Candida albicans is an opportunistic fungal pathogen in immunocompromised patients. The fungus has to adapt to a variety of environments within the host. At the chromosome level, C. albicans can adapt to the host via gross chromosomal rearrangements (GCRs) and ploidy changes. The diploid genome of the fungus consists of eight pairs of homologous chromosomes (chromosome R, 1 – 7). Except for chromosomes 3, all other chromosomes contain at least one functional copy of the structure called major repeat sequence (MRS). It can be contracted and expanded and is frequently the site of translocation where chromosomes exchange parts of their chromatids. Such changes at MRS can cause chromosome-length polymorphism in chromosome homologs where homologous chromosomes can have different length. Furthermore, aneuploidy can arise during mitosis via chromosome non-disjunction and, as a result, two daughter cells will have different number of chromosome copies.

To find evidence of how C. albicans changes its chromosomes during infection (in vivo), oropharyngeal candidiasis (OPC) and blood stream infection (BSI) mouse models were utilized. These models mimic infection types found in patients. Chromosome karyotypes of post-in vivo isolates were compared to that of parental strain using contour-clamped homogeneous electric field (CHEF) electrophoresis. An example of karyotypes of C. albicans chromosomes separated by size is shown in figure 1. Band shifting and intensity changes relative to parental strain karyotype can suggest that translocation or non-disjunction might have occurred.

In the study of chromosomes 5-7 of OPC isolates, the rates of band shifting and intensity changes are similar in most homologs (approximately 30%). However, the rate is significantly lower in the larger homolog of chromosome 6, in which there is no change in band intensity or band shifting in any isolates that were studied. This project will be continued in this fall semester more karyotypes (for example, of larger chromosomes R, and 1-4) of both OPC and BSI models will be studied. In the future, strains that showed evidence of ploidy changes and GCRs will be analyzed more using microarray technique to determine the events that the strains had undergone.

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