

# The Effect of Genetic Connectivity on Natural Selection in *Chlamydomonas reinhardtii*



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## What Are Genetic Networks?

- Genetic networks represent metabolites or genes (nodes) and their interactions (edges)
- Networks can be used to represent connections such as gene co-expression and metabolic pathways
- Chlamydomonas reinhardtii*'s network:
  - ChlamyNet Gene Co-expression network<sup>1</sup> accounts for 5,897 genes

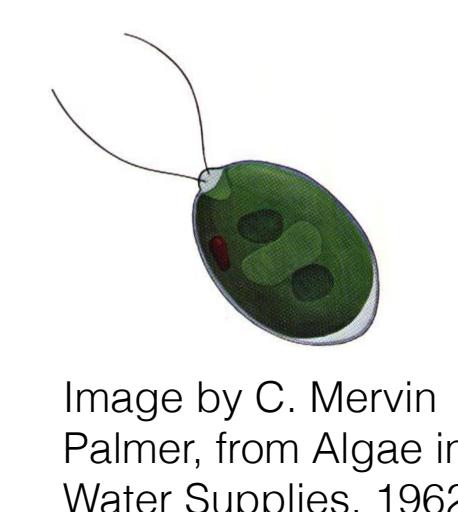


Image by C. Mervin Palmer, from Algae in Water Supplies, 1962

## Network Measures Degree & Betweenness Centrality

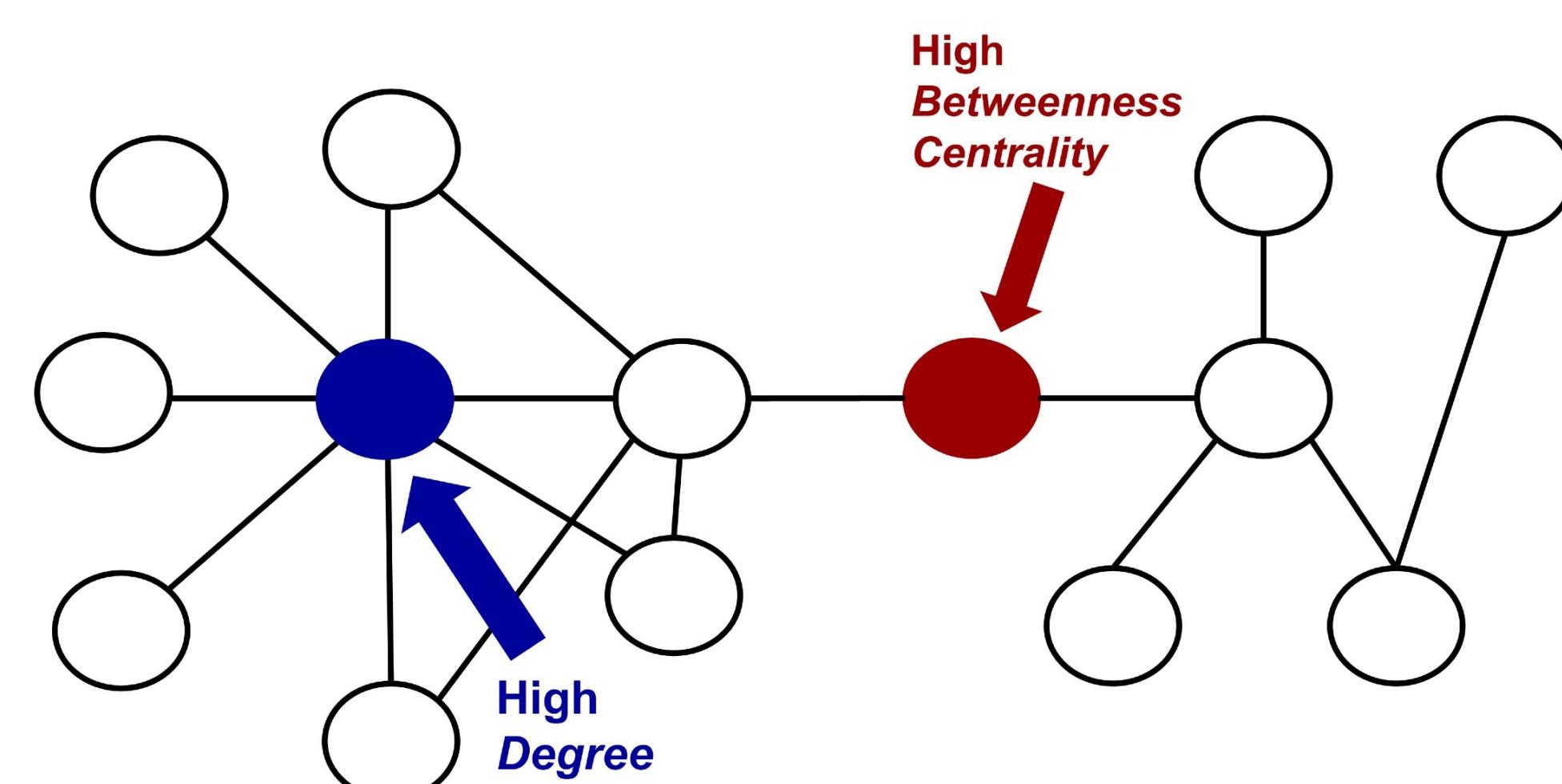


Fig 3. Visualization of network parameters

- Degree** measures the number of direct connections the node has to other nodes
- Betweenness centrality** measures the extent to which a node lies on path between other nodes

## How does the network predict the distribution of fitness effects of new mutations?

- DFE-alpha method<sup>2</sup> uses divergence and diversity data to estimate:
  - Proportion of deleterious mutations in 4 categories of  $N_{eS}$
  - Rate of adaptive molecular evolution ( $\alpha$ )
  - Adaptive over neutral rate of substitution ( $\omega_a$ )

