



SHEFFIELD INSTITUTE
of GLUTEN RELATED DISORDERS



Sheffield
Gastroenterology



A genome-wide association study of celiac disease identifies novel risk variants in the 5p15.33 locus: results from a population-based screening of adults, the HUNT4 study.

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Introduction

- Conditions:
 - Genetically susceptible
 - Environmental factors
- Screening revealed:
 - 55% carry the HLA-DQ risk heterodimers
 - 1-2% of the risk carriers develop the disease
- Genetic variation:
 - HLA + Non HLA: 50%
 - Unknown: 50%

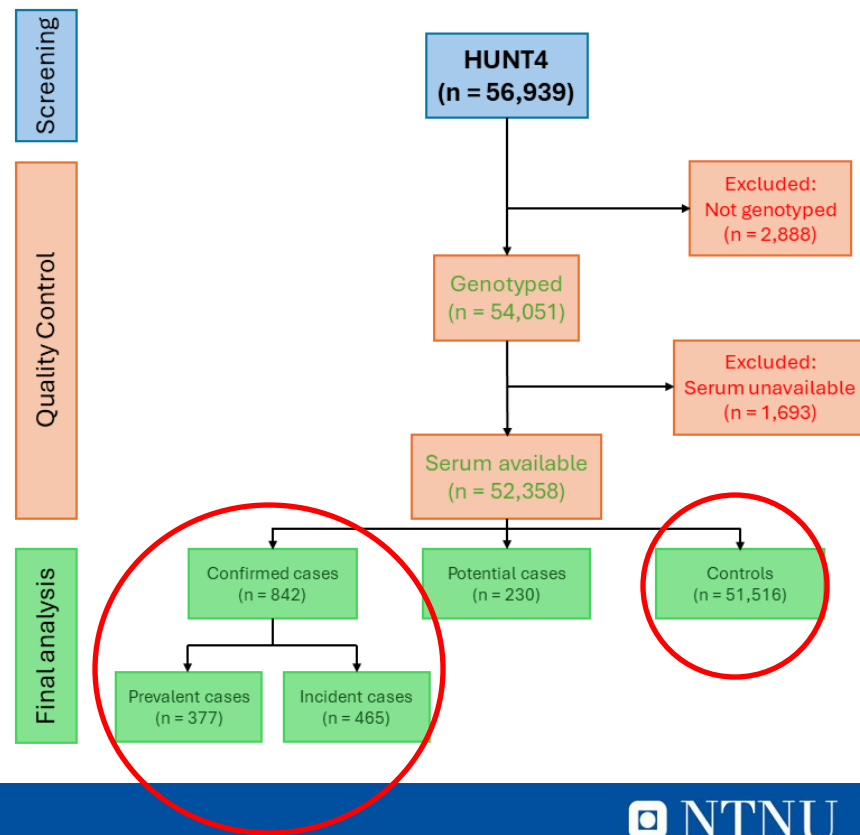
Methods - Cohort

- Study:
 - HUNT4 (2017-2019)
 - Participation:
 - Sample size = ~57,000
 - Participation rate = ~54%
 - Female proportion = ~54%



Methods - CeD screening

- Inclusion and exclusion:
 - Seropositivity cutoff:
 - TG2-IgA ≥ 0.7 mg*/L or
 - TG2-IgG ≥ 1 mg*/L
 - Biopsy:
 - Marsh grade 3
 - Ruling out *H pylori* and NSAIDs
- Final analysis:
 - ~51,000 controls
 - 842 cases (465 incident, 377 prevalent)



Methods - Genetics

- Genotyping:
 - ~360,000 SNPs
 - Panels:
 - Illumina HumanCore Exome
 - UM HUNT Biobank
- Imputation:
 - IMPUTE5 tool
 - Haplotype Reference Consortium
 - 24.9 mill variants ≥ 0.3 imputation score

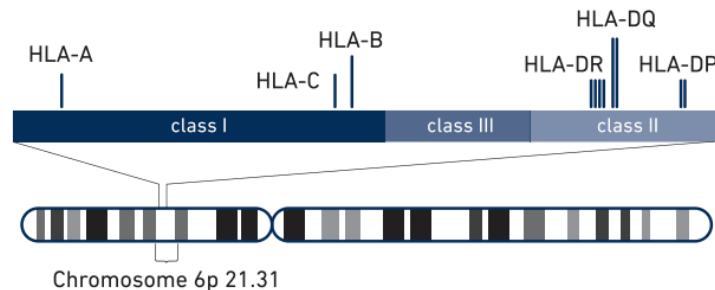


Methods - GWAS and validation

- SAIGE
 - Case-control imbalance
 - Relatedness
- Six randomly selected population subsets

