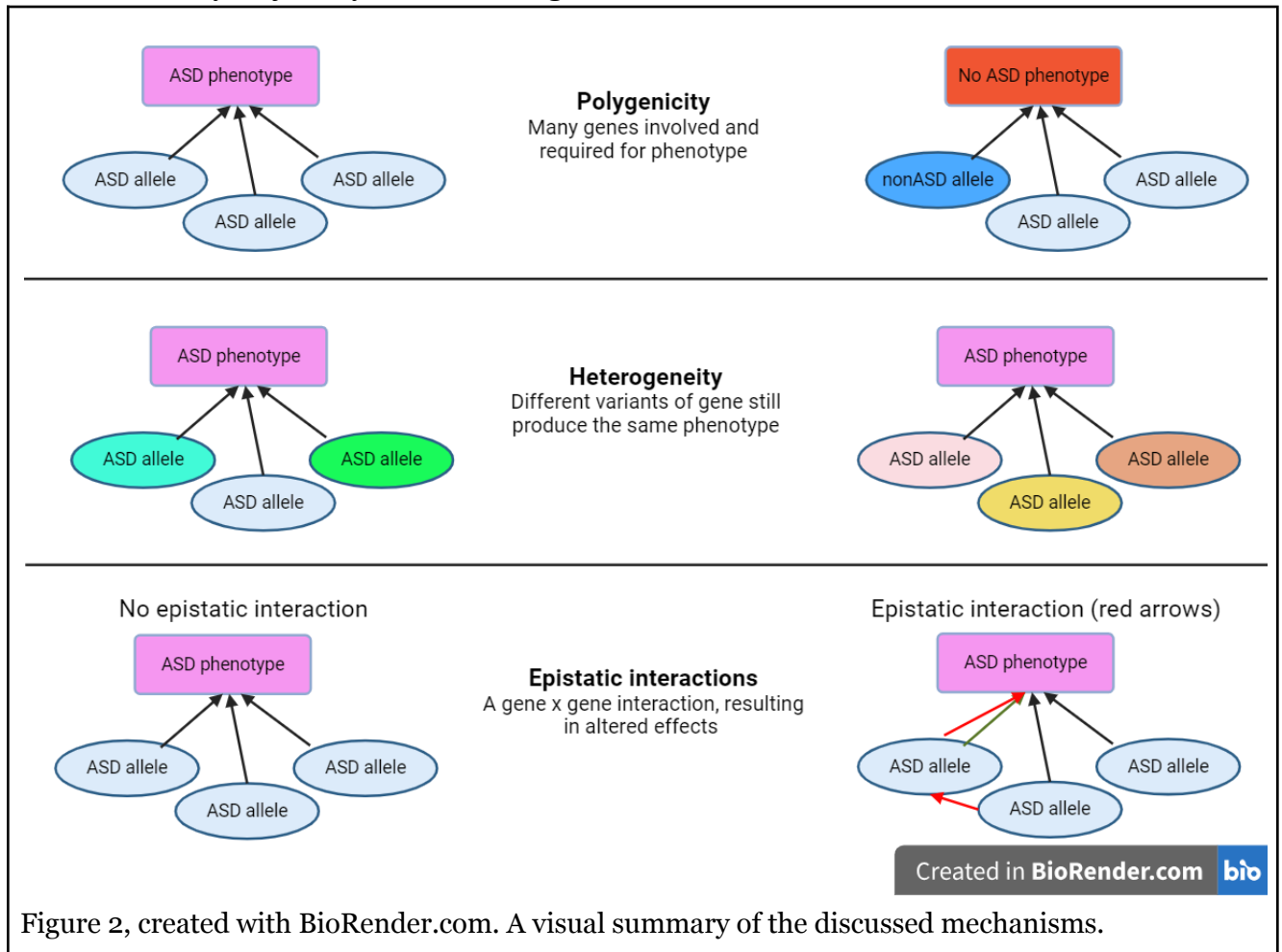


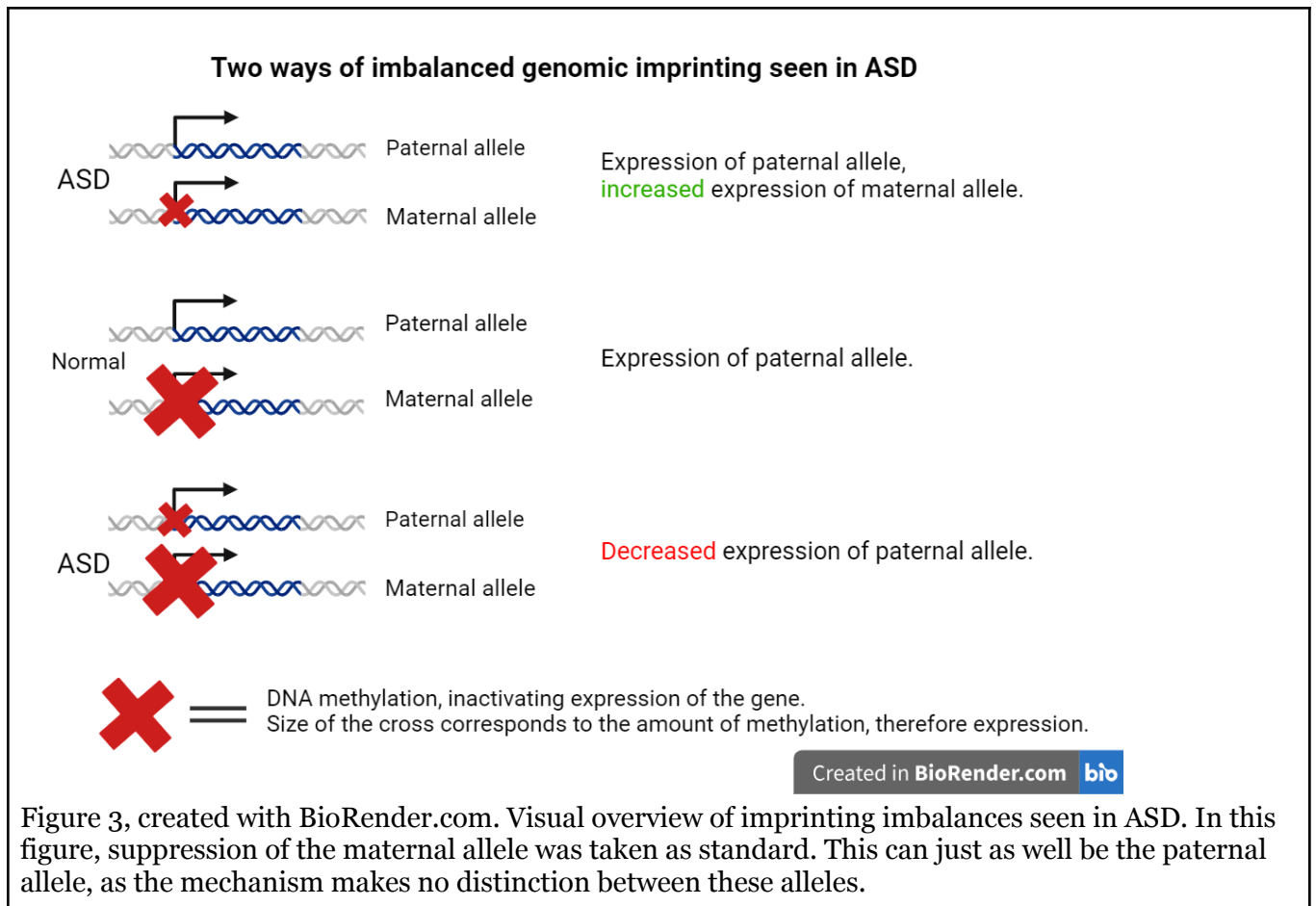
Figure 2, created with BioRender.com. A visual summary of the discussed mechanisms.

Chapter 1, Where do the ASD alleles come from

Chapter 0 concerned only the situation once the specific alleles associated with ASD are present. It discussed how these alleles come together to result in ASD. In this chapter, the theories about mechanisms that produce these alleles will be articulated.

Imbalanced imprinting

When analyzing the genes playing a role in ASD, an overlapping characteristic becomes apparent. A large portion of ASD genes are subjected to parental imprinting (Li et. al., 2020). Parental imprinting refers to sex-specific epigenetic inactivation of one of the two alleles representing a gene (Reik & Walter, 2001). So for these imprinted genes, a male only expresses the paternal copy while a female only expresses the maternal copy. Thus, the total expression pattern is now determined solely by the genetics of one of the parents, thereby only one allele. This mechanism leads to parent-of-origin effects and enhanced mutative risk (Ryan & Heron, 2023). Many of these genes are found to be important in neuronal and brain development (Davies et. al., 2005). The evolutionary reasoning behind the existence of this epigenetic mechanism addresses a *tug-of-war* hypothesis (Moore, 1991). This hypothesis centralizes the different optimum expression patterns for mother and father, referring to the expression of the imprinted genes in their child. Imbalanced imprinting has recently been a frequently proposed causal mechanism of ASD, as the relation between ASD and imprinting is being better elucidated (Ryan & Heron, 2023; Badcock & Crespi, 2006). Additional evidence for the role of imprinting in ASD refers to disorders comorbid with ASD, which are caused by imbalanced imprinting (Grafodatskaya et. al., 2010). The most well-known of these comorbid disorders are Prader-Willi and Angelman syndrome, both caused by imprinting errors. Lastly, strong epistatic interactions are reported with imprinted genes in the brain (Patten et. al., 2016). In conclusion, distorted imprinting and the epistatic interactions of these imprinted genes may alter neurodevelopment in a way that results in ASD.



