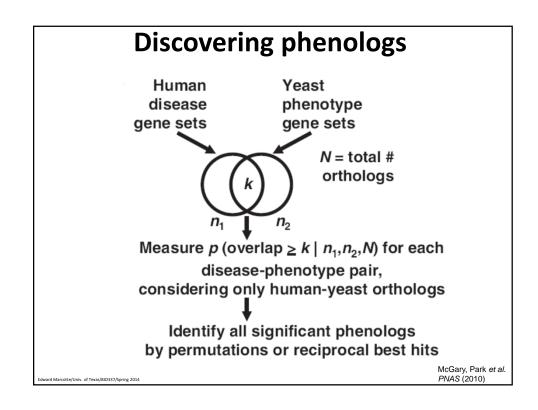
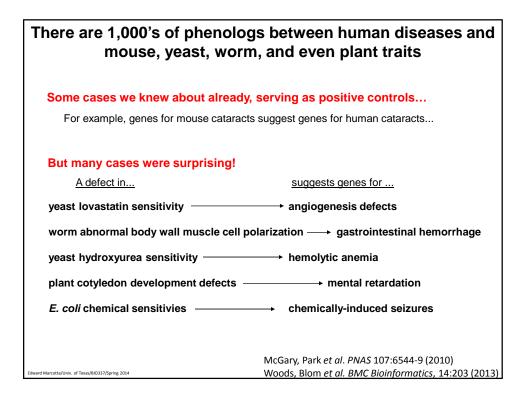
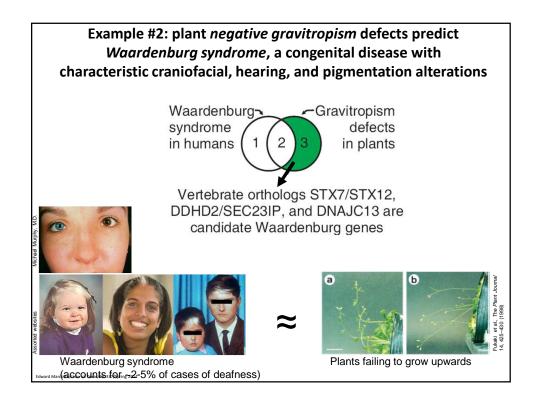
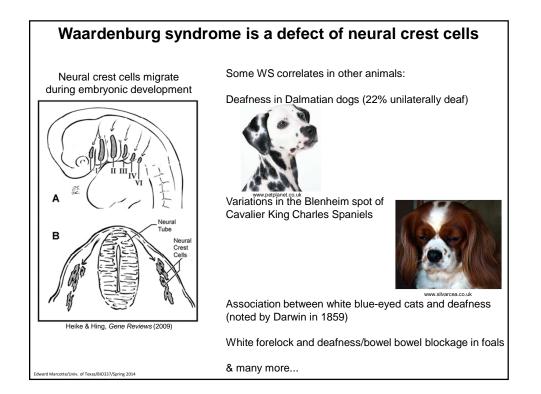


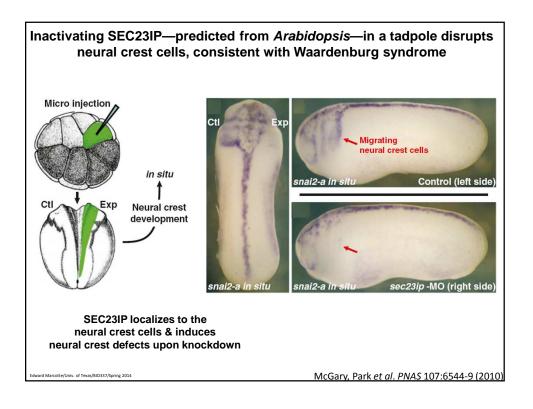
Building & searching a collection of phenotypes	
Mining available databases +	
manual collection from the primary literature \downarrow	
# gene-phenotype	
Organism	associations
human	1,923
mouse	74,250
worm	27,065
yeast	86,383
Arabidopsis	22,921
Spanning ~300 human diseases,	
>7,000 model organism mutational phenotypes	
Computational scan phenotypes for novel models of a disease of interest, identify significant phenologs using permutation tests McGary, Park <i>et al.</i> <i>PNAS</i> (2010)	

