

Past, Present, and Future: A literature review of the genetic research into the evolution of human language

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1. Introduction

Since Forkhead box P2 (FOXP2) was first identified as being a gene involved in speech and language in 2001 (Lai et al., 2001) the amount of research into the genetic basis for human language has grown exponentially. Despite FOXP2 being initially hailed as the “language gene”, over the last 20 years it has since become abundantly clear that the situation is much more complex than that (Deriziotis & Fisher, 2017; Fisher, 2019). Language is clearly a complex cognitive trait meaning that it is influenced by multiple genes and genomic pathways. To untangle this complex genetic architecture multiple streams of evidence (both genomic and otherwise) will need to be analysed together, including considering multiple genetic targets at once, to create a clearer picture (Deriziotis & Fisher, 2017; Eising et al., 2022).

2. Methods

A State-of-the-Art (SotA) literature review was conducted to analyse the current landscape of genetic research on the evolution of human language, alongside identifying historic trends in this research area, and themes for future research. This type of literature review specifically seeks to synthesise a summary of current thinking, examine how such perspectives may have changed over time, look at the historical trends within the research literature, and suggest areas for future directions of research (Barry et al., 2022b). This SotA review was conducted using Covidence (a cloud-based software) and the six stage methodological approach for SotA reviews suggested by Barry et al. (2022a). The process pathway for papers to be included in this review is shown in Fig. 1 below.

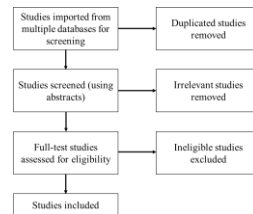


Figure 1. The Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) flow diagram for this review

The Web of Science database was used for this review, using the search expressions “Language evolution genetic”, “Genome language evolution”, and “Gene human language”. From this search 9,585 studies were imported to Confidence for screening, 876 removed as duplicates, and 8,709 taken to manual screening (title and abstract, followed by full text review) and further analysis.

3. Discussion

3.1 Future research areas

One area suggested for future research is a shift away from “popular” genes to ensure that all genes of potential interest are equally investigated. For example, even in 2015 it was clear that some genes were more studied than others (Brown, 2015). This is likely as FOXP2 was dubbed “the language gene” upon its discovery, garnering substantial news interest and thus skewing research focus in this direction (Brown, 2015). As well as language being multigenetic, several transcription factors have been identified as involved in language evolution (Brown, 2019). Thus complex intersecting pathways are underlying language evolution, promoting a broad approach to this research. While still underrepresented in the literature there is beginning to be a shift towards this type of multigene/genome-wide work (Eising et al., 2022).

3.2 Limitations

A clear limitation of this review is that it was conducted with a single reviewer, which can compound the effects of the relativism and subjectivism that can be said to be inherent to this type of review (Barry et al., 2022a). When conducting a literature review we bring our own experiences, perspectives, and biases to the work, and thus this can affect the data interpretation. In order to conduct a stronger review it is suggested that this work be replicated with multiple reviewers, who may collaborate via Covidence to vote at each stage of the PRISMA process, with the goal of creating a consensus and reducing bias.

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