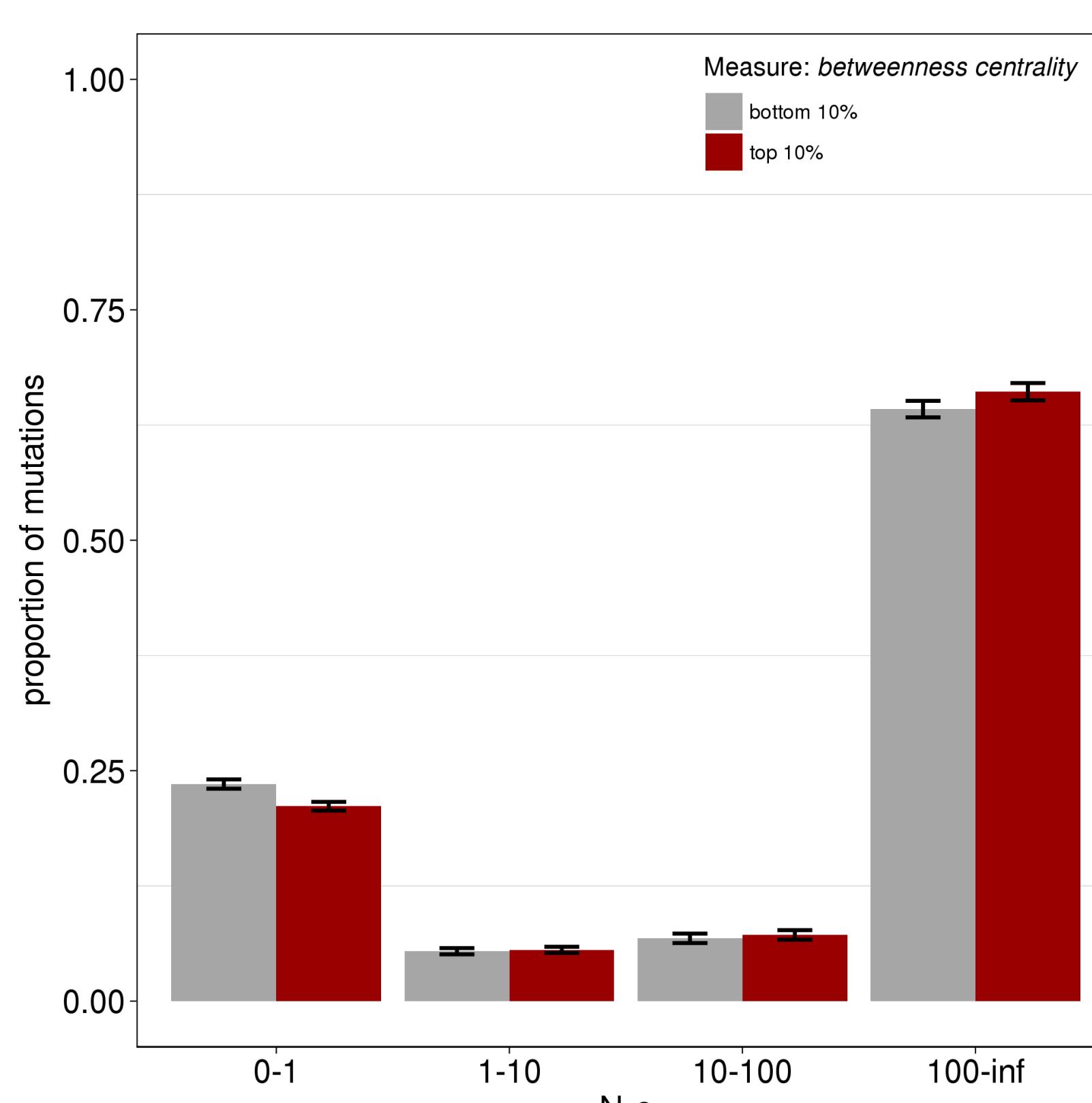


Fig 4. Distribution of fitness effects ( $N_{eS}$ ) of mutations by betweenness centrality

- Similar DFE of high and low betweenness centrality
- Indicates constraint across the network is similar