Interactions with intelligence

Intelligence is a concept bearing much meaning, as there is hardly one true definition of the word. The articles cited in this paper foremostly define intelligence according to various cognitive processes measured in a verbal-perceptual-rotation model (VPR) (Johnson & Bouchard Jr, 2005). This model assesses specific sorts of cognitive abilities, including comprehension, perception, and verbal capabilities. The model tests similar aspects of the brain as the IQ test. Often, these methods for measuring intelligence are interchangeably used. This is done with the notion that intelligence refers most primarily to cognitive abilities, thereby centralizing how well a specific brain area executes its functions. The definition of intelligence handled in this thesis refers to the average cognitive ability of the brain, not accounting for differences in ability between specific brain regions.

ASD and intelligence seem to have a strongly intertwined genetic basis (Rao et. al., 2022). As mentioned in the introduction, the established interplay has shifted in dynamics over time. The original consensus portrayed ASD to affect IQ only in a negative sense, increasing the prevalence of intellectual disorders. Recent findings have

however decidedly shown that ASD skews IQ both to the lower and to the higher end (Wolff et. al., 2022). ASD is characterized by uneven brain development, leading to large variations in abilities between different cognitive functions within an ASD-diagnosed individual (*The Neuropsychology of Autism*, 2011). This has complex effects on IQ, as some parts of the brain might be classified as better developed than the average while others remain underdeveloped. This leads to the IQ of individuals with ASD varying per case and making the concrete interplay mechanism less clear (*The Neuropsychology of Autism*, 2011). So regardless of the strong correlation and overlap between genes involved in intelligence and ASD, the nature of the relationship remains unknown.