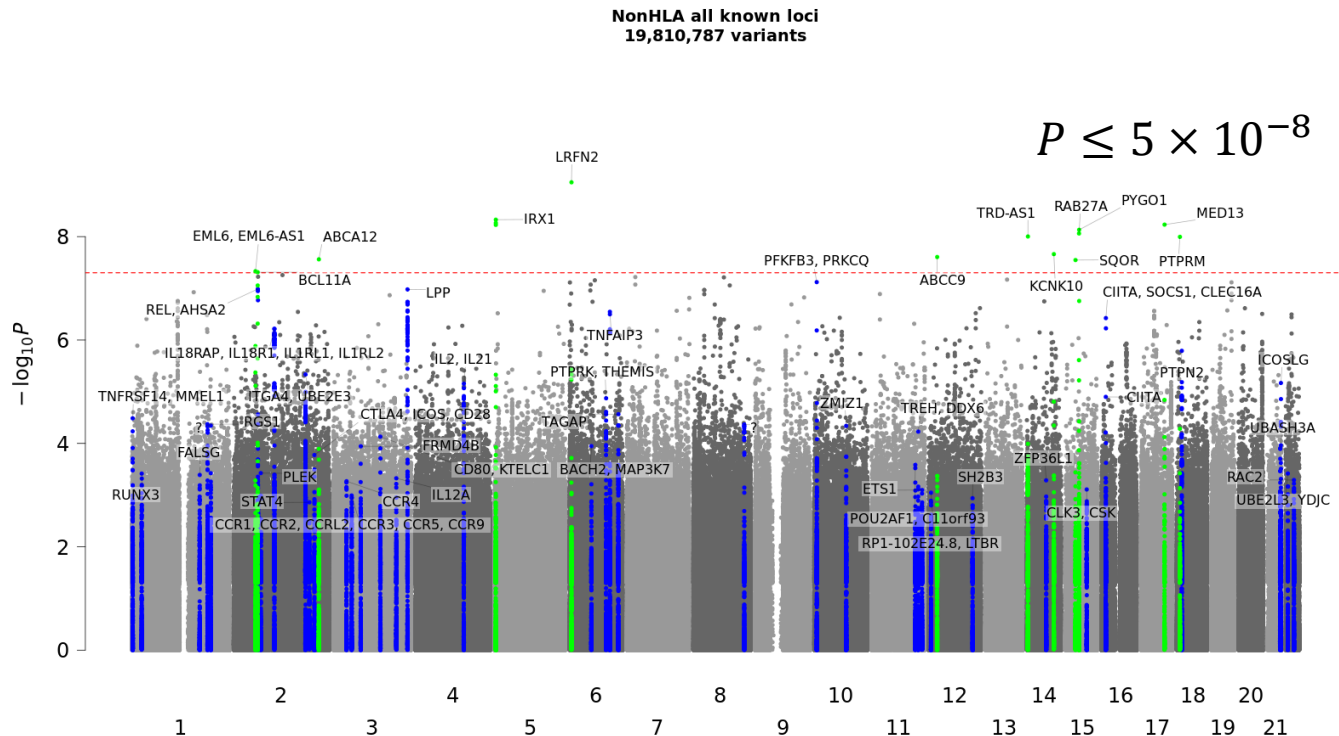
Methods – HLA and downstream

- HLA:
 - CHR6: 29MB – 34MB [hg19]
 - ~12,000 variants ≥ 0.8 imputation score
 - Conditional analysis
- FUMA:
 - SNP2GENE
 - GENE2FUNC



