THE GENETIC BASIS OF ADAPTATION TO NOVEL ENVIRONMENTS IN *CHLAMYDOMONAS REINHARDTII*

Torsten Bernhardt
Department of Biology
McGill University, Montreal
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Abstract

Four pairs of selection lines of *Chlamydomonas reinhardtii* were each founded by mt^+ and mt^- spores from the same zygote. They were cultured asexually under light (photoautotrophic) and dark (heterotrophic) conditions for several hundred generations. The light and dark lines derived from each spore had by then diverged, each becoming adapted to its selection environment. Sister lines were then crossed. Crosses between lines selected in the same environment (mt^+light x mt^-light and mt^+dark x mt^-dark) showed that adaptation was heritable and generally additive; however, some lines showed substantial epistasis. Crosses between lines selected in different environments (mt^+light x mt^-dark and mt^+dark x mt^-light) suggested that chloroplast and mitochondrial genomes contributed to adaptation, genes evolving in the light being borne on the chloroplast and those evolving in the dark on the mitochondrion.

Résumé

Quatre paires de lignées de *Chlamydomonas reinhardtii* ont été dérivées de spores mt$^+$ et mt$^-$ issues d'un même zygote. Chacune de ces lignées a ensuite été soumise à selection, d'une part à la lumière (croissance autotrophe), d'autre part à l'obscurité (croissance hétérotrophe), pendant plusieurs centaines de générations. Les lignées "lumière" et "obscurité" issues de chaque spore ont ainsi divergé, chacune s'adaptant à son environnement. Des croisements entre lignées sélectionnées dans le même environnement (mt$^+$ "lumière" x mt$^-$ "lumière" et mt$^+$ "obscurité" x mt$^-$ "obscurité") montrent que l'adaptation est héritable et généralement additive; néanmoins, certaines lignées présentent des effets épistatiques non négligeables. Les croisements entre lignées sélectionnées dans des environnements différents (mt$^+$ "lumière" x mt$^-$ "obscurité" et mt$^+$ "obscurité" x mt$^-$ "lumière") suggèrent une contribution du génôme chloroplastique à l'adaptation à la croissance autotrophe, et du génôme mitochondrial à l'adaptation à la croissance hétérotrophe.

Introduction

Differing responses to selection

It has long been recognized that conspecific populations may adapt to identical selection pressures in different ways (Wright, 1931, Simpson, 1950). Selection acts upon the phenotype of the organism, rather than directly on the genotype, so that adaptation is achieved differently in different cases. There are many examples in which populations have adapted differently to similar agents of selection (see Cohan, 1984b, for review), such as resistance to T4 phage in *Escherichia coli* (Lenski, 1988), copper tolerance in *Agrostis tenuis* (Nichols and McNeilly, 1979) and *Saccharomyces cerevesiae* (Ashida, 1965), herbicide tolerance in *Cucumis sativus* (Miller et al., 1973a, 1973b), DDT resistance in *Aedes aegypti* (Brown and Abedi, 1962), and warfarin resistance in *Rattus norvegicus* (Greaves and Ayres, 1977). In some cases, the physical or biochemical mechanisms involved in the variability of response have been elucidated. A European population of the red spider mite *Tetranychus urticae* increased its tolerance to organophosphate insecticides by reducing its neural sensitivity, while a New York population achieved the same result by detoxifying the compounds (Matsumura and Voss, 1967). Different human populations have adapted differently to the threat of malaria: populations in the Mediterranean region have evolved thalassemia, whereas populations in Africa have reduced susceptibility through sickle-cell hemoglobin (Livingstone, 1971, Luzzatto, 1979).

Populations selected in similar environments may diverge for several reasons. In the first place, no two environments are precisely the same. Slight differences in food (Falconer, 1960, Robertson, 1960) or temperature (Druger 1962), for example, have been shown to cause different responses to artificial selection. This can happen even when the variation is only temporal, in the sense of changing the order in which selection at different rates or different directions is applied (Lewontin, 1967).

Secondly, differences in response between populations can be caused by differences in their initial state. This has been found experimentally for resistance to ethanol knockdown in *Drosophila melanogaster* (Cohan et al., 1989), where different alleles were present in the base populations from which the selection lines were founded. Alternatively, even if the same alleles are present in both populations, a difference in their initial frequencies could lead to different rates of response, although eventually the same degree of adaptation should be reached in all populations, as has been reported for selection for sternopleural bristle number in *Drosophila melanogaster* (López-Fanjul and Hill, 1973).