There are several theories implementing interactions with intelligence to explain the origin of ASD. ASD has been suggested as a by-product of intelligence (Pickard et. al., 2011). Nonetheless, there are also studies performed that indicate a causal role of ASD in the development of intelligence, suggesting the co-emergence of intelligence and ASD alleles (Crespi, 2016; Leisman et. al., 2022). This argumentation is supported by the involvement of ASD alleles in brain development. Here the “chicken and egg problem” is mentioned, referring to atypical brain development and atypical behavior (Leisman et. al., 2022). Thus facing the following problem: is the atypical ASD behavior a consequence of the abnormal brain development that rose due to intelligence, or has intelligence risen from the abnormal brain development provided by ASD? Which came first, and thereby initiated the other, cannot be said according to the current knowledge available. In all of the theories discussed above, the origin of alleles involved in ASD is seen to be a consequence of its interactions with intelligence.

A large general population cohort study found a positive correlation between polygenic ASD risk and intelligence, stating that individual ASD alleles contribute positively to intelligence (Clarke et. al., 2015). Once more, this emphasizes this deep intertwinement of intelligence and ASD. It also opens up the hypothesis that the intelligence aspect of ASD alleles relieves evolutionary pressure, as it provides some aspect of positive selection. Theories regarding ASD and intelligence will be more elaborately discussed from an evolutionary perspective in the next chapter.

Chapter 2, Why did the ASD alleles persist in our society

The previous chapter discussed some of the many theories speculating where the original alleles involved with ASD came from. Disrupted imprinting and intricate interactions with intelligence were established as probable mechanisms for the creation of these ASD alleles. This chapter will build on this foundation, i.e. the presence of alleles involved with ASD, to hypothesize evolutionary theories about their maintenance in the population throughout time. Two approaches will be taken. One assessing possible indirect beneficial factors via intelligence and one looking at feasible direct advantages of ASD.

Intelligence

There are two important points to consider when taking an evolutionary approach to the aforementioned intelligence and ASD intertwinement. The first relates to the notion of extreme complexity in the formation and evolution of intelligence (Bouchard Jr, 2014). The second point emphasizes again the intricate but prominent interplay between genes involved in intelligence and ASD (Rao et. al., 2022). Keeping these principles in mind, there are several theories discussing the shared evolutionary trajectory ASD and intelligence could have taken. All theories assume that the emergence of intelligence has been a beneficial characteristic, and therefore spread (McNally et. al., 2012).

The first theory bases on the uneven brain development seen in ASD. Dysregulation of development seems to allow for specific brain areas to excel compared to the general population (Crespi, 2016). This supposedly allowed for pioneering by ASD to create alternate investment in the brain development of certain regions. If enlargement of this region was deemed more beneficial at the time than the burdens of ASD, genetic makeup leading to the larger brain area might be maintained as a variant in the population. The hypothesis is supported by a study simulating incomplete selection, findings showed that ASD-involved alleles were positively selected for (Polimanti & Gelernter, 2017). Specifically, genes involved in neurogenesis and cognitive ability. The theory transcends the evolution of intelligence and might take part in explaining the evolution of cognitive enhancement in all regions affected by ASD. Since the theory bases on the burdens of ASD being lower than the benefits of intelligence, mild ASD is the most realistic to fulfill this criterion, as it has the least burdens.

A second theory introduces the concept of freeloading. This theory centralizes maintenance and therefore benefit of the ASD alleles individually, rather than the disorder altogether. It states that because of the epistatic and polygenic nature of ASD, many of the genes can present themselves in the form of “ASD alleles” without causing pathology (Ploeger & Galis, 2011). And because the ASD-involved genes have so much overlap with intelligence genes, the ASD alleles might be selected for. Evidence for this resides in the fact that polygenic ASD risk has been positively correlated with IQ, as previously mentioned (Clarke et. al., 2015). Then ASD is just the result of an extremely unlucky combination of all the involved genes together, while a near ASD state is still favored due to its ties with intelligence.

Strategy-related fitness benefits

A crucial consideration to make when theorizing about the direct benefits of ASD relates to the severity of the disorder. As seen in the introduction, the severity of the disorder determines for a large part how impactful the disorder is. Therefore, more severe cases of ASD are increasingly detrimental to an individual, to the point where they cannot

look after themselves. In all to be mentioned theories in this paragraph, the presence of ASD should be considered as a mild case, to be able to maintain the credibility of the theories.

There are many foreseeable situations where ASD may have had beneficial prospects. Many of the theories are implemented as advantageous solely because of strategic choices. One of them is titled 'The solitary forager hypothesis' (Reser, 2011). Here the behavioral profile seen in ASD is centralized, with the hypothesis that reduced social behavior is accompanied by obsessive tendencies towards foraging. This combination results in a completely independent individual, a strategy that might flourish due to probable periodical circumstances. These circumstances include, amongst others, times of food scarcity and local war. The theory stresses "partially solitary" as the most plausible dynamic, due to the necessity of mating. As a consequence, it attributes possible advantages only to mild ASD. More severe cases are explained by the article as a consequence of assortative mating in ASD.

Argumentation of a second theory takes on a mating strategy, proposing maintenance of ASD through sexual selection via mate choice (Giudice et. al., 2010). The primary conceptions are based again on the behavioral patterning of ASD, highlighting a highly specific mating strategy. The male strategy, contrary to the conventional, allegedly comprises long-term resource allocation, high parental investment, and low mating effort. So, this strategy comprises relatively high paternal care, as well as reliability, as there is low mating effort. This strategy can be successful in humans if recognized and trusted by a female, as paternal care is beneficial for the female.

A third theory points out the unorthodox way associations are made between and about personal possessions (Spikins et. al., 2018). There is less of a tendency towards attaching relational or conceptual meaning to their possessions, leaving more attachment to the practical use of this possession. This necessity for an object to be of practical use may have had a selective advantage in the development of the modern human.

There are many remaining theories that acknowledge the neurodiversity beared by ASD in their argumentation of advantages. This argument stands strong especially in the distant past, as back then, humans had many concepts to endeavor, figure out, and learn that we currently take for granted. ASD could have been vital in the development of the modern human and our many, now common and realized, concepts (Spikins, 2009). Alternative thinking, as provided by ASD, can be of aid in e.g. the discovery of music and art, but also rulemaking and social order (Masataka, 2020; Spikins, 2013).

