

# QTL mapping in MAGIC populations

## Part 1

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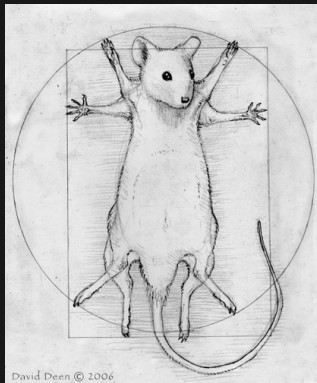
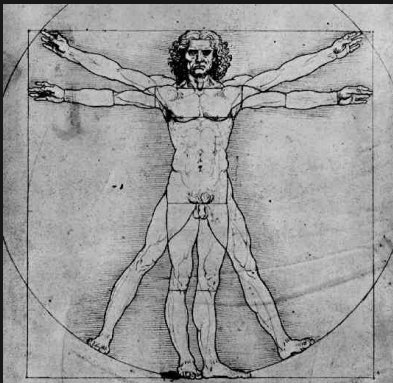
[github.com/kbroman](https://github.com/kbroman)

@kwbroman

Slides: [kbroman.org/Talk\\_MAGIC2021](http://kbroman.org/Talk_MAGIC2021)

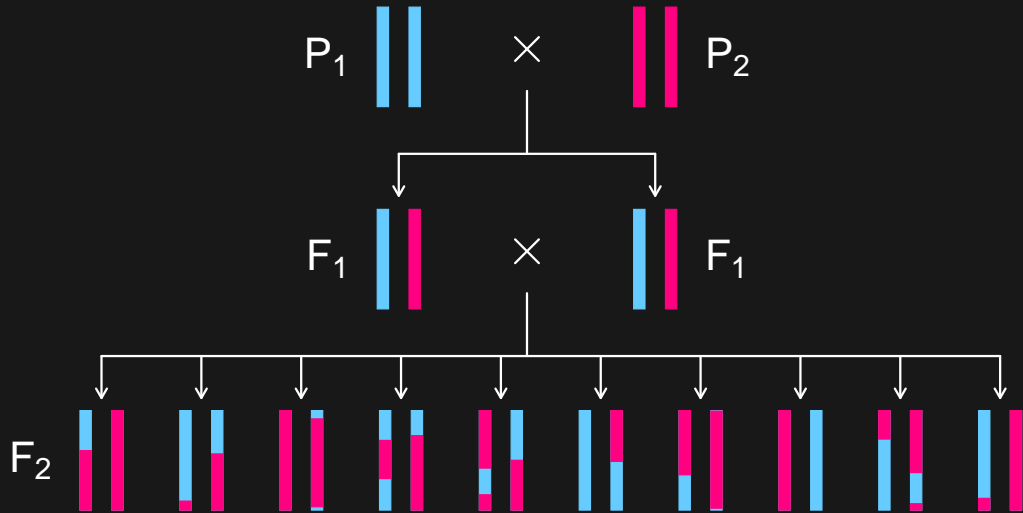




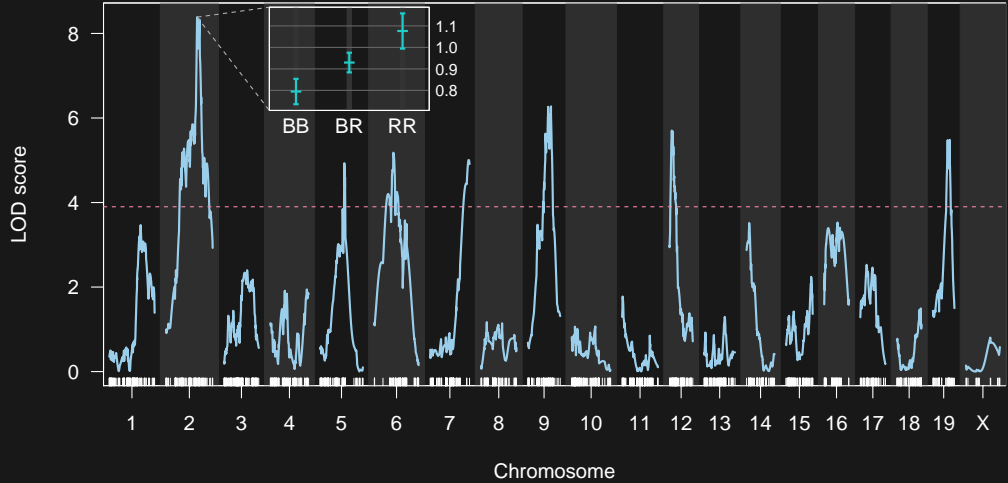


daviddeen.com

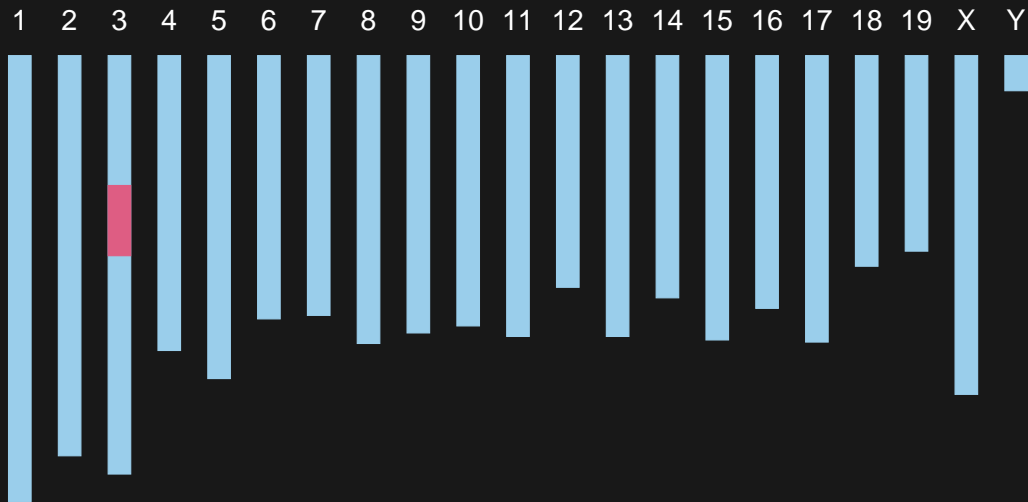
# Intercross



# QTL mapping



# Congenic line/NIL



# Improving precision

- ▶ more recombinations
- ▶ more individuals
- ▶ more precise phenotype
- ▶ lower-level phenotypes
  - transcripts, proteins, metabolites