Finally, differences may arise by chance during the course of selection and accumulate through time, so that the divergence of replicate lines is a historical process. The first and most obvious cause of historicity is mutation. Mutations arise independently in different selection lines (Clarke et al., 1988). If the fitness of a new mutant generally depends on the mutations that have previously been fixed in the line, then each line will favour a different evolutionary trajectory. The second cause of historicity is genetic drift. Drift can cause divergence by fixing different alleles at the same locus in different populations, regardless of selection and recurrent mutation. The effects of drift are most pronounced when the effective population size is small. In *Drosophila melanogaster*, drift was found to be important for the dynamics of abdominal bristle number (Yoo, 1980). Weak selection combined with drift can also cause divergence in populations, sometimes more so than drift alone (Cohan, 1984b).

The shifting balance theory

The best-known attempt to express the contingent nature of evolutionary change is Wright's shifting balance theory (Wright 1931, 1932). By way of an analogy, populations are seen as inhabiting an "adaptive landscape." This landscape is usually viewed as a three-dimensional surface, with two axes representing allele frequencies at different loci. The third axis, usually height, represents population mean fitness. The surface would require many more dimensions to portray reality, but the three axes suffice to convey the idea. Selection acts to drive populations uphill until they reach a point of maximum fitness, the "adaptive peak." If there are large interactions among loci in their effects on fitness there may be several adaptive peaks, any given allele being selected for or against, depending upon which genetic background it is found in. If populations are initially different, their uphill progress may take them to different peaks. Alternatively, drift or mutation may drive populations that are initially similar to different peaks. The movement of a population from one peak to another is constrained because the transitional genotypes have lower fitness. The more highly-adapted the population (i.e. the taller the peak), the greater the reduction in fitness away from the peak, and the stronger the constraint on movement away from the peak. The offspring from matings between parents from the same peak will inherit a well-adapted combination of genes. On the other hand, mating between parents from different peaks brings together different combinations of genes, producing new and probably ill-adapted genotypes through recombination. Evidence supporting the theory has been found from studies of DDT resistance (King, 1955) in *Drosophila*, modification of ci^D expression (Cohan, 1984a) in *Drosophila*, and pupal weight in *Tribolium* (Enfield, 1977). However, the theory was not supported by experiments involving crossveinlessness (Milkman, 1964, 1979) and ethanol knockdown resistance (Cohan et al., 1989) in *Drosophila melanogaster.*

Extranuclear adaptation

Theories of the inheritance of adaptation have as a rule been concerned with the mendelian inheritance of nuclear genes. However, eukaryotes also contain extranuclear genomes in mitochondria and chloroplasts. These organellar genomes are usually (but not always) transmitted uniparentally through the female line. Non-mendelian inheritance has unfamiliar genetic properties, the evolutionary implications of which have yet to be fully explored (Asmussen et al., 1987, Lande and Kirkpatrick, 1989, 1990).

The quantifiable effect of these extranuclear genomes is identified as a maternal effect. This may arise in two ways. The first is through a developmental or physiological effect, such as the effect of the body size of the mother on the offspring or the seed size of plants; this is more properly known as the maternal environmental effect (Platenkamp and Shaw, 1993). The second is the effect that the mother has on her offspring through the inheritance of her cytoplasmic genomes; this is the maternal genetic effect. These two aspects of the maternal effect are often not distinguished, the summed effect being referred to as the maternal effect.

Phenotypic variation of traits coded for by organellar genomes is often low; for instance, heritability due to maternal genetic effects for seed weight in plants is about zero (Platenkamp and Shaw, 1993). This lack of phenotypic variation could be due to the erosion of variation by natural selection (Fisher, 1930, Endler, 1986). However, organellar genomes evolve quickly at the molecular level, and have been used to construct phylogenies at low taxonomic levels (Avise et al., 1987, Avise, 1989), and even geographically adjoining conspecific populations can be distinguished (Quattro et al., 1991, Zwanenburg et al., 1992). This variation may be neutral. However, mutations in organellar genomes, when occurring under new conditions, can lead to qualitative phenotypic variation, most notably with exposure to antibiotics and herbicides (Grun, 1976, Gillham, 1978). Whether selection in novel environments will often lead to adaptation based on modification of the extranuclear genomes is unclear.

The Chlamydomonas reinhardtii *system*

The unicellular chlorophyte *Chlamydomonas reinhardtii* is especially useful for investigating the genetic basis of adaptation. It is vegetatively haploid, the only diploid structure being the zygote. It has been extensively examined both physiologically and genetically (Harris, 1989). It is usually grown photoautotrophically in minimal medium, obtaining energy from light and carbon from dissolved CO_2. It can also be maintained in the dark in medium supplemented by acetate (Sagar and Granick, 1953, Bamberger et al., 1982), obtaining energy and carbon skeletons from the acetate by using the glyoxylate shunt of the tricarboxylic acid cycle (Kornberg and Elsden, 1961). These light and dark environments represent two extremes, photoautotrophism and heterotrophism, and obviously make very different metabolic demands upon the cell. They are thus appropriate environments in which to study adaptation and divergence in *Chlamydomonas reinhardtii.*

