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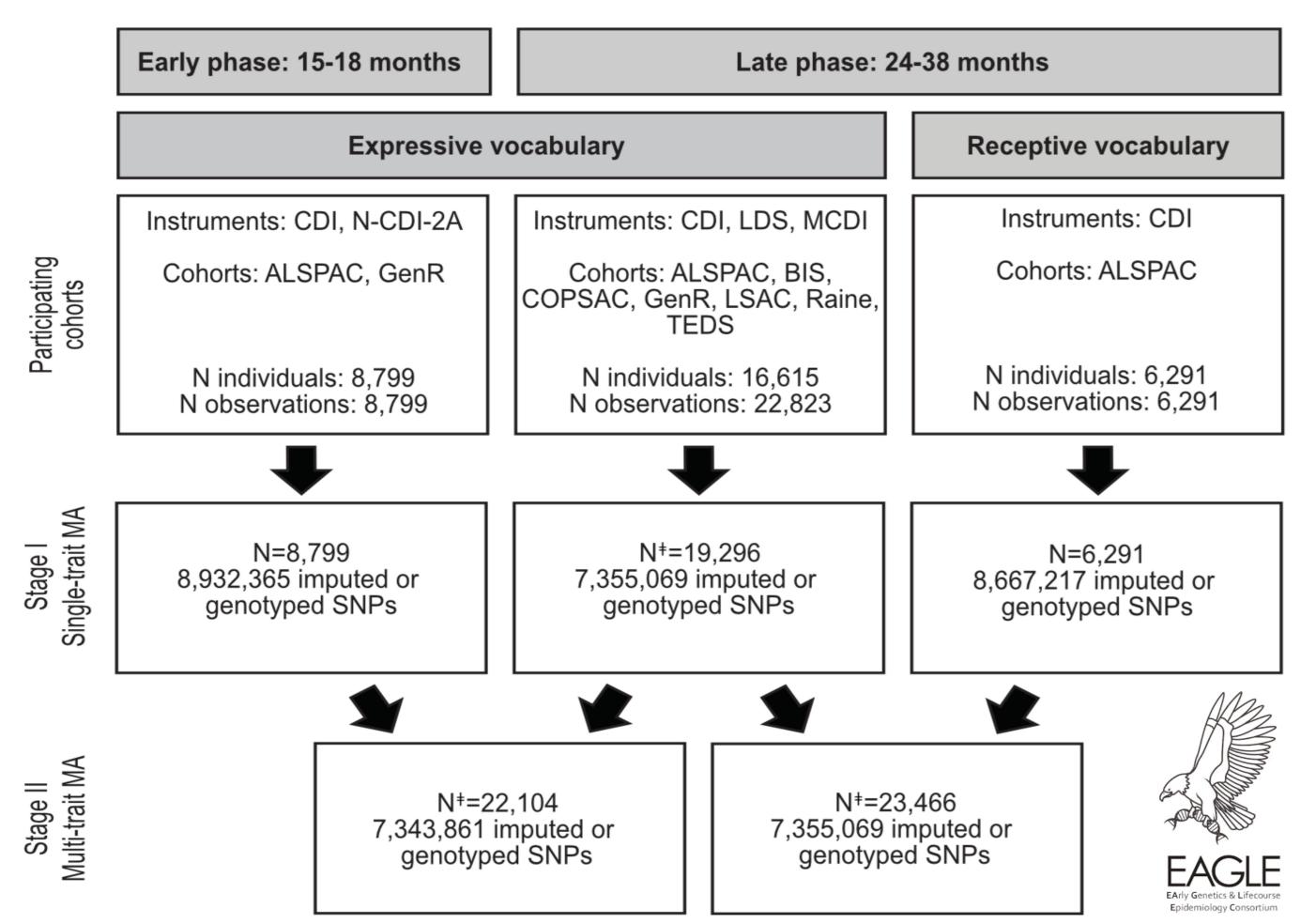
In a nutshell - we aimed to ...

(i) identify genome-wide association signals for early vocabulary, (ii) elucidate the underlying genetic architecture and (iii) characterise polygenic links with later-life cognitive, behavioral and health outcomes.

Background

The genetic architectures underlying expressive and receptive vocabulary in early life are complex and little characterised. Here, we present the largest metagenome-wide association study (meta-GWAS) of early vocabulary (15-38 months) till date, based on 37,913 observations and 17,298 individuals, within the Early Life Course Epidemiology (EAGLE) Genetics and Consortium.

