An exploratory literature review of DNA methylation related to a rapid eating rate

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Introduction

- The prevalence of obesity has grown to epidemic level proportions, with the WHO estimating that it has tripled since 1975.
- One factor that has been linked to obesity is an individual's eating rate, or how rapidly one finishes a meal.
- However, there is little information available about whether a rapid eating rate may epigenetically modify DNA or if there is an epigenetic predisposition in individuals with a rapid eating rate.

Objective

The goal of this exploratory literature review is to identify if prior research identified a connection between eating rate and methylated DNA regions.

Methods

 A key word listed was generated for both eating rate and methylation and an exploratory review of the literature in English was conduced through the PubMed database.

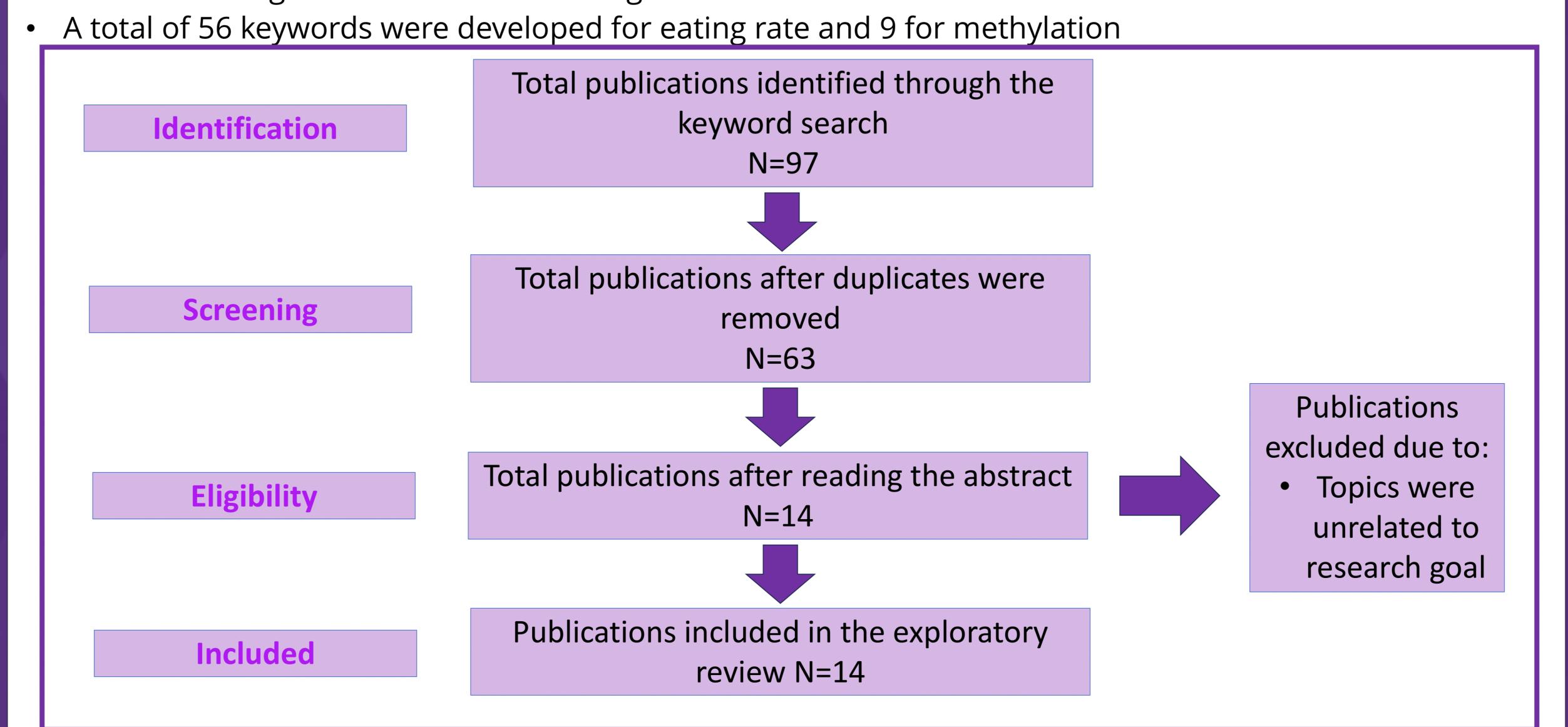


Figure 1: Flow Chart of Review Process for Methylation and Eating Rate keyword search

Rodriguez et al. Human Study

Number of participants	Demographics	Tissue	Methylation Studies	Genes of Interest	Justification for Inclusion
N=46	12 Male 34 Female 25 with BN 21 BED Adolescents from Mexico City	Whole Blood	Illumina Infinium Methylation EPIC microarray beadchip	PRKAG2, ST3GAL4, FRK	 The definition of binge eating is consuming a large amount of food in a short period Therefore, it can be said that those who binge eat exhibit a rapid eating rate

Table 1. Summary of Rodriguez et al. paper BN: Bulimia Nervosa, BED: Binge Eating Disorder

Results

- The keyword list generated 97
 possible publications tied to eating
 rate and methylation.
- 14 were identified as relevant
- 5 human studies
- 6 animal experiments
- 3 reviews publications
- However, there was little overlap of DNA regions among the publications.



Conclusion

Eating rate and methylation has been explored in other studies, justifying a more scoping review of the literature to identify DNA regions for future work

Future Directions

- Determine what has already been identified in the current field by reviewing the 3 review publications
- Identify any common candidate genes from the remaining animal and human study publications

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