Chlamydomonas reinhardtii can be maintained indefinitely in asexual culture under laboratory conditions. Sexuality can be induced by transferring the cells to nitrogen-free medium. The nitrogen-starved cells undergo gametogenesis when the internal nitrogen reserves have been depleted, transforming into either mating-type plus (mt^+) or mating-type minus (mt^-) gametes, and will subsequently mate with cells of the opposite mating type. Organellar genomes in the chloroplast and mitochondria are inherited uniparentally but asymmetrically, with the mitochondria being transmitted by the mt^- parent and the single chloroplast by the mt^+ parent. Thus, the three genomes (nuclear, mitochondrial and chloroplast) are each inherited through different pathways.

Selection lines of *Chlamydomonas reinhardtii* were maintained in the light photoautotrophic and dark heterotrophic environments for about a year, representing several hundred generations of selection (for details, see Bell and Reboud, unpublished). These lines were then crossed. The progeny of crosses between sister lines from the same selection environment received chloroplast and mitochondrial genomes that had been selected in the same direction. These were used to investigate the nuclear genetics of adaptation, with the expectation that progeny would on average be inferior to the midparent if adaptation had been achieved through epistatic combinations of genes. The progeny of crosses between sister lines from different selection environments received chloroplast and mitochondrial genomes that had been selected in different directions. These were used to identify any extranuclear contribution to adaptation; in particular, we expected that progeny might be superior to the midparent if they received their chloroplast from a mt^+ line selected in the light, and their mitochondria from a mt^- parent selected in the dark.

Materials and Methods

Base Population

Spores were isolated from crosses of natural isolates of *Chlamydomonas reinhardtii* (see Harris, 1989, for details): mt^+ CC-1010 and CC-2343 stocks were mated with mt^- CC-1952 and CC-2342, resulting in the four sets of selection lines. Details of mating and other basic procedures can be found in Harris (1989). One random mt^+ and one random mt^- spore from each cross were each used to inoculate one light and one dark flask, giving a total of (4 pairs of sister lines)*(2 mating types)*(2 selection environments)=16 selection lines. These selection lines were named by letter and mating type; lines A+ and A- (CC-1010xCC-1952), B+ and B- (CC-1010xCC-2342), C+ and C- (CC-2343xCC-1952) and D+ and D- (CC-2343xCC-2342). Note that every flask was founded by a single clone. The original parental spores were stored on agar slants in dim light to maintain the cultures but keep growth to a minimum.

Selection

Selection took place in liquid batch culture. The flasks which comprised the light environment were filled with 300ml Bold's medium, a standard minimal algal growth medium (Harris, 1989), and illuminated by cool white fluorescent bulbs. Flasks in the dark environment were filled with 300ml Bold's medium supplemented with 1.2g/l anhydrous sodium acetate, and were wrapped in aluminum foil to occlude light. All flasks were bubbled continuously with filtered air. Cultures were initially transferred whenever cultures were dense enough for 1ml of inoculant to permit growth in the newly-inoculated flasks; eventually, transfers were possible every week for the dark flasks and twice weekly for the light flasks. In total, an estimated 700 generations of growth and selection occurred in the light environment and 450 in the dark environment, during the twelve months of the experiment. Results for the genotypes obtained from the selection flasks before mating have been described in a previous paper (Bell and Reboud, unpublished) and are not reported here.

Matings

Two spores were isolated at random from each flask, giving two mt^+ and two mt^- genotypes for each selection environment for each pair of sister selection lines. Together with the founding spore of each line, this material was used to set up a 5x5 set of crosses for each pair of sister selection lines. These matings resulted in four "cross types": light/light, dark/light, light/dark, and dark/dark. In each case, the first term designates the selection environment of the mt^+ parent, and the second the selection environment of the mt^- parent. Thus, dark/light indicates a dark-selected mt^+ genotype being mated with a mt^- genotype that had been selected in the light.