All of the hypotheses noted above are not mutually exclusive, therefore the validity of one does not question the credibility of the other. Extended integration of the various theories discussed can be found in the next chapter.

Chapter 3, Integration

Up until now, scientific literature was brought together to argue individual findings and theories. This was done to explain either the emergence of ASD genetics or the maintenance of the disorder overall. This chapter aims to integrate these individual points into an overview of the trajectory of ASD, from its origin to its passage through time.

Summary

ASD is a highly multifactorial disorder with a large but complex genetic architecture. The genetic side of the etiological package is polygenic, heterogeneous, and highly epistatic. These characteristics are the consequence of the genetic mechanisms producing ASD-involved alleles. There are many of these genetic mechanisms proposed, two of which are articulated in this thesis. As discussed, the creation of ASD-involved alleles can be the result of improper genomic imprinting or an interaction with genes involved in intelligence. Several evolutionary theories were raised, regarding the maintenance of the alleles in the population once they are present. The first theory expands on the prominent interaction with the beneficial intelligence genes, while the latter theories all pursue potential direct advantages ASD brings. Severity seems to be of underlying importance in all these theories, as the theories appear more applicable in the milder cases.

Integration of intelligence theories

The intelligence-related theories are the most straightforward to band together. The alleles involved in ASD emerged alongside intelligence and came to be partly due to this evolution of intelligence. This genetic intertwinement, with many epistatic interactions between ASD and intelligence-involved genes, has influenced the evolutionary trajectory of both phenotypes. As the genes are dependent on each other, selective forces on either of the phenotypes will affect the other. Thereby, the genetic ties between intelligence and ASD constrict evolution to act on the cumulative effects of these two phenotypes where they overlap, rather than as their own trait. This has led to a substantial amount of theories incorporating the positive effects of intelligence to explain the maintenance of ASD.

Integration of genetic and evolutionary theories

Distorted genomic imprinting and strategy-related evolutionary theories do not seem to be connected. Their presence is however a necessity for the other theory to be credible, establishing an indirect connection. Evolutionary theories require a genetic mechanism

that conveys the specific alleles through generations. Vice versa, for the genetic mechanism, evolutionary selection is requisite too. The specific alleles only hold meaning in case they exert an effect on the environment and fitness. So, while this codependency of the genetic and evolutionary mechanisms does not require the specific theories discussed, they do require some mechanism to be there. With respect to this explanation, anomalies in genomic imprinting may actually directly cause the changes in the brain that lead to the altered behavioral patterns discussed. If and to what extent this correlation exists, can however only be formulated as speculation with current literature.

Timeline

It is important to give thought to the evolutionary timeline and define which theory is applicable where. Genomic imprinting is a mechanism present throughout mammals, thereby this principle could very well have been a factor in the evolution of ASD (Sleutels & Barlow, 2002). This also holds true for intelligence-related origin theories. As intelligence and ASD likely co-emerged, intelligence is seen to be an important factor in the origin and evolutionary maintenance of ASD. The role of intelligence has been subjected to change over time, as societal structure came to be. More on this can be found in the next paragraph, where all theories are placed in the current society and assessed for applicability.

Lastly, the strategy-related theories, which are harder to pinpoint timescale-wise. Archeological records estimate the origin of ASD to be in the Paleolithic, approximately 100.000 years ago (Spikins, 2013). This was a time with much development in both societal structure and cognitive ability. The solitary forager hypothesis requires foraging as an important part of survival, which was seen to be the case at the proposed origin of ASD and for a long time after (*The Oxford Handbook of the Archaeology and Anthropology of Hunter-Gatherers*, 2014). Mating strategies will forever be under pressure of sexual selection, therefore the ASD-related mating strategy was likely to be credible at the origin of ASD and after. The advantages of this strategy depend on the standard for paternal care, the lower the standard, the more attractive the high parental care provided by ASD. In hunter-gatherers, paternal care has been hypothesized to be present, but in relatively low proportions (*Fatherhood*, 2010). The remaining theories point out the alternative brain development in ASD as an asset. All of these theories may very well be applicable throughout the evolution of ASD (Spikins, 2013) To conclude, each of the theories has been placed in a timeline that is in agreement with the timing of the origin and maintenance of ASD. Therefore, the timing of ASD origin supports the described effects the theories could have had on ASD.

The current society

In this paragraph, it will be assessed whether the evolutionary theories are still applicable in the current society, even though they were not proposed as such. This could provide some illumination of the prospects of ASD and its prevalence.

In the distant past, an edge on cognitive ability could have had large advantages, considering there were many optimizable concepts in our environment, such as tool use (Tague, 2016). Nowadays, the environment has drastically changed, and intelligence has not remained that strong of a selective marker (Međedović, 2017). As a result, theories that account for the benefits of intelligence affecting ASD might face diminished validity in the current society.

The strategy-dependent theories are more intricate to compare with our current society. Whereas solitary foraging is no longer seen as an option, some of its associated behaviors may still be of use in the current scenario. The repetitive and even obsessive behavior might aid in a workforce where repetitive labor is demanded. A work field like science, where some form of obsessive behavior can be beneficial, encompasses ASD-diagnosed individuals at a higher-than-chance level (Wei et. al., 2012). The extent to which these characteristics are generalizable, or even beneficial at all, is hard to say. Therefore, further research should be executed, focusing specifically on theories about ASD maintenance revolving around the situation at hand.

Several arguments can be made both for and against the mating strategy still being of relevance. Mating has of course remained as an essential component of evolution, thereby its evolutionary selective force should still be adequate. There is however a higher standard of paternal care, likely to be a product of a shift from polygyny to monogamy. This shift is estimated to have taken place approximately 5.000-10.000 years ago (Dupanloup et. al., 2003). Therefore, the mating strategy associated with ASD was likely more warranted before this shift.