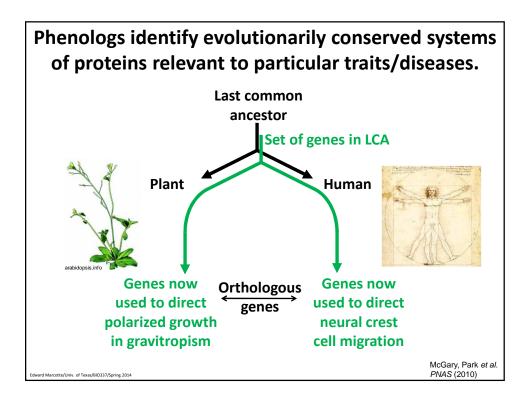


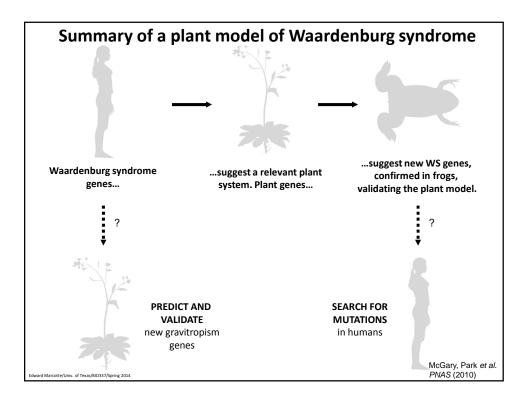


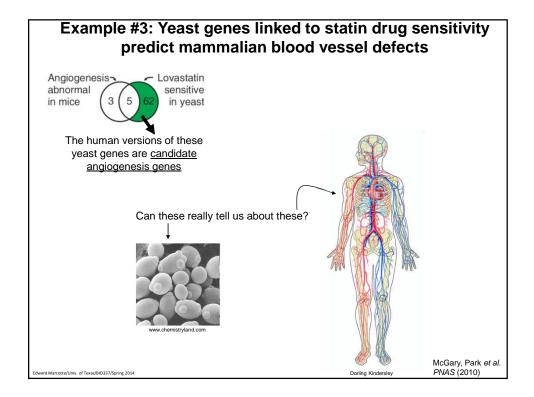


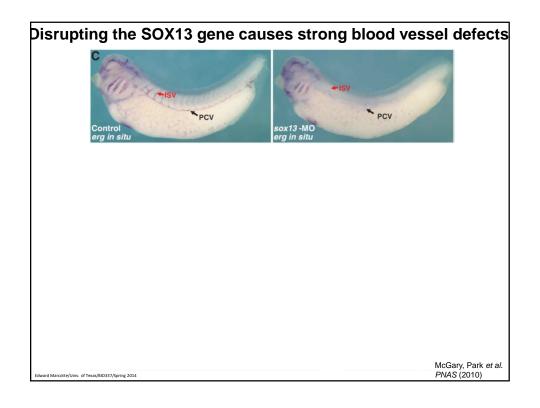


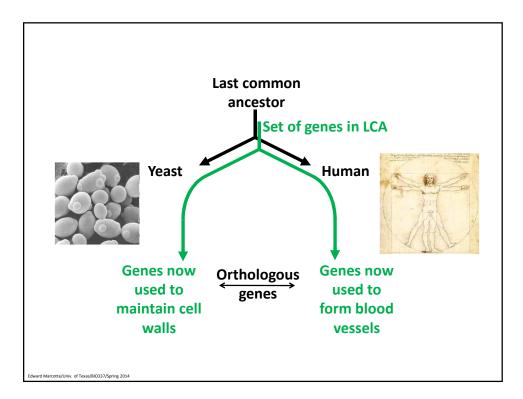


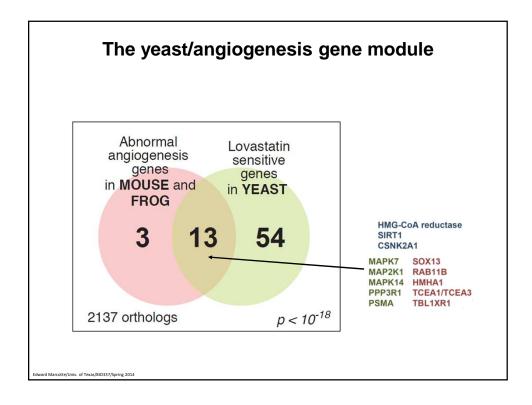


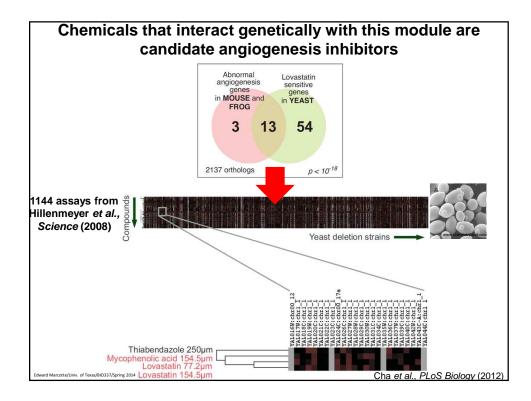


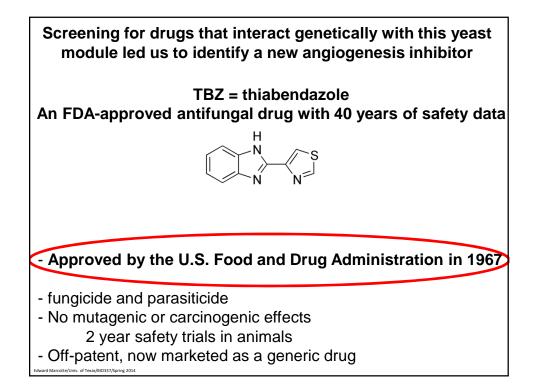


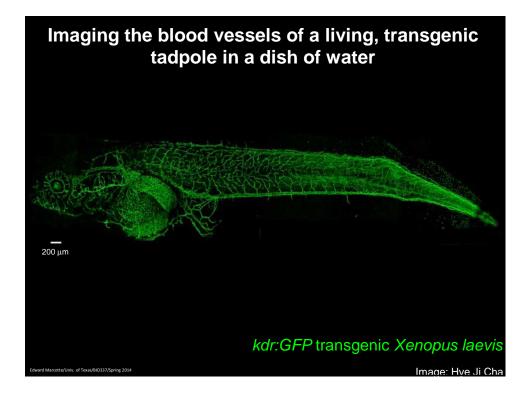


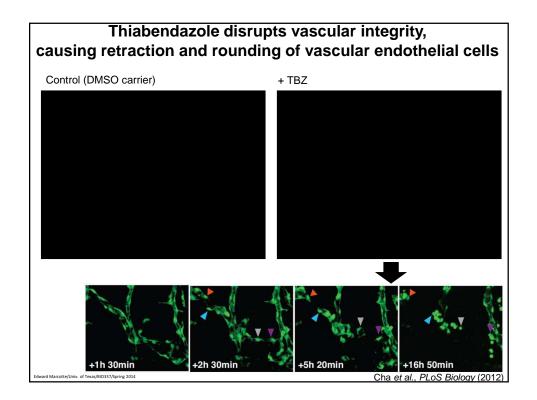


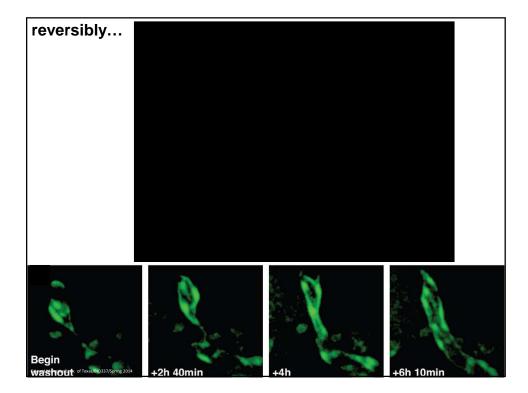


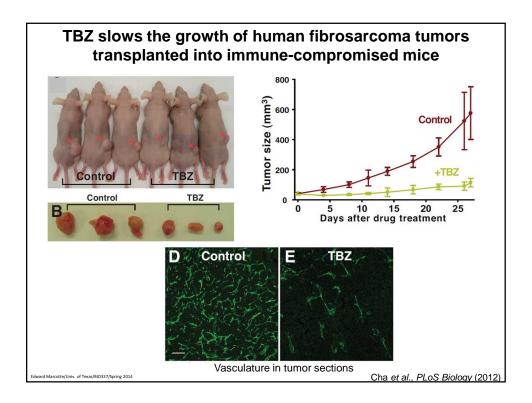


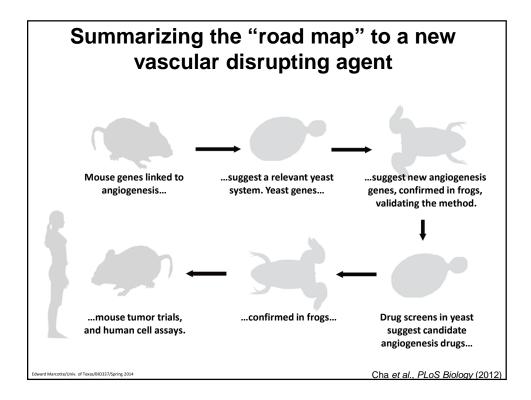












Summary of the major themes

- Genetic traits and diseases often arise from perturbing any one (or more) of a set or module of genes, e.g. components of the same pathway or protein complex
- Pathways and complexes can be deeply evolutionarily conserved, often more deeply than the diseases or traits they are linked to
- Knowing the underlying module of genes thus predicts new candidate genes for any of the linked traits across organisms, e.g. as for yeast lovastatin sensitivity predicting vertebrate angiogenesis genes

Edward Marcotte/Univ. of Texas/BIO337/Spring 2014