The procedure for isolation and mating was as follows. A loopful of medium containing cells from the selection flasks was spread onto Bold's 1.5% agar plates. The plates were placed in the light and left for three to four days to let the individual spores grow into colonies, after which two random colonies were scraped from the plate with an inoculating loop and placed in 40ml of Bold's medium in 80ml culture tubes. The cultures were left in the light for two to three days, until they were visibly green. The medium was then centrifuged at 2000*g* for 15 minutes and the supernatant decanted. 15ml of nitrogen-free medium was then added and the pellet resuspended. The mixture was then centrifuged again, the supernatant decanted, and the pellet resuspended in 15ml of nitrogen-free medium. Mating was done in 24-well microtitre plates. 1ml of a mt^+ isolate was mixed with 1ml of a mt$^-$ isolate, and the plates left under lights until a zygote mat (Harris, 1989) had formed, within one to four days. Mating was often slow and sparse; we attributed this to the loss of mating ability in long-continued vegetative cultures (see da Silva and Bell, 1992, Bell, 1994). The mated culture was then spread on an agar plate and left in under lights for one day and then in the dark for four to five days. Plates were then exposed to chloroform vapour for 45s to kill vegetative cells. The plates were then placed under lights for three to four days, until colonies were just visible to the naked eye. At this point, each colony contained four genotypes originating from the zygospore. Random zygospore colonies were respread thinly onto new agar plates and cultures under lights. When colonies were just large enough to be seen with the naked eye, random colonies were picked and placed in 20ml of Bold's medium in pre-inoculation culture tubes. These cultures were grown in the light until faintly green.

Growth Assays

The assay took place in 80ml culture tubes containing 20ml of medium identical to that used in the selection flasks; either unsupplemented Bold's minimal medium in the light or Bold's minimal medium supplemented with 1.2ml/l anhydrous sodium acetate in the dark. Each assay tube was inoculated with 0.1ml of culture from the corresponding pre-inoculation tube. Two replicates of each spore were grown in each environment. The tubes were arranged as two unreplicated randomized blocks, each with a border row of blank uninoculated tubes of the appropriate medium. The tubes were vortexed and scored every one to two days for three weeks using a digital Spectronic 20D spectrophotometer set at 665nm. Percent transmittance was measured, and the measure of cell density used was 1000-10*transmittance, which is equivalent to turbidity (see Bell,1991, for more details on this and other techniques used here) and gives a more intuitive growth value than transmittance alone. These values obtained for a given spore, V_t, were fitted to the logistic equation (Bell, 1991)

$$V_t=K/[1+(K/V_0-1)\exp(-rt)]$$

by nonlinear least-squares, using the Gauss-Newton option on PROC NLIN of SAS release 6.3 (SAS Institute, 1988), where *r* is the maximum rate of growth as density approaches zero, *K* is the maximum population density, and *t* is time measured in days since inoculation. Ideally, V_0 would be made identical among all tubes by diluting the pre-inoculation tubes to a constant cell density, but this was impracticable because of the large number of tubes involved. Corrections were made for differences in V_0 by regressing *r* against V_0 and adjusting *r* accordingly. The raw score ten days after inoculation, P_{10}, was also used as a measure of growth. Estimates were adjusted slightly (less than 0.5%) by setting both replicate blocks to the same mean.

Genotypes sometimes failed to grow for a week or more in the dark before suddenly beginning what seemed to be normal growth. The reasons for this phenomenon are unknown. This lag resulted in low *r* values or a failure for PROC NLIN to converge at all. In such cases, the logistic equation was fitted by ignoring all points before population density increased by a minimum of1.0% transmission between two successive readings. The lag seems to be a real phenomenon that contributes to fitness in the dark, but is not analyzed further in this paper.

Several different measures of growth are necessary because assays could not be performed in flasks in the same environment as selection. Fitness does not therefore correspond to a particular period of growth in assay conditions. P_{10} is the simplest measure of fitness of the three measured here, but batch selection in flasks usually results in selection for *r* in microorganisms (Dykhuizen, 1990). To ensure that an appropriate measure of fitness was used, *r*, *K*, and P_{10} were all analyzed .

Results

Assessing parental adaptation

The selection lines used as parents in the crosses had become differentially adapted to the light and dark environments (table 1, fig 1). Differences between light- and dark-selected parents were most exaggerated in the dark, suggesting that selection for dark growth had been more effective. Growth was usually higher in the light environment, and *Chlamydomonas reinhardtii* was probably better adapted to the light environment from the outset. *C. reinhardtii* is usually maintained in well-lit conditions. Light-selected lines grew well from the start, whereas many genotypes initially failed to grow at all in the dark, especially the B lines (Bell and Reboud, unpublished).

Heritability of adaptation

The genetic changes resulting in selection can be evaluated by comparing the offspring of the crosses of sister lines selected in the light and in the dark. Since the two original parents of these lines were the same, any difference between the progeny of light/light and dark/dark crosses must be attributed to genetic changes occurring in the course of selection. An analysis of variance was used to compare the two crosses, with spores nested within crosses being the error term. In all selection lines, the crosses had higher P_{10} values in the environment in which their parents had been selected, even if not all the results are formally significant at $p=0.05$ (table 2). Results for r mirrored those for P_{10} in all lines. Results for K also generally paralleled P_{10}, the only exception being for the C lines in the dark. Again, the differences between lines were greater in the dark, and growth overall was generally better in the light, even for offspring whose parents were dark-adapted.