# Genome-scale phenotypes

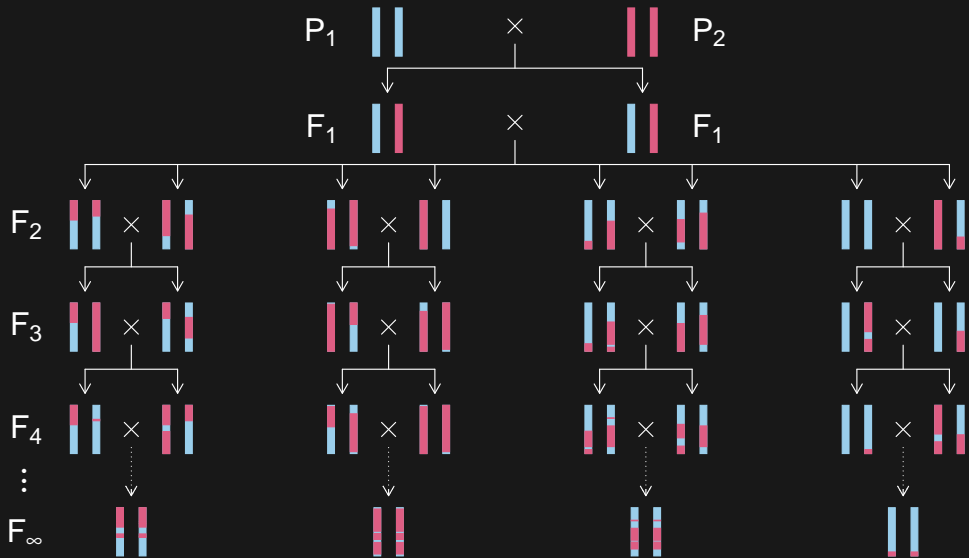




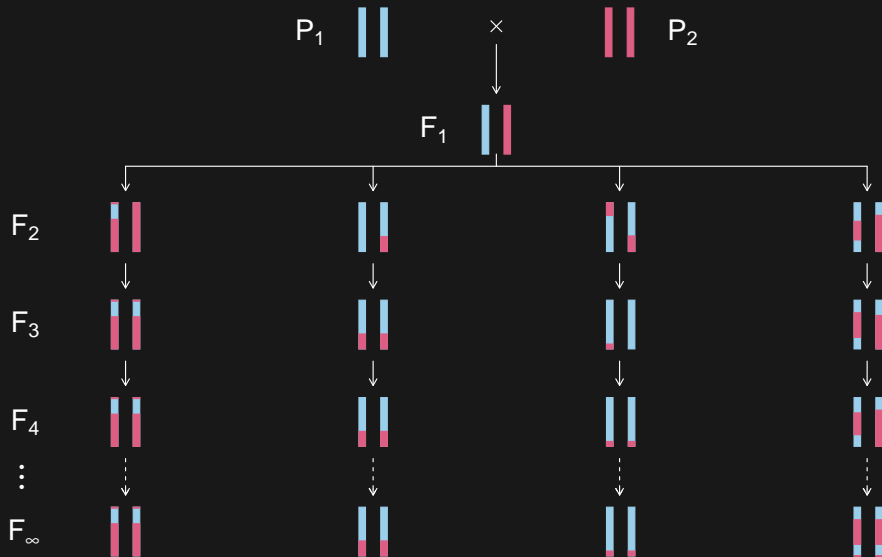
# Advanced intercross lines



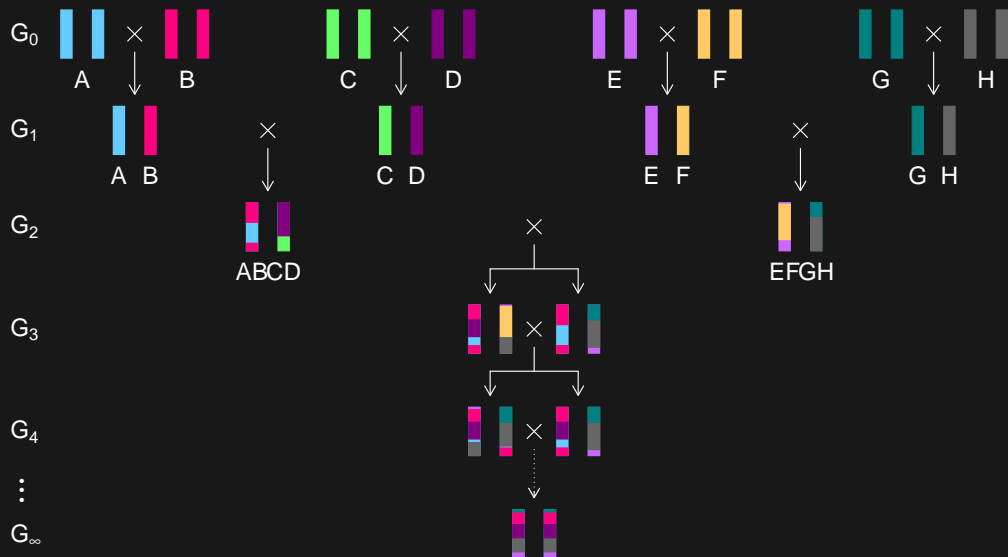
# Recombinant inbred lines



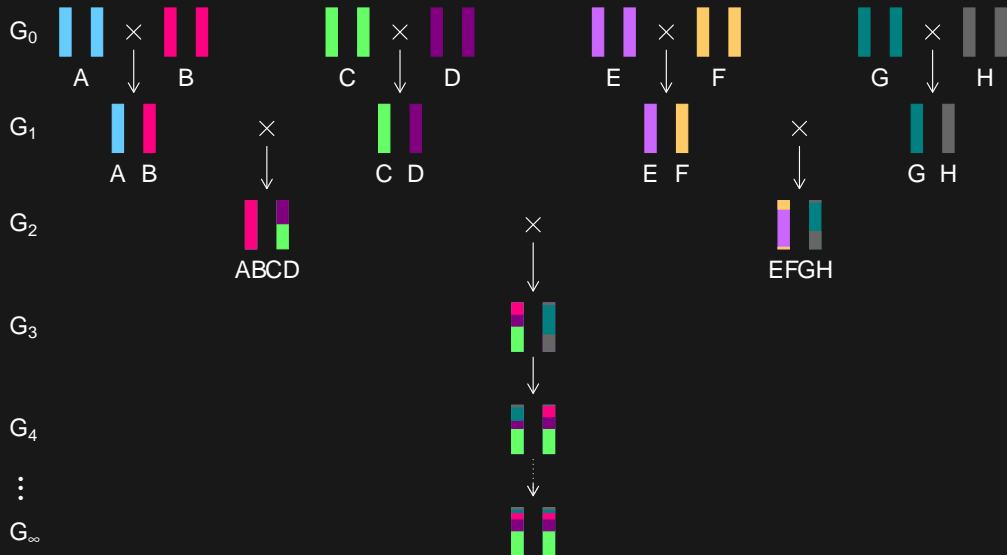
# Recombinant inbred lines



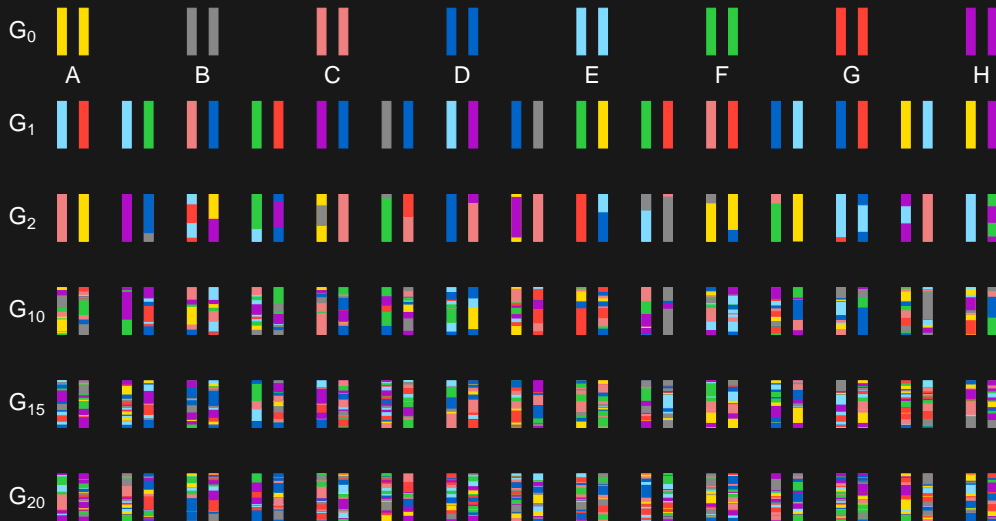