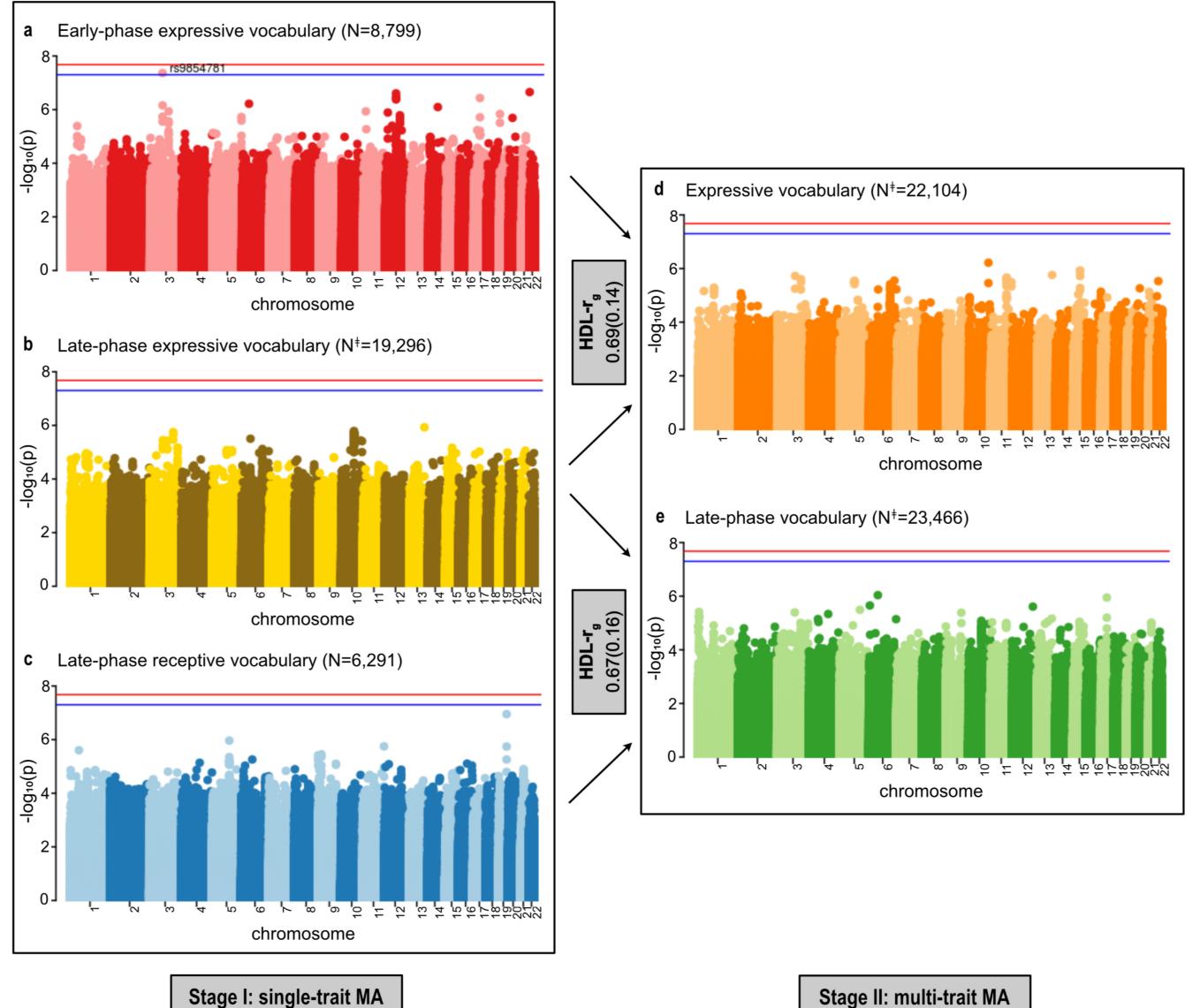
Study design



Expressive and/or receptive vocabulary was assessed using parent questionnaires in children of European descent from seven independent population-based or community-based cohorts. Meta-GWASs were performed for early-phase expressive vocabulary, late-phase expressive vocabulary, and late-phase receptive vocabulary using METAL as part of stage I. To increase statistical power, multi-trait SNP-vocabulary associations were examined by combining genetically related vocabulary traits using MTAG as part of stage II. + Estimated sample size based on the increase in mean χ^2 statistic using MTAG. Abbreviations: CDI, Communicative Development Inventory; LDS, Language Development Survey; MA, meta-analysis; SNP, Single-Nucleotide Polymorphism