Genetic additivity of adaptation

Chlamydomonas reinhardtii is vegetatively haploid, and thus expresses no dominance effects. A simple additive model for inheritance is therefore appropriate, with expected progeny means equal to the value of the midparent, and only the F_1 need be scored. At the level of sister selection lines, progeny means were satisfactorily explained by the additive model in all lines except B, where progeny grew significantly better than their parents in both environments (table 3). The lines behaved in a similar way in both assay environments, except that the D progeny grew better than the midparent in the dark but worse than the midparent in the light. Results for *r* generally followed the trend of P_{10}, and again *K* seemed to be poorly correlated with P_{10}.

Progeny were also examined for nonadditivity of adaptation in greater detail, at the level of cross types, to identify any effect of the parents' selection environments. Results for the light/light and dark/dark crosses are presented in table 4. Progeny means were generally neither better nor worse than the midparent, but the results were not very consistent between the two assay environments. The light/light cross types deviated significantly from the additive model only when assayed in the dark; there, the A progeny did better and the C progeny worse than their midparents. The dark/dark cross types showed some non-additive effects in both assay environments; in the dark, both A and B progeny did better than the midparent, while in the light only the B progeny did significantly better than the midparent. Again, *r* seemed better correlated to P_{10} than was *K*.

Reciprocal Crosses

The additivity of reciprocal cross types, light/dark and dark/light, is analyzed in table 5. Again, r more closely mirrored P_{10} than did K. The B and C lines show a fairly consistent pattern of deviations, the deviations from the midparent being positive for the light/dark cross types and the deviations being negative for the dark/light cross types. These deviations were often individually significant, in both the light and dark environments. The A lines showed this trend only in the light, and the D lines did not show the trend in either environment. The most dramatic deviation was the light/dark cross type of the B lines in the dark, which not only exceeded the midparental value, but also outgrew the better parent (difference=233, t=3.42, df=8, p<0.01).

Crosses between non-sister selection lines

The crosses between the A and D lines showed only additive effects when tested in the light. In the dark, however, there were strong and consistent non-additive effects, the progeny of AxD crosses exceeding their parents whereas the DxA progeny are inferior to the parental mean for all growth parameters analyzed (table 6).

The pattern found for the crosses as a whole was also found at the level of cross types (table 7). In the light assay environment, the only significant results were for the dark/dark cross type from the AxD cross, which had significantly larger values than the midparent. In the dark, however, all AxD cross types did significantly better than the midparent. All the DxA cross types in the dark scored significantly lower than the midparent. The only exception in the DxA cross was the dark/light cross type, which scored greater than the parent.

The AxD progeny in the dark not only grew better than the midparent, but better than the superior parent too (table 8). Although these results are not always formally significant, they are larger than any other deviation from the midparent. There were no other inter-line crosses or cross types that grew better than the superior parent; the effect was limited to the AxD crosses in the dark environment.

Discussion

Additivity of adaptation

Every flask was inoculated with a single genotype at the outset of selection. All subsequent genetic adaptation must then have arisen through sequential mutation and selection. The mutations could have acted additively or epistatically. If the cultures had been maintained sexually, mutations would have found themselves in a new genetic background every sexual cycle. The epistatic mutations would have lost the interactions that provided the selective advantage, and so the epistatic mutations would not have been selected for. Instead, additive mutations would have been favoured, as they would produce the same effect regardless of the genetic background.

However, the lines were all maintained in asexual culture. All mutations would thus have experienced a unique genetic environment, which would have changed only through other subsequent mutations, for up to several hundred generations. As such, adaptation could have occurred epistatically without being selected against, and adaptation could have been additive or epistatic without penalty during the selection process.

The results obtained were a mix of additive and non-additive adaptation. At the level of non-sister selection lines (table 4), there was no general trend. Only in the B lines was there a significant difference between the offspring and midparent, and significance levels were low. The light/light and dark/dark cross type results were more often and more significantly non-additive than results at the higher levels. The B lines had the most significant differences, although again there was no overall trend of either superiority or inferiority compared to the midparent. Wright's shifting-balance theorem would have predicted that the epistasis and co-adapted gene complexes underlying adaptation would have been broken down by recombination, resulting in offspring with lower fitness than the midparent. Given the asexual maintenance of the cultures, this trend should have been especially pronounced. However, this trend was formally significant only in the light/light cross type in the C lines assayed in the dark, and the highest significance values were for progeny that performed better than expected. This directly contradicted the expectations of the shifting balance hypothesis.