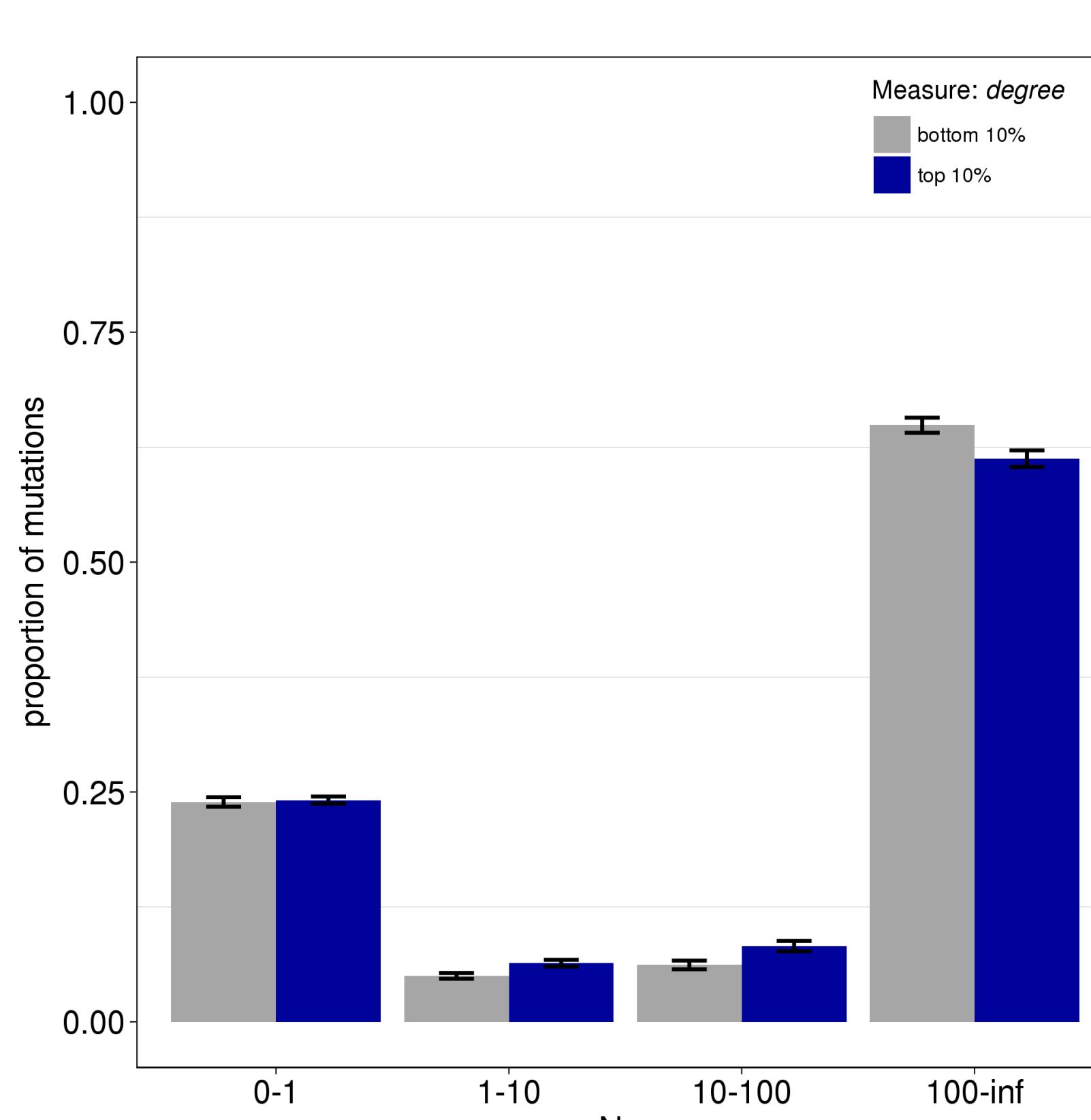


Fig 5. Distribution of fitness effects ( $N_{eS}$ ) of mutations by degree

- Similar DFE of high and low degree genes
- Indicates constraint across the network is similar