Discussion

This thesis aimed to answer the research question “What could be the origin of ASD and why does ASD remain prevalent in human society throughout time?”. This was achieved by addressing and integrating existing theories. Additionally, these theories were expanded on where possible, according to updates in the literature. Key points made regarding the origin of ASD alleles relate to the involvement of imbalanced genomic imprinting and the intertwined nature of ASD alleles with intelligence genes. The key points made regarding the maintenance of ASD throughout time involve positive selection. This can be provided either by the dependence of intelligence on ASD or adaptive strategies compatible with ASD behavioral patterns.

One theory distinctly contradicted the consensus regarding the mechanism by which intelligence may have aided in the development of ASD-involved alleles. The opposing theory suggested ASD to be a byproduct of intelligence, while other theories attribute a more intricate interplay to the ASD-intelligence interaction. The contradiction can be explained by comparing the setup of the experiment. While the study perceiving ASD as a byproduct took an archeological approach, all the others did not. This alternative perspective can easily lead to differing interpretations and therefore outcomes. Comparing the credibility of these hypotheses is not easily done, as the studies all provide only limited evidence, which can potentially explain an unknown fraction of the cause of ASD. The scientific literature is far from complete regarding this matter, further research with more perspectives will need to be executed to better grasp the interaction between intelligence and ASD.

Integration of all mentioned theories shows dependence, the genetic theories require evolutionary transmission and the evolutionary theories require a genetic mechanism. Most theories are also compatible with each other, likely because there are many sides to ASD both genetically and phenotypically, which necessitates a multitude of involved factors.

Throughout time, there has been a large change in standards regarding mating strategies (*Fatherhood*, 2010; Dupanloup et. al., 2003). How the ASD mating strategy can still be translated and assessed for its advantages, cannot be stated due to a lack of research. ASD-related mating strategies in the current society should be incorporated into future research, as they can provide valuable perspectives on ASD. After all, the principle of sexual selection taken on by the original theory in this thesis is still relevant.

Evolutionary speaking, our current society is very young. The effects of it, e.g. sharply improved healthcare, may not yet have exerted its evolutionary effects on ASD. Therefore, assessment of accuracy for the theories placed in our current society can be done only in the future, and are for now just hypothetical. Nevertheless, these theories do provide a valuable perspective on ASD, and could further research be conducted providing theories specifically designed for our current society.

Conclusion

Contributing factors to the origin of ASD are dysregulated genomic imprinting as well as codependence with intelligence. Contributing factors to the maintenance of ASD throughout time are indirect positive selection through codependence with intelligence as well as direct positive selection through adaptive strategies. An important conception relies on the extreme array of genetics as well as phenotypes involved in ASD. These characteristics are a complication in answering the research question, as the answer will

always be incomplete. There are always more genetic mechanisms found capable of generating ASD alleles. Similarly, there are always more phenotypes and ways the phenotypes affected the total fitness of an individual with ASD in the past.

Acknowledgements

My lovely peer reviewers: Vlaicu David, Lia Suru, and Julia Datema. Thank you for the insightful comments that helped me write a better thesis than I could have done by myself.

And of course, a declaration of gratitude to my supportive and considerate supervisor: Lysanne Jorna.

References

1. Tick, B., Bolton, P., Happé, F., Rutter, M., & Rijdsdijk, F. (2015). Heritability of autism spectrum disorders: a meta-analysis of twin studies. *Journal Of Child Psychology And Psychiatry And Allied Disciplines*, 57(5), 585–595. <https://doi.org/10.1111/jcpp.12499>
2. Idring, S., Lundberg, M., Sturm, H., Dalman, C., Gumpert, C., Rai, D., Lee, B. K., & Magnusson, C. (2014). Changes in Prevalence of Autism Spectrum Disorders in 2001–2011: Findings from the Stockholm Youth Cohort. *Journal Of Autism And Developmental Disorders*, 45(6), 1766–1773. <https://doi.org/10.1007/s10803-014-2336-y>
3. Chiarotti, F., & Venerosi, A. (2020). Epidemiology of Autism Spectrum Disorders: A Review of Worldwide Prevalence Estimates Since 2014. *Brain Sciences*, 10(5), 274. <https://doi.org/10.3390/brainsci10050274>
4. Association, N. A. P. (2013). *Diagnostic and Statistical Manual of Mental Disorders*. <https://doi.org/10.1176/appi.books.9780890425596>
5. Kim, Y. S., Fombonne, E., Koh, Y., Kim, S., Cheon, K., & Leventhal, B. L. (2014). A Comparison of DSM-IV Pervasive Developmental Disorder and DSM-5 Autism Spectrum Disorder Prevalence in an Epidemiologic Sample. *Journal Of The American Academy Of Child And Adolescent Psychiatry*, 53(5), 500–508. <https://doi.org/10.1016/j.jaac.2013.12.021>
6. Stevens, E., Dixon, D. R., Novack, M. N., Granpeesheh, D., Smith, T., & Linstead, E. (2019). Identification and analysis of behavioral phenotypes in autism spectrum disorder via