The predictions of the hypothesis are applicable only if the parents involved in the crosses had reached different adaptive peaks. The two initial genotypes used for each pair of sister selection lines were full sibs. Cohan (1984a) found that even identical populations of *Drosophila melanogaster* had a 41% chance of diverging morphologically, so full-sib relatedness does not seem to be an undue hindrance. The mt^+ and mt^- parents used in the crosses had also undergone several hundred generations of mutation and selection in a constant environment. Although this may have driven them to higher fitness on the same adaptive peak, mutations may also have by chance driven the lines to the domain of attraction of different peaks; this effect of historicity is similar to what may happen in sexual lines through drift (Yoo, 1980).

The B selection lines began with the weakest ability to grow in the dark; early on, the cultures in the flasks were often of such low density that transfer to a new flask had to be delayed for two or three weeks until sufficient growth had occurred. By the end of selection, the B lines had improved markedly, and also showed the most evidence for non-additive adaptation (tables 3, 4). What the actual cause of the non-additive results for any lines was is unknown for the light/light and dark/dark cross types.

Organellar inheritance: Reciprocal crosses

Deviations from additivity could be caused either by interactions among nuclear genes or by the transmission of chloroplast or mitochondrial genomes. In the light/dark and dark/light crosses, half the nuclear genome was donated by either parent, with one parent light-adapted and one dark-adapted in both type of crosses. The deviation of the progeny from the midparent would have been expected to be the same in either cross if it were determined only by the nuclear genome. However, the organelle genomes that the offspring received had been selected in different backgrounds. Mating type in *Chlamydomonas* is determined by a mating type locus, so there would be no sex chromosomes to contribute to asymmetry.

In the light/dark crosses, progeny received light-selected chloroplast genomes and dark-selected mitochondrial genomes. The organelles had thus been selected in the environment in which they were expected to have made the greatest contribution to fitness. The mean value of the progeny would then have been expected to be significantly higher than the mean midparental value, because the organelles would have biased the progeny's fitness towards that of the more adapted parent. In the dark/light crosses, on the other hand, the progeny would have received dark-selected chloroplast genomes and light-selected mitochondrial genomes. In this case, the organelles would have been expected to bias the progeny's growth parameter towards that of the less adapted parent in either environment, causing mean progeny growth to fall below the mean midparental value.

The most support for the hypothesis that organelle genomes responded to selection was for the B and C lines, in both environments (table 5). In both cases, the light/dark and dark/light performance relative to the midparent was as expected. The B lines were not only the most likely to have organellar adaptation, but had also progressed the farthest in the dark relative to their parents. If there were more opportunity for improvement in the B lines, at least some of that improvement could have been in the organelle genomes. The ability of the light/dark cross type of the B lines to outgrow even the best parent must have been due to epistatic effects. These non-additive results could have been obtained by many means. Being vegetatively haploid, however, heterosis, dominance effects and the like could not have contributed to the phenomenon. More complex interactions are a possible in length (Michaelis et al., 1990), shorter than the mitochondrial genomes of most higher plants, fungi and animals. The genome codes for three tRNAs, those for tryptophan, glutamine, and methionine. It also codes for eight proteins: five subunits of the NADH-Q1 complex, cytochrome *b*, a subunit of the cytochrome oxidase complex, and a poorly understood gene encoding a reverse transcriptase-like product. Molecular genetic analysis to find which of the genes in the mitochondria produce the adaptation would not be difficult, given the small size of the genome and the small number of factors coded therein.

Although obviously vital in the light to carry out photosynthesis, the chloroplast, as a structural entity, is not essential in the dark. Several yellow (*y*) mutants are known (Sagar, 1955, Harris, 1989), in which the thylakoid membranes breaks down in the dark. The cells continue to grow while supplied with acetate, with the existing chlorophyll being diluted in the progeny and no new chlorophyll being produced. Such mutants acquire a pale yellow colour, giving the class of mutations its name. The effect is reversible; upon exposure to light, the chloroplast structure is reconstituted, chlorophyll is produced, and the mutant cells cannot be distinguished phenotypically in the light from non-mutant genotypes. Chloroplasts are still required in the dark for protein synthesis, and it can be assumed that in this respect the chloroplast genome is required for the survival of the cell; even obligately heterotrophic algae have never been documented to lose their chloroplasts entirely (W. Birky, pers. comm.). Three of the four dark selection lines (A^+, B^-, and D^-) became fixed for spontaneous *y* mutations during the course of this experiment. In one case the mutation seemed to be allelic to *y*-7, whereas the other two were at different loci (James Van Loon, unpublished results).