## Does the rate of adaptive evolution vary across the genetic network?

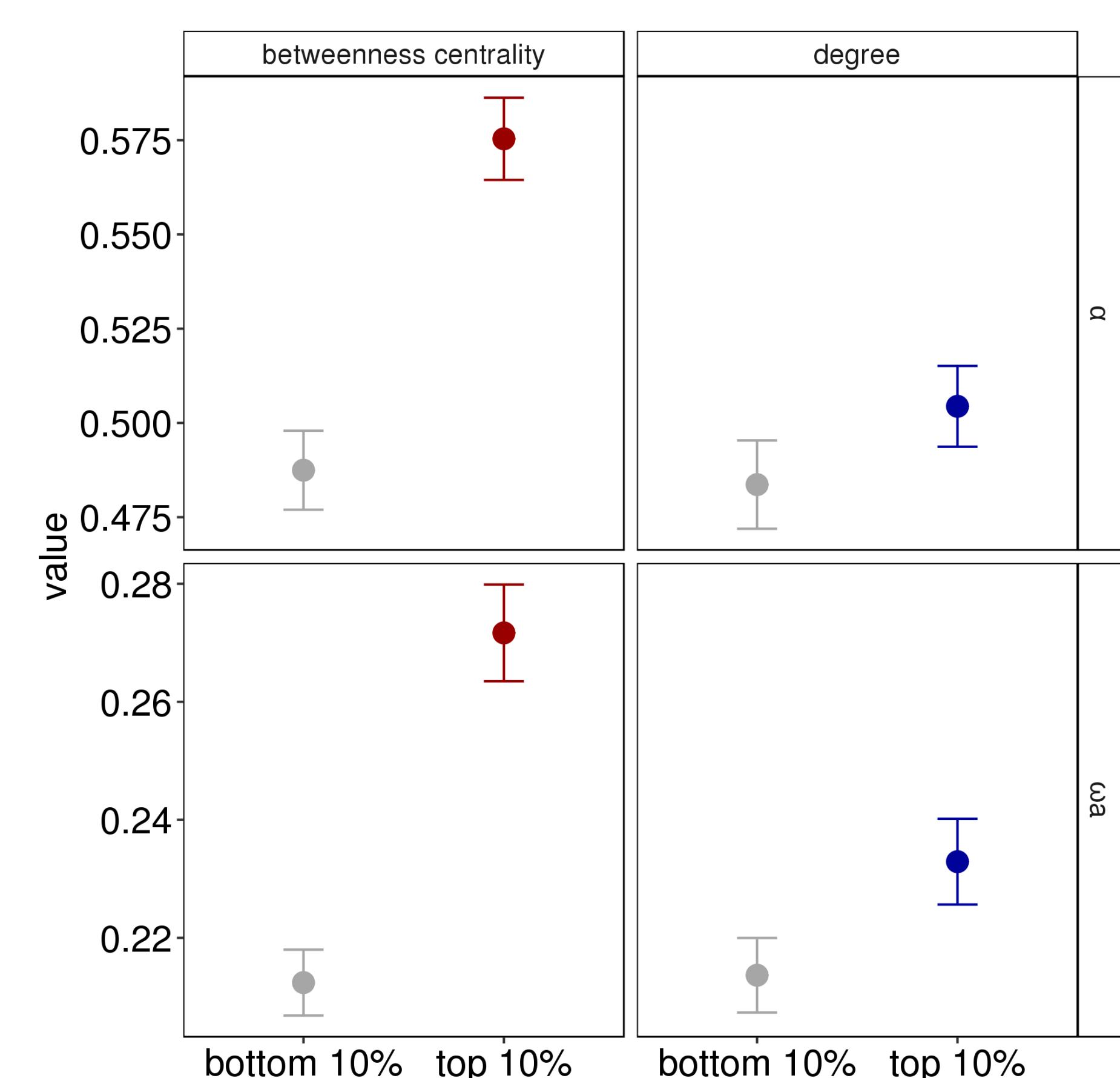


Fig 6. Values of  $\alpha$  and  $\omega_a$  at different degree and betweenness groups

- ~20% increase in proportion of adaptive substitutions in high betweenness genes
- ~30% increase in rate of adaptive substitutions in high betweenness genes
- Highly connected genes have marginally higher values of  $\alpha$  and  $\omega_a$
- Error bars represent 95% CI from bootstraps

## What It All Means

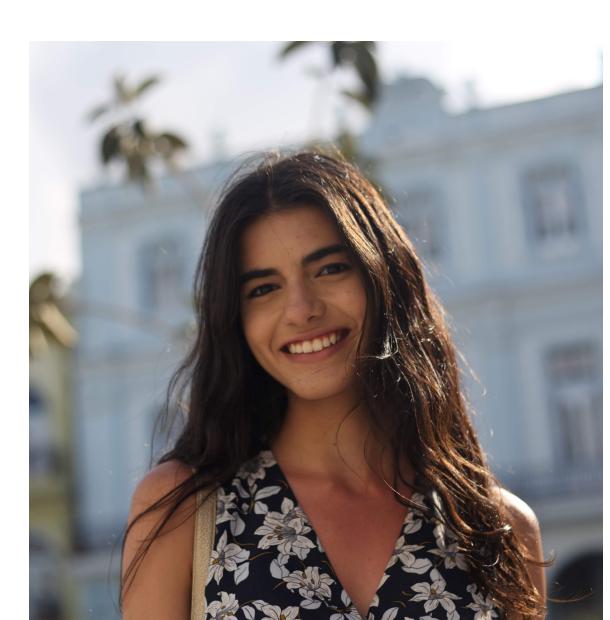
- Distribution of deleterious fitness effects of mutations is similar across genes regardless of connectivity or betweenness centrality.
- Proportion of adaptive substitutions and rate of adaptive substitution is higher in highly connected genes and especially in those with high betweenness.
  - Purifying selection is strong across most genes in the genome.
  - Positive selection is more prevalent in genes with strong connections in the network and genes between major clusters in the network adapt significantly faster than other genes in the genome.

## References & Acknowledgements

- Romero-Campero et al. 2016, BMC Genomics 17
- Eyre-Walker and Keightley 2009, MBE 26: 2097



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