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The human pathogen *Candida albicans*' genome varies substantially between clinical isolates, yet it is currently unknown how this variation affects infection. Since many genetic variants are located in gene regulatory sequences, Dr. Petra Vande Zande predicts that there is substantial divergence in gene-regulatory networks between different *C. albicans* isolates that modifies their fitness. Dr. Vande Zande will use gene expression data from different isolates to model gene regulatory networks and identify key differences that impact fitness. Vande Zande will conduct these experiments in [Dr. Anna Selmecki's lab](#) at the University of Minnesota. This research will provide direct insight into genetic differences that impact *C. albicans* infections. It may also provide clues into other genetically diverse systems with differences in gene-regulatory networks, including human cancers.

As a graduate student in [Dr. Patricia Wittkopp's lab](#) at the University of Michigan, Vande Zande studied gene expression in the context of adaptive evolution. In particular, Dr. Vande Zande discovered that [mutations affecting a gene's expression from a distance are more pleiotropic and more detrimental to fitness than mutations occurring proximally to the gene of interest](#). With her experience in the evolution of gene expression, Dr. Vande Zande is now interested in understanding divergence in gene-regulatory networks between different clinical isolates of yeast infections.

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