In contrast, the mitochondria are vital as structural entities both in the light and the dark. In the dark, acetate is metabolized through the glyoxylate shunt in the tricarboxylic acid cycle, which takes place in the mitochondria. Loss of the mitochondria in the dark can therefore be assumed to be lethal. Artificially induced mutations affecting various regions of the mitochondrial genome have been described (Bennoun et al., 1992, Dorthu et al., 1992), and in all cases increased mutation was found to lower fitness under heterotrophic conditions, although growth under photoautotrophic conditions did not seem affected. However, gross damage or complete loss of the mitochondrial DNA in the light is lethal. Minute mutants (Alexander et al., 1974), equivalent to the petite mutants in *Saccharomyces cerevisiae* (Ephrussi and Hottinguer, 1950, 1951), exist. These mutants have lost their mitochondria, and form tiny colonies that grow slowly for eight to nine generations in the light before dying, and only divide once at most in the dark. Mutations in the organellar genomes have generally only been recognized when dramatic or debilitating; examples include the *poky* mutants in *Neurospora* (Mitchell and Mitchell, 1952), the *petite* mutations in *Saccharomyces*, and the *yellow* and *minute* mutants in *Chlamydomonas*. These mutations are all well documented as being detrimental with the exception of the *yellow* mutants, whose effects on fitness have yet to be examined. Organellar mutations that result in an increase in fitness have not previously been described, with the exception of mutations that confer resistance to antibiotics (Grun, 1976).

The heritability of traits with genetic maternal effect is generally low (e.g. Platenkamp and Shaw, 1993). This could be explained by an erosion of variability by natural selection (Fisher, 1930). Variability of the organelles in crosses between non-sister selection lines could not be determined, but the variability within each flask could have been low, especially if periodic selection was in effect (Crow and Kimura, 1970). However, judging by the results for the non-sister selection lines crosses, it seems as if natural selection has produced heritable organellar adaptation.

Crosses between non-sister selection lines

The results found for the crosses of non-sister selection lines seem to be the result of differences present in the base populations rather than to changes occurring during selection. Selection may have brought about divergence between the cross types within the non-sister selection line (i.e. AxD and DxA) crosses, but the differences seem to be primarily between the AxD and DxA crosses as a whole, and are evident only in the dark environment. In the dark, the AxD crosses do much better than the midparent, while the DxA crosses do worse than expected. This result would be expected if the mitochondria of the D lines were superior to those of the A lines before selection, and if that ranking had not changed noticeably during selection. Parents from the D line had higher P_{10} values in the dark than those of the A-line parents, which may in part have been due to superior mitochondria. Epistatic effects also seem to play a part in the dark, as all of the AxD crosses do better than even the best parent (table 8). What these interactions are is uncertain, but they are robust , as they are shown by all cross types. It could be that the interactions occur between the mitochondria and chloroplast; interactions of various types between the two are common (Govindarajan and Gnanam, 1982, Lemaire et al., 1988, Rebeille and Gans, 1988), and this could explain the consistent effect of the interaction in all cross types.

Better mitochondria would bias growth in the AxD crosses towards that of the better parent, while the inferior A-line mitochondria would do the reverse in the DxA crosses. This effect is so strong as to mask possible effects from selection as seen in the non-sister selection lines crosses, assuming that those effects do exist; the deviations from the midparental value are the largest found in any of the matings. As the mitochondria have the greatest effect in the dark, the difference is manifested there. Since deviations from the midparent are virtually nil in the light, it would seem that the chloroplasts from the two lines were approximately equal in quality, with no significant subsequent change from selection. This result also leads to the possibility that the mitochondria have relatively little effect in the light, as the differences found in the dark are not shown when the lines are assayed in the light. If this is true, then the test for organellar adaptation performed in the non-sister selection lines crosses tests for a specific organelle: mitochondrial adaptation in the dark and chloroplast adaptation in the light, since the two would seem to have very little effect in the contrasting environment. On the other hand, there could be little variation left for mitochondrial effects in the light if selection in the light is the standard situation for *Chlamydomonas reinhardtii* in nature. Pre-inoculation culture enrichment in this study was also performed in the light for two reasons, the first being to accelerate the process as much as possible, so that a minimum of generations of universal selection in a given environment happened between the controlled selection and the assays. The other reason was that the dark was assumed to be a novel environment at the beginning of selection, and it was decided to avoid growing light-selected spores in dark conditions to avoid selection in a novel environment. Thus, the dark environment was truly a novel environment for light-selected genomes, with hidden variation revealing itself, while the light was expected to be more similar to past conditions.

These results also indicate the selection has most likely been most effective in the past in light-like environments, probably due to selection occurring as a rule in that type of environment. Divergence among the dark-selected parents was greater than among the light-selected parents. In addition, light-selected parents improved to a lesser degree than those selected in the dark, indicating greater latitude for adaptation in that environment. Although there was only one cross performed between non-sister selection lines, large amounts of variation were present only in the dark, indicating that variation in the dark was neutral in the light, where selection usually takes place. Selection in the light may have long ago eroded variability in that environment, while in the dark much variability remains, so much so that it is still present after hundreds of generations of selection.