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Genome-wide association meta-analysis of expressive and receptive vocabulary from infancy to early childhood E. Verhoef¹, T.S. Ahluwalia^{2,3}, P. Jansen^{4,5}, K. Lange^{6,7}, A. Allegrini⁸, C. Wang⁹, C. Symeonides^{6,7,10}, A. Morgan^{6,7,10}, EAGLE working group, S.E. Fisher^{1,11}, B. St Pourcain^{1,11,12}



Single-trait (stage I) and multi-trait (stage II) SNP-vocabulary associations were assessed using METAL and MTAG, respectively. No SNP-vocabulary associations passed the adjusted threshold (red line, P<2.1x10⁻⁸). rs9854781 was associated with early-phase expressive vocabulary at the unadjusted genome-wide significance threshold (blue line, *P*<5x10⁻⁸). Genetic correlations among single-trait vocabulary summary statistics were derived with HDL. **+** Estimated sample size based on the increase in mean χ^2 statistic using MTAG. Abbreviations: HDL, High-Density Llkelihood; MA, meta-analysis.

SNP-vocabulary associations

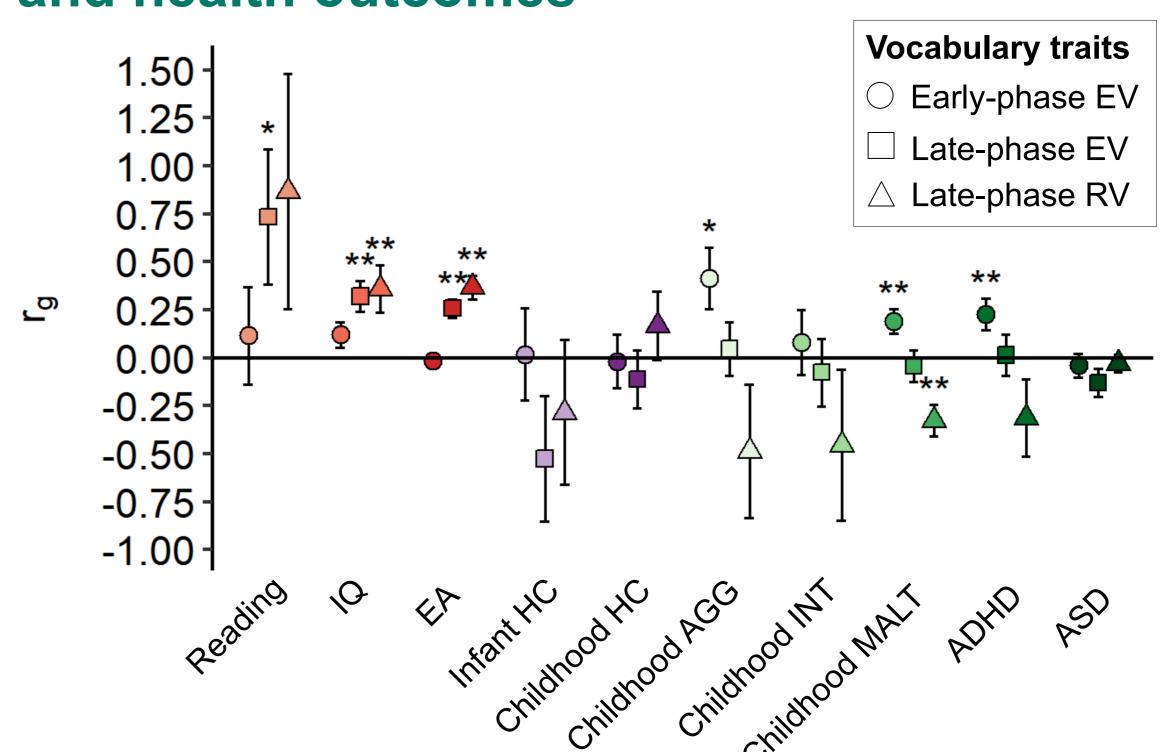
SNP-heritability of early vocabulary					
Analysis	Trait	SNP-h ² (SE)	Z-score	Р	Ν
Stage I: single-trait MA	Early-phase EV	0.24(0.02)	8.64	<1x10 ⁻¹⁰	8,799
	Late-phase EV	0.08(0.01)	5.53	3x10 ⁻⁸	19,296 [‡]
	Late-phase RV	0.20(0.04)	5.21	2x10 ⁻⁷	6,291
Stage II: multi-trait MA	EV	0.10(0.01)	6.91	<1x10 ⁻¹⁰	22,104 [‡]
	Late-phase vocabulary	0.07(0.01)	5.00	5x10 ⁻⁷	23,466‡