# Collaborative Cross



# MAGIC



# Heterogeneous stock



# MAGIC is magic

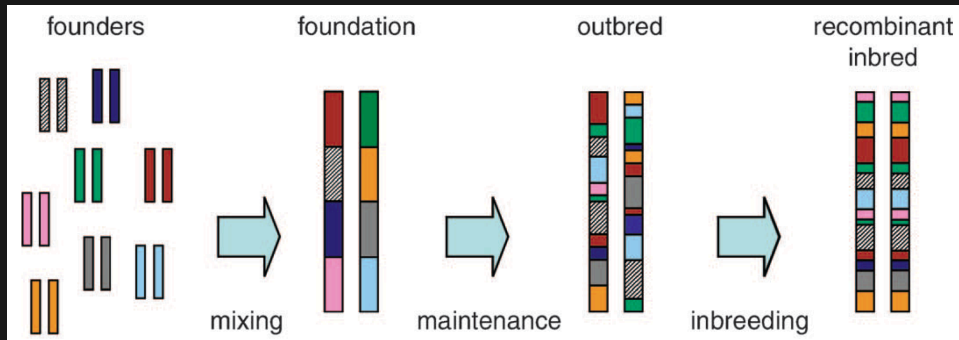
- ▶ Genetic diversity
- ▶ High-precision mapping
- ▶ Predictable linkage disequilibrium
- ▶ Phenotype replicates to reduce individual variation
- ▶ Pool phenotypes from multiple labs, environments, treatments
- ▶ Genotype once