- unsupervised machine learning. *International Journal Of Medical Informatics*, 129, 29–36.
<https://doi.org/10.1016/j.ijmedinf.2019.05.006>
7. Delli, C. K. S., & Papaefstathiou, E. (2019). Review of cluster analysis of phenotypic data in Autism Spectrum Disorders: distinct subtypes or a severity gradient model? *International Journal Of Developmental Disabilities*, 66(1), 13–21.
<https://doi.org/10.1080/20473869.2018.1542561>
 8. Matson, J. L., Wilkins, J., & Macken, J. (2008). The Relationship of Challenging Behaviors to Severity and Symptoms of Autism Spectrum Disorders. *Journal Of Mental Health Research in Intellectual Disabilities/Journal Of Mental Health Research in Intellectual Disabilities.*, 2(1), 29–44. <https://doi.org/10.1080/19315860802611415>
 9. Mouridsen, S. E., Brønnum-Hansen, H., Rich, B., & Isager, T. (2008). Mortality and causes of death in autism spectrum disorders. *Autism*, 12(4), 403–414.
<https://doi.org/10.1177/1362361308091653>
 10. Woolfenden, S., Sarkozy, V., Ridley, G., Coory, M., & Williams, K. (2012). A systematic review of two outcomes in autism spectrum disorder – epilepsy and mortality. *Developmental Medicine And Child Neurology/Developmental Medicine & Child Neurology*, 54(4), 306–312.
<https://doi.org/10.1111/j.1469-8749.2012.04223.x>
 11. DaWalt, L. S., Hong, J., Greenberg, J. S., & Mailick, M. R. (2019). Mortality in individuals with autism spectrum disorder: Predictors over a 20-year period. *Autism*, 23(7), 1732–1739.
<https://doi.org/10.1177/1362361319827412>
 12. Lin, L., & Huang, P. (2017). Quality of life and its related factors for adults with autism spectrum disorder. *Disability And Rehabilitation*, 41(8), 896–903.
<https://doi.org/10.1080/09638288.2017.1414887>
 13. Kohane, I. S., McMurry, A., Weber, G., MacFadden, D., Rappaport, L., Kunkel, L., Bickel, J., Wattanasin, N., Spence, S., Murphy, S., & Churchill, S. (2012). The Co-Morbidity Burden of Children and Young Adults with Autism Spectrum Disorders. *PLoS One*, 7(4), e33224.
<https://doi.org/10.1371/journal.pone.0033224>

14. Khachadourian, V., Mahjani, B., Sandin, S., Kolevzon, A., Buxbaum, J. D., Reichenberg, A., & Janecka, M. (2023). Comorbidities in autism spectrum disorder and their etiologies. *Translational Psychiatry*, 13(1). <https://doi.org/10.1038/s41398-023-02374-w>
15. *Treatment of Disorders in Childhood and Adolescence*. (z.d.). Google Books. <https://books.google.nl/books?hl=en&lr=&id=RouDDwAAQBAJ&oi=fnd&pg=PA376&dq=klinger+et+al+2014+ASD&ots=dv7Gcfu9Rq&sig=P4e92azi8Bsn1VvDw5cdalkXy30#v=onepage&q=klinger%20et%20al%202014%20ASD&f=false>
16. Sealey, L., Hughes, B., Sriskanda, A., Guest, J., Gibson, A., Johnson-Williams, L., Pace, D., & Bagasra, O. (2016). Environmental factors in the development of autism spectrum disorders. *Environment International*, 88, 288–298. <https://doi.org/10.1016/j.envint.2015.12.021>
17. Willsey, A. J., & State, M. W. (2015). Autism spectrum disorders: from genes to neurobiology. *Current Opinion in Neurobiology*, 30, 92–99. <https://doi.org/10.1016/j.conb.2014.10.015>
18. Kubota, T., & Mochizuki, K. (2016). Epigenetic Effect of Environmental Factors on Autism Spectrum Disorders. *International Journal Of Environmental Research And Public Health/International Journal Of Environmental Research And Public Health*, 13(5), 504. <https://doi.org/10.3390/ijerph13050504>
19. *Philosophy of Biology*. (z.d.). Google Books. https://books.google.nl/books?hl=nl&lr=&id=tBxGpaV-ocsC&oi=fnd&pg=PA103&ots=2NsvWAIk5L&sig=sbofJaJS8cTKkDkCoJrUCWbXeLc&redir_esc=y#v=onepage&q&f=false
20. Tsur, E., Friger, M., & Menashe, I. (2016). The Unique Evolutionary Signature of Genes Associated with Autism Spectrum Disorder. *Behavior Genetics*, 46(6), 754–762. <https://doi.org/10.1007/s10519-016-9804-4>
21. Warrier, V., Zhang, X., Reed, P., Havdahl, A., Moore, T. M., Cliquet, F., Leblond, C. S., Rolland, T., Rosengren, A., Group, E. L., Group, I. A., Consortium, S. 1. A. A., Rowitch, D. H., Hurles, M. E., Geschwind, D. H., Børglum, A. D., Robinson, E. B., Grove, J., Martin, H. C., . . . Baron-Cohen, S. (2022). Genetic correlates of phenotypic heterogeneity in autism. *Nature Genetics*, 54(9), 1293–1304. <https://doi.org/10.1038/s41588-022-01072-5>