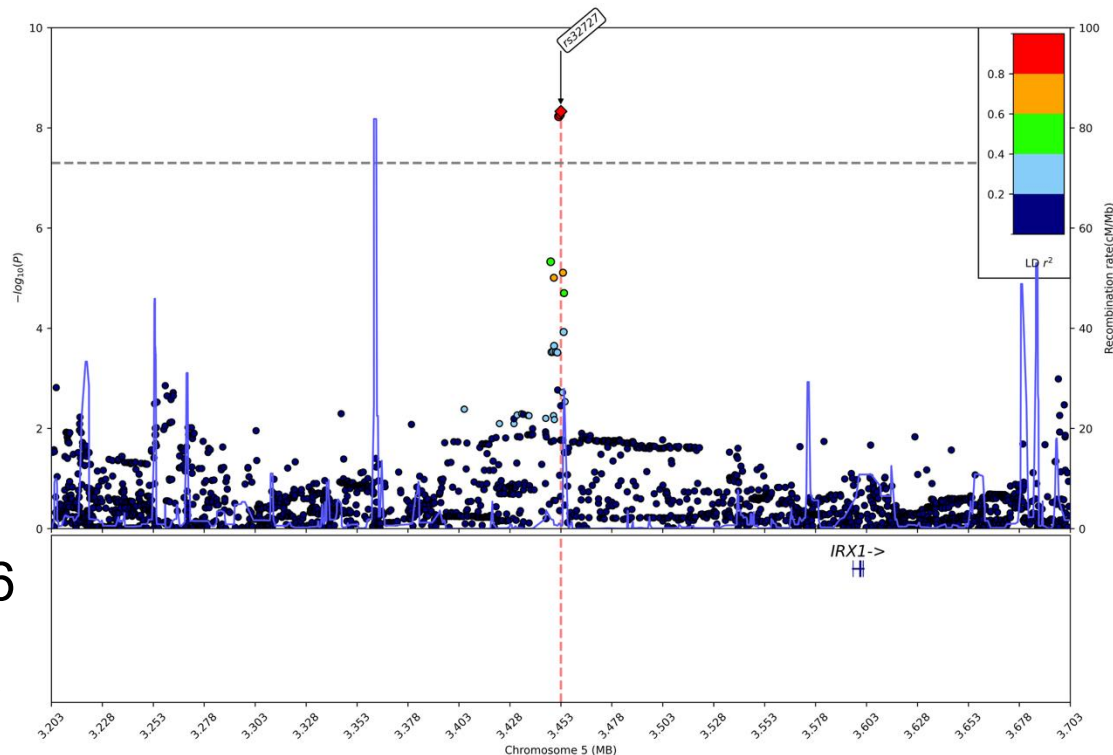
Results

- Novel findings:
 - 13 SNPs (Green)
- Replicated observation:
 - 38 out of 42 autosomal loci (blue)



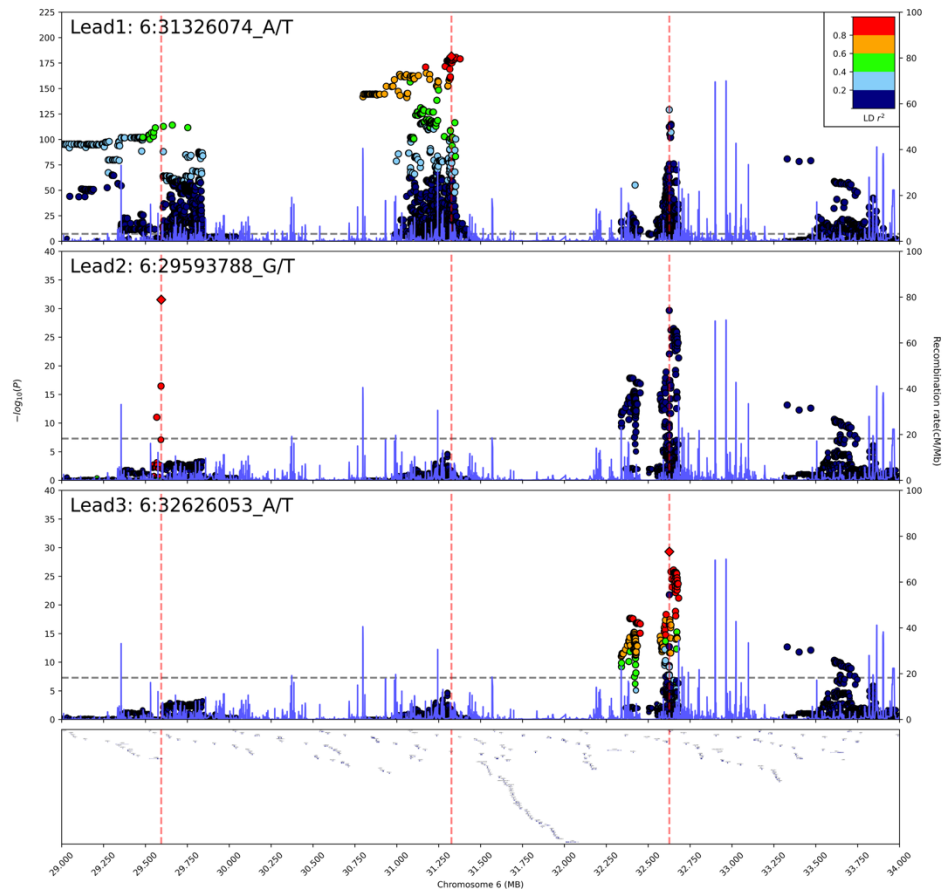
Results (contd.)

- Locus post filtering:
 - $MAF \geq 5\%$
 - $MAC \geq 10$
 - **5p15.33**
- SNPs
 - Lead: rs32727
 - In LD: rs32723, rs32726
- Heritability of non-HLA region = 23%



Results (contd.)

- Lead SNP in HLA region:
 - rs28633132 (HLA-DQB1)
 - rs2853999 (HLA-B)
 - rs715044 (GABBR1)



Discussion

- 5p15.33 locus:
 - rs32737 is a long non-coding RNA SNP
 - reached significance in validation subsets too
 - closest gene *IRX1*, also associated with rheumatoid arthritis
- Strengths:
 - Screening: inclusion of histologically confirmed incident cases
 - SAIGE: controlling relatedness and imbalanced dataset
- Limitations:
 - Missing young cohort, limited cases, European ancestry only

Conclusion

- The lncRNA might be involved in key gene regulations
- Close to *IRX1* linked to RA
- RA is known to share loci with CeD

The 5p15.33 is a novel locus associated with CeD

Thank you for your attention!



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