SNP-heritability (SNP-h²), corresponding standard error (SE) and P-value were estimated with High-Density Likelihood (HDL) software using a HapMap3 reference panel. SNP-h² Z-scores were calculated by dividing SNP-h² by its standard error. \pm Estimated sample size based on the increase in mean χ^2 statistic using MTAG. Abbreviations: EV, expressive vocabulary; MA, meta-analysis

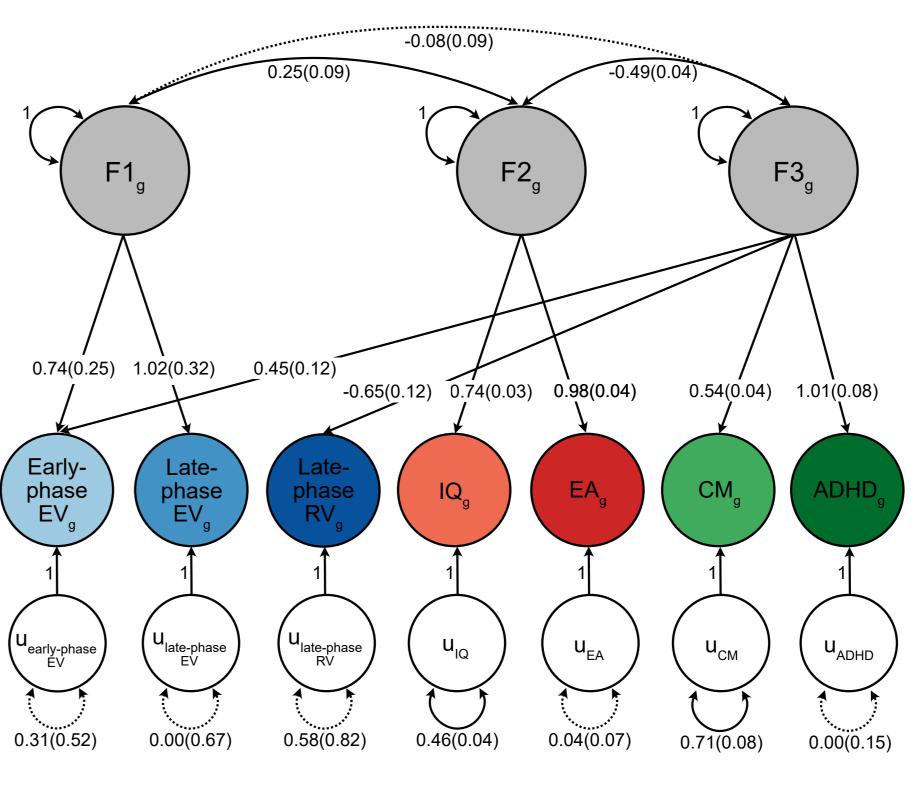
Gene-, gene-set and gene-property analyses All analyses were carried out within FUMA software. No results passed multiple-testing-adjusted thresholds.

Stage II: multi-trait MA

Genetic links with later-life cognitive, behavioral and health outcomes



Genetic correlations of vocabulary traits with later-life cognitive, behavioral and health outcomes estimated using HDL software. Bars represent standard errors. * P<0.05; ** P<5.3x10⁻³. Abbreviations: ADHD, Attention-Deficit/ Hyperactivity Disorder; AGG, aggression, ASD, Autism Spectrum Disorder; EA, educational attainment; EV, expressive vocabulary; HC, head circumference; INT, internalising symptoms; IQ, general intelligence; MALT, maltreatment; RV, receptive vocabulary



In a nutshell - we found that ...

the genetic architecture underlying early vocabulary changes during development:

- genetic relationships with cognition trace back to word use and understanding in toddlerhood, but not infancy

- exposure to maltreatment in childhood has a negative genetic link with word understanding in toddlers, while the link with single-word production in infants is positive



AIC CFI SRMR 40.81 10 1.2x10⁻⁵ 76.81 0.99 0.11 Confirmatory factor analysis (CFA) with GenomicSEM for genetically correlated traits with early vocabulary (see above). Factors that explained >0.2 variance and paths with a standardised factor loading >0.35 in exploratory factor analysis were CFA standardised path included. coefficients are shown. Dashed lines path coefficients with represent *P*>0.05. Model fit was assessed with chi-square, Akaike information criterion (AIC), Comparative Fit Index (CFI) and Standardised Root Mean ^{0.00(0.15)} Squared Residual (SRMR).