22. An, J. Y., & Claudianos, C. (2016). Genetic heterogeneity in autism: From single gene to a pathway perspective. *Neuroscience & Biobehavioral Reviews/Neuroscience And Biobehavioral Reviews*, 68, 442–453. <https://doi.org/10.1016/j.neubiorev.2016.06.013>
23. Alonso-Gonzalez, A., Calaza, M., Rodriguez-Fontenla, C., & Carracedo, A. (2019). Novel Gene-Based Analysis of ASD GWAS: Insight Into the Biological Role of Associated Genes. *Frontiers in Genetics*, 10. <https://doi.org/10.3389/fgene.2019.00733>
24. Schaaf, C. P., Betancur, C., Yuen, R. K. C., Parr, J. R., Skuse, D. H., Gallagher, L., Bernier, R. A., Buchanan, J. A., Buxbaum, J. D., Chen, C., Dies, K. A., Elsabbagh, M., Firth, H. V., Frazier, T., Hoang, N., Howe, J., Marshall, C. R., Michaud, J. L., Rennie, O., . . . Vorstman, J. A. S. (2020). A framework for an evidence-based gene list relevant to autism spectrum disorder. *Nature Reviews. Genetics*, 21(6), 367–376. <https://doi.org/10.1038/s41576-020-0231-2>
25. Wei, H., Zhu, Y., Wang, T., Zhang, X., Zhang, K., & Zhang, Z. (2021). Genetic risk factors for autism-spectrum disorders: a systematic review based on systematic reviews and meta-analysis. *Journal Of Neural Transmission*, 128(6), 717–734. <https://doi.org/10.1007/s00702-021-02360-w>
26. Choi, L., & An, J. (2021). Genetic architecture of autism spectrum disorder: Lessons from large-scale genomic studies. *Neuroscience & Biobehavioral Reviews/Neuroscience And Biobehavioral Reviews*, 128, 244–257. <https://doi.org/10.1016/j.neubiorev.2021.06.028>
27. Ploeger, A., & Galis, F. (2011, 1 juni). *Evolutionary approaches to autism- an overview and integration*. PubMed Central (PMC). <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3277413/>
28. Mitra, I., Lavillaureix, A., Yeh, E., Traglia, M., Tsang, K., Bearden, C. E., & Rauen, K. A. (2017). Reverse pathway genetic approach identifies epistasis in autism spectrum disorders. *PLOS Genetics*, 13(1), e1006516. <https://doi.org/10.1371/journal.pgen.1006516>
29. Lvovs, D., Favorova, O., & Favorov, A. (2012, 1 september). *A Polygenic Approach to the Study of Polygenic Diseases*. PubMed Central (PMC). <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3491892/#:~:text=Polygenic%20diseases%20are%20caused%20by,be%20small%20or%20even%20unnoticeable>
30. Webber, C. (2017). Epistasis in neuropsychiatric disorders. *Trends in Genetics*, 33(4), 256–265. <https://doi.org/10.1016/j.tig.2017.01.009>

31. Bishop, D. V. M. (2010). Overlaps Between Autism and Language Impairment: Phenomimicry or Shared Etiology? *Behavior Genetics*, 40(5), 618–629.
<https://doi.org/10.1007/s10519-010-9381-x>
32. Wang, H. Z., Qin, H., Guo, W., Samuels, J., & Shugart, Y. Y. (2013). New insights into the genetic mechanism of IQ in autism spectrum disorders. *Frontiers in Genetics*, 4.
<https://doi.org/10.3389/fgene.2013.00195>
33. Li, J., Lin, X., Wang, M., Hu, Y., Xue, K., Gu, S., Lv, L., Huang, S., & Xie, W. (2020). Potential role of genomic imprinted genes and brain developmental related genes in autism. *BMC Medical Genomics*, 13(1). <https://doi.org/10.1186/s12920-020-0693-2>
34. Reik, W., & Walter, J. (2001). Genomic imprinting: parental influence on the genome. *Nature Reviews. Genetics*, 2(1), 21–32. <https://doi.org/10.1038/35047554>
35. Ryan, N. M., & Heron, E. A. (2023). Evidence for parent-of-origin effects in autism spectrum disorder: a narrative review. *Journal Of Applied Genetics/Journal Of Applied Genetics*, 64(2), 303–317. <https://doi.org/10.1007/s13353-022-00742-8>
36. Davies, W., Isles, A. R., & Wilkinson, L. S. (2005). Imprinted gene expression in the brain. *Neuroscience & Biobehavioral Reviews/Neuroscience And Biobehavioral Reviews*, 29(3), 421–430. <https://doi.org/10.1016/j.neubiorev.2004.11.007>
37. Moore, T. (1991). Genomic imprinting in mammalian development: a parental tug-of-war. *Trends in Genetics*, 7(2), 45–49. [https://doi.org/10.1016/0168-9525\(91\)90230-n](https://doi.org/10.1016/0168-9525(91)90230-n)
38. Badcock, C., & Crespi, B. (2006a). Imbalanced genomic imprinting in brain development: an evolutionary basis for the aetiology of autism. *Journal Of Evolutionary Biology*, 19(4), 1007–1032. <https://doi.org/10.1111/j.1420-9101.2006.01091.x>
39. Grafodatskaya, D., Chung, B., Szatmari, P., & Weksberg, R. (2010). Autism Spectrum Disorders and Epigenetics. *Journal Of The American Academy Of Child And Adolescent Psychiatry*, 49(8), 794–809. <https://doi.org/10.1016/j.jaac.2010.05.005>
40. Patten, M. M., Cowley, M., Oakey, R. J., & Feil, R. (2016). Regulatory links between imprinted genes: evolutionary predictions and consequences. *Proceedings - Royal Society. Biological Sciences/Proceedings - Royal Society. Biological Sciences*, 283(1824), 20152760.
<https://doi.org/10.1098/rspb.2015.2760>