# MAGIC is magic

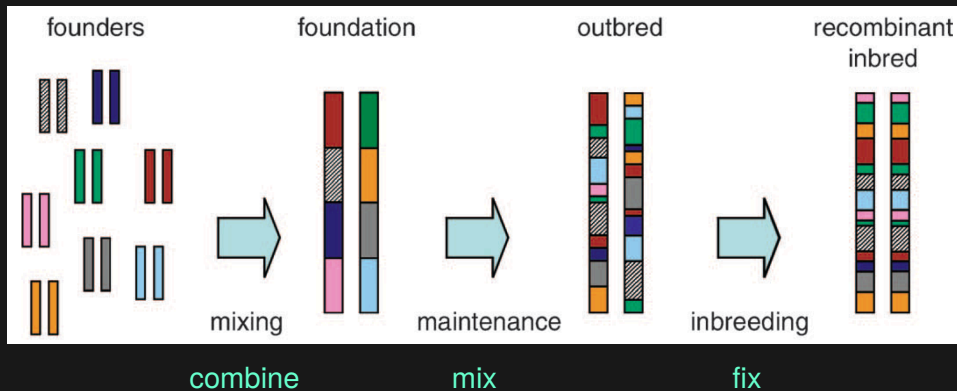
- ▶ Genetic diversity
- ▶ High-precision mapping
- ▶ Predictable linkage disequilibrium
- ▶ Phenotype replicates to reduce individual variation
- ▶ Pool phenotypes from multiple labs, environments, treatments
- ▶ Genotype once
- ▶ Cool name



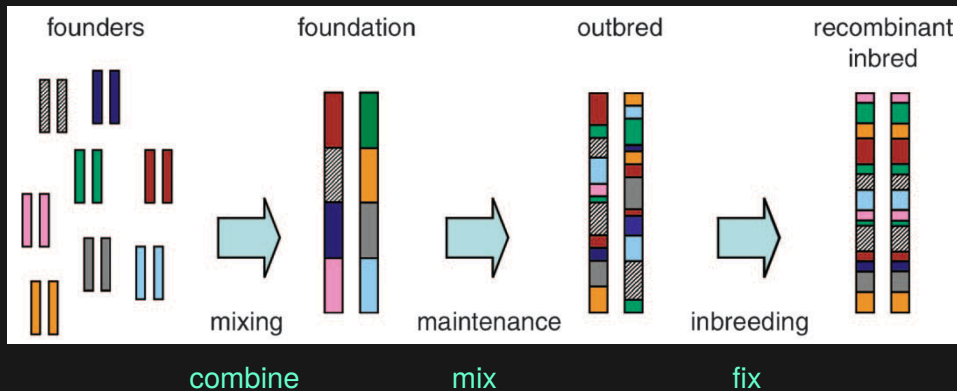
# MAGIC lines



# MAGIC lines

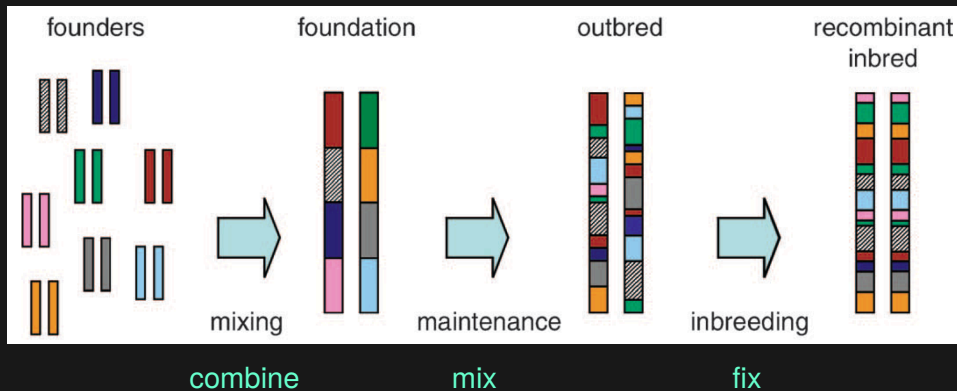


# MAGIC lines



How many?

