FILE S1

Supporting Materials and Methods

Statistical analysis of preferential co-segregation of two different homologues into sister spores

Following a triploid meiosis, there are only two ways to distribute the twelve copies of two different homologous chromosomes within a single tetrad: 1) double disomes (two sister spores disomic for both chromosomes and the remaining two sister spores monosomic for both chromosomes) or 2) mixed disomes (two sister spores disomic for one homologue and monosomic for the other with the other sister pair receiving the reciprocal arrangement of chromosomes). If segregation of the chromosomes into four-viable spore tetrads is random, these two events should occur at equal frequencies. Among the MH10/JSC2 data set, for all 120 two-chromosome combinations, we found some tetrads with double-disomes (indicating no double-disome combination is lethal). In addition, since we also recovered some tetrads with mixed disomes for all two-chromosome combinations, there is no situation in which disomy for one type of homologue requires disomy for another type of homologue for viability.

We calculated whether the numbers of double disomes and mixed disomes were significantly different for each two-chromosome combination by comparing the number of tetrads in each class for each homologue with the expectation of equality by using the chi-square "Goodness of Fit" test on the Vassar Stat Website (http://faculty.vassar.edu/lowry/VassarStats.html). After correcting for the false-discovery rate (BENJAMINI and HOCHBERG 1995), no significant departures from equality were observed. We point out, however, that because of the relatively small number of tetrads examined and the large number of comparisons examined, this statistical test is not particularly sensitive.

Statistical analysis of preferential co-segregation of three different homologues into sister spores

There are 560 combinations of three-chromosome disomes. Among the tetrads of MH10 and JSC2, we found all 560 of these combinations, demonstrating that no combination of three-chromosome disomes is lethal.

There are four possible ways to distribute 18 copies of three homologues within a tetrad as shown below:

	Chromosome 1	Chromosome 2	Chromosome 3
Meiotic pair 1	monosome	monosome	monosome
Meiotic pair 2	disome	disome	disome
Meiotic pair 1	monosome	disome	disome
Meiotic pair 2	disome	monosome	monosome
Meiotic pair 1	monosome	disome	monosome
Meiotic pair 2	disome	monosome	disome
Meiotic pair 1	monosome	monosome	disome
Meiotic pair 2	disome	disome	monosome

As with the two-chromosome combinations, each of these situations should occur at equal frequencies if presence of a disome is independent of all other disomes. Because there were so many missing homologues in the MH10 experiment, we tested this expectation with only the JSC2 data. Using the chi-square "Goodness of Fit" test and the BENJAMINI-HOCHBERG correction as described above, we did not detect any significant deviation from random. As discussed above, because of the relatively small numbers of tetrads examined, this test is not sensitive.

Statistical analysis of the non-random segregation of disomic chromosomes in JSC2 based on whether the chromosomes are derived from S288c, JAY291, or YJM789

We also examined whether disomes had a non-random pattern with respect to which genetic background they were derived from. For each spore with a disomic chromosome, there are three possible patterns: 1) one chromosome derived from S288c and one derived from JAY291, 2) one chromosome derived from S288c and one derived from YJM789, and 3) one chromosome derived from JAY291 and one derived from YJM789. In the absence of preferential segregation, these three patterns should be found with equal frequencies. We examined the JSC2 tetrad data for any deviation from random pairing for all 16 chromosomes with both the chi-square "Goodness of Fit" test and the BENJAMINI-HOCHBERG method as described above. No evidence for preferential segregation was obtained.

References

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