41. Johnson, W., & Bouchardjr, T. (2005). Constructive replication of the visual–perceptual-image rotation model in Thurstone’s (1941) battery of 60 tests of mental ability. *Intelligence*, 33(4), 417–430. <https://doi.org/10.1016/j.intell.2004.12.001>
42. Rao, S., Baranova, A., Yao, Y., Wang, J., & Zhang, F. (2022). Genetic Relationships between Attention-Deficit/Hyperactivity Disorder, Autism Spectrum Disorder, and Intelligence. *Neuropsychobiology*, 81(6), 484–496. <https://doi.org/10.1159/000525411>
43. Wolff, N., Stroth, S., Kamp-Becker, I., Roepke, S., & Roessner, V. (2022). Autism Spectrum Disorder and IQ – A Complex Interplay. *Frontiers in Psychiatry*, 13. <https://doi.org/10.3389/fpsyt.2022.856084>
44. *The Neuropsychology of Autism*. (z.d.). Google Books. <https://books.google.nl/books?hl=en&lr=&id=dSpVikpnJgcC&oi=fnd&pg=PA281&dq=IQ+in+asd&ots=11aN5T7d-X&sig=fXKnU3pu8Tsk8GWcpPdoPnAg3S8#v=onepage&q=IQ%20in%20asd&f=false>
45. Pickard, C., Pickard, B., & Bonsall, C. (2011). Autistic spectrum disorder in prehistory. *Cambridge Archaeological Journal*, 21(3), 357–364. <https://doi.org/10.1017/s0959774311000412>
46. Crespi, B. J. (2016). Autism As a Disorder of High Intelligence. *Frontiers in Neuroscience*, 10. <https://doi.org/10.3389/fnins.2016.00300>
47. Leisman, G., Melillo, R., Melillo, T., Machado, C., Machado-Ferrer, Y., Chinchilla, M., & Carmeli, E. (2022). Taking Sides: Asymmetries in the Evolution of Human Brain Development in Better Understanding Autism Spectrum Disorder. *Symmetry*, 14(12), 2689. <https://doi.org/10.3390/sym14122689>
48. Clarke, T., Lupton, M. K., Fernandez-Pujals, A. M., Starr, J., Davies, G., Cox, S., Pattie, A., Liewald, D. C., Hall, L. S., MacIntyre, D. J., Smith, B. H., Hocking, L. J., Padmanabhan, S., Thomson, P. A., Hayward, C., Hansell, N. K., Montgomery, G. W., Medland, S. E., Martin, N. G., . . . McIntosh, A. M. (2015). Common polygenic risk for autism spectrum disorder (ASD) is associated with cognitive ability in the general population. *Molecular Psychiatry*, 21(3), 419–425. <https://doi.org/10.1038/mp.2015.12>
49. Bouchard, T.J. Genes, Evolution and Intelligence. *Behav Genet* 44, 549–577 (2014). <https://doi.org/10.1007/s10519-014-9646-xb>

50. McNally, L., Brown, S. P., & Jackson, A. L. (2012). Cooperation and the evolution of intelligence. *Proceedings - Royal Society. Biological Sciences/Proceedings - Royal Society. Biological Sciences*, 279(1740), 3027–3034. <https://doi.org/10.1098/rspb.2012.0206>
51. Polimanti, R., & Gelernter, J. (2017). Widespread signatures of positive selection in common risk alleles associated to autism spectrum disorder. *PLOS Genetics*, 13(2), e1006618. <https://doi.org/10.1371/journal.pgen.1006618>
52. Reser, J. E. (2011). Conceptualizing the Autism Spectrum in Terms of Natural Selection and Behavioral Ecology: The Solitary Forager Hypothesis. *Evolutionary Psychology*, 9(2), 207–238. <https://doi.org/10.1177/147470491100900209>
53. Del Giudice, M., Angeleri, R., Brizio, A., & Elena, M. R. (2010). The evolution of autistic-like and schizotypal traits: a sexual selection hypothesis. *Frontiers in Psychology*, 1. <https://doi.org/10.3389/fpsyg.2010.00041>
54. Spikins, P., Wright, B., & Scott, C. (2018). Autism spectrum conditions affect preferences in valued personal possessions. *Evolutionary Behavioral Sciences*, 12(2), 99–112. <https://doi.org/10.1037/ebs0000105>
55. Spikins, P. (2009). Autism, the Integrations of ‘Difference’ and the Origins of Modern Human Behaviour. *Cambridge Archaeological Journal*, 19(2), 179–201. <https://doi.org/10.1017/S0959774309000262>
56. Masataka, N. (2020). Were Musicians As Well as Artists in the Ice Age Caves Likely with Autism Spectrum Disorder? A Neurodiversity Hypothesis. In *Springer eBooks* (pp. 323–345). https://doi.org/10.1007/978-981-15-4250-3_9
57. Spikins, P. (2013). The Stone Age Origins of Autism. In *InTech eBooks*. <https://doi.org/10.5772/53883>
58. Sleutels, F., & Barlow, D. (2002). 5 The origins of genomic imprinting in mammals. In *Advances in genetics* (pp. 119–163). [https://doi.org/10.1016/S0065-2660\(02\)46006-3](https://doi.org/10.1016/S0065-2660(02)46006-3)
59. *The Oxford Handbook of the Archaeology and Anthropology of Hunter-Gatherers*. (z.d.). Google Books. <https://books.google.nl/books?hl=en&lr=&id=U5uzAwAAQBAJ&oi=fnd&pg=PA177&dq=hunter>

[+gatherer+timeline&ots= kpBPvVAgV&sig=PZoqCFQrtCuMQglEcaE-i3Dadn8#v=onepage&q=unter%20gatherer%20timeline&f=false](#)

60. Fatherhood. (z.d.). Google Books.

https://books.google.nl/books?id=v8bmEAAAQBAJ&dq=first+record+of+paternal+care+in+humans&lr=&source=gbs_navlinks_s

61. Tague, G. F. (2016). Prehistory and Mind. In *BRILL eBooks* (pp. 16–54).

https://doi.org/10.1163/9789004319486_003

62. Mededović, J. (2017). Intelligence and Fitness: The Mediating Role of Educational Level.

Evolutionary Psychology, 15(2), 147470491770693. <https://doi.org/10.1177/1474704917706936>

63. Wei, X., Yu, J. W., Shattuck, P., McCracken, M., & Blackorby, J. (2012). Science, Technology, Engineering, and Mathematics (STEM) Participation Among College Students with an Autism Spectrum Disorder. *Journal Of Autism And Developmental Disorders*, 43(7), 1539–1546.

<https://doi.org/10.1007/s10803-012-1700-z>

64. Dupanloup, I., Pereira, L., Bertorelle, G., Calafell, F., Prata, M. J., Amorim, A., & Barbujani, G. (2003). A Recent Shift from Polygyny to Monogamy in Humans Is Suggested by the Analysis of Worldwide Y-Chromosome Diversity. *Journal Of Molecular Evolution*, 57(1), 85–97.

<https://doi.org/10.1007/s00239-003-2458-x>