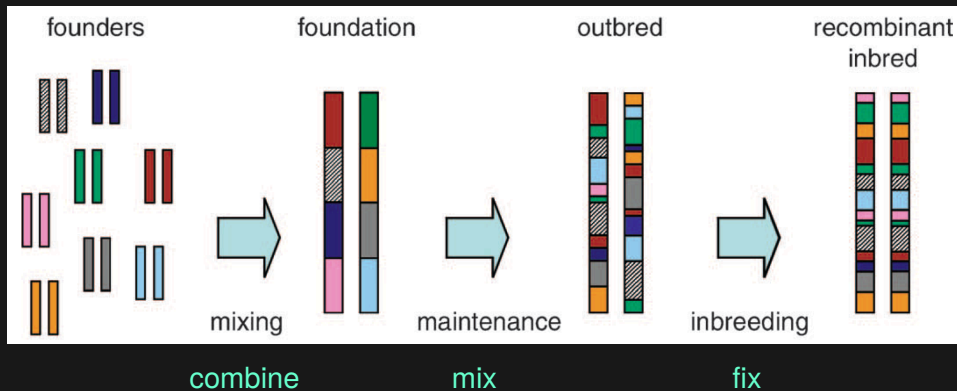
# MAGIC lines



How many?

Which?

# MAGIC lines



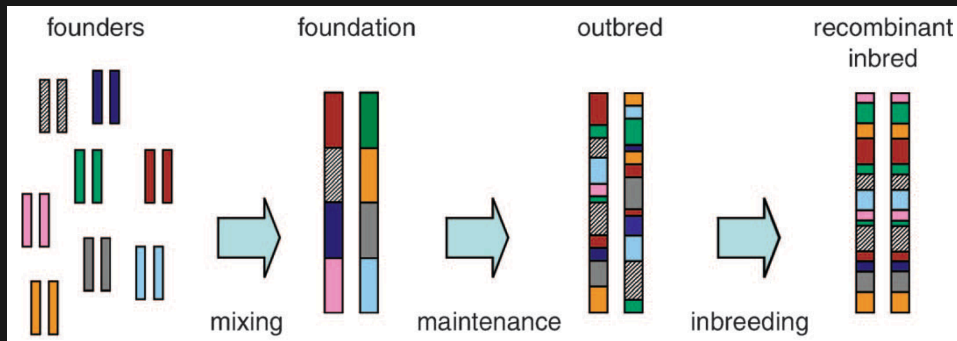
How many?

How long?

Which?

Valdar et al., Genetics 172:1783, 2006

# MAGIC lines



combine

mix

fix

How many?

How long?

How?

Which?

Valdar et al., Genetics 172:1783, 2006

# The goal

Identify QTL

- ▶ Power
- ▶ Mapping precision

# The goal

Identify QTG

- ▶ Power
- ▶ Mapping precision



# The goal

Identify QT**G**

- ▶ Power
- ▶ Mapping precision
- ▶ Estimate QTL allele frequencies

# Principles

- ▶ Avoid population structure
- ▶ Tradeoff between *power for de novo discovery* and *mapping precision*
- ▶ More QTL to find  $\Rightarrow$  more QTL getting in the way?
- ▶ More QTL alleles  $\Rightarrow$  less information about each
- ▶ Are QTL alleles common or rare?

# How many founders?

## More

- ▶ More general use
- ▶ More QTL
- ▶ Greater precision
- ▶ Estimate allele frequencies
- ▶ Haplotype analysis in founders

## Fewer

- ▶ Lower residual variance
- ▶ Greater power for a particular QTL?
- ▶ Better power for epistasis
- ▶ Rare alleles are less rare

# Which founders?

- ▶ Diverse
- ▶ Interesting
- ▶ No breeding problems
- ▶ Balanced: star phylogeny

# How much mixing?

- ▶ More mixing  $\Rightarrow$  Greater mapping precision
- ▶ ...but lower power for *de novo* mapping
- ▶ Potential for population structure, missing alleles
- ▶ Random mating or curated mating?
- ▶ Start with many random cross directions?

# Selfing or DH?

- ▶ Inbreeding gives added recombination
- ▶ But not so much as at the mixing stage
- ▶ If doubled haploids are feasible, use them

# Sharing is also key

- ▶ The greatest power of MAGIC comes from sharing  
Pooling data, exploring multiple environments/treatments
- ▶ Common software needs  
Analysis software, database infrastructure
- ▶ Many students need to learn the same stuff  
Joint training opportunities

Slides: [kbroman.org/Talk\\_MAGIC2021](https://kbroman.org/Talk_MAGIC2021)



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