There have been many reports of populations adapting differently to the same selection pressure, and there have been many ways of analyzing whether these differences have occurred (see Cohan, 1984b for review). Mechanistic explanations are difficult to elucidate, and so divergence is usually explained through statistical means. In this study, different sister selection lines seem to have responded in different ways. Some sister selection lines and cross types responded in an additive fashion, while others were found to

Table 1. Adaptation of parents: mean values. The first value in the r, K and P_{10} columns is for the light-selected parents; the second is for the dark-selected parents. The number of observations are given in parentheses, in the same order as above.

Assay Environment	Selection Line	r	K	P_{10}
Dark	A	171/465 (15/16)	519/478 (15/16)	10/242 (16/16)
	B	229/450 (10/14)	214/441 (16/12)	28/93 (16/16)
	C	552/697 (6/7)	511/545 (8/8)	412/424 (8/8)
	D	375/608 (6/8)	486/643 (6/8)	192/466 (8/8)
Light	A	619/481 (16/16)	878/853 (16/16)	659/474 (16/16)
	B	598/549 (16/16)	843/748 (16/16)	643/497 (16/16)
	C	560/446 (8/8)	840/797 (8/8)	610/473 (8/8)
	D	640/534 (8/7)	832/738 (8/8)	714/555 (8/8)

Table 2. Genetic basis of adaptation. the first value is that of the light/light crosses, the second is for dark/dark crosses. Significance values are from an ANOVA testing for a difference between the crosses, using spores within cross types as the error term. Degrees of freedom for the denominator are given in parentheses; in each case, the numerator had one degree of freedom.

Assay Environment	Selection Line	r	K	P_{10}
Dark	A	249/579**** (13)	470/505 (13)	65/305**** (13)
	B	191/516**** (11)	362/425 (12)	51/230**** (12)
	C	405/490 (13)	688/482* (14)	291/323 (14)
	D	469/593 (13)	442/661 (14)	266/479* (14)
Light	A	677/422*** (13)	868/803 (13)	694/399*** (13)
	B	663/654 (12)	810/806 (12)	629/604 (12)
	C	537/369* (14)	790/659 (13)	604/333*** (14)
	D	620/534 (14)	826/750* (14)	683/562** (14)

*=$P<0.05$
**=$P<0.01$
***=$P<0.001$
****=$P<0.0001$

Table 3. Additivity of adaptation by selection line. Values are midparent subtracted from progeny, with probability values obtained by Student's t-test with the null hypothesis that all mean differences are zero. Degrees of freedom are 32 unless otherwise noted in parentheses.

Assay Environment	Selection Line	r	K	P_{10}
Dark	A	25 (30)	-20 (30)	7 (31)
	B	139** (24)	-2 (22)	84* (30)
	C	-85* (22)	35	-59
	D	47 (30)	65	54
Light	A	19 (31)	-20 (31)	8 (31)
	B	76** (30)	31* (30)	52* (30)
	C	-37	-48	-53
	D	-14	7	-17

*=$P<0.05$

**=$P<0.01$

Table 4. Check for additivity of response by cross type. Values given are of midparent subtracted from parent. Significance determined by Student's t-test with the null hypothesis that the mean difference is zero. Degrees of freedom are 8 unless otherwise noted in parentheses.

Assay Environment	Selection Line	Cross Type	r	K	P_{10}
Dark	A	light/light	78** (5)	-44 (7)	44** (7)
	B	light/light	16 (5)	121 (6)	22 (6)
	C	light/light	-124** (4)	178	-121* (7)
	D	light/light	161 (7)	68	74
	A	dark/dark	113*	27	68*
	B	dark/dark	106*	-125**** (4)	112****
	C	dark/dark	-180	-63	-121
	D	dark/dark	-14	18	13
Light	A	light/light	60 (7)	-10 (7)	73 (7)
	B	light/light	63 (6)	-26 (6)	-27 (6)
	C	light/light	-23	-49***	-6
	D	light/light	-20	-6	-31
	A	dark/dark	-59	-50	-127
	B	dark/dark	108***	58*	107***
	C	dark/dark	-78	-135	-157
	D	dark/dark	0	11	7

*=$P<0.05$

**=$P<0.01$

***=$P<0.001$

****=$P<0.0001$

Table 5. Comparison of reciprocal crosses. Values are for midparent subtracted from progeny. Significance values are from Student's t-test, with the null hypothesis expectation that mean differences are zero. Degrees of freedom are 8 unless otherwise noted in parentheses.

Assay Environment	Selection Line	Cross Type	r	K	P_{10}
Dark	A	dark/light	134 (7)	-104 (7)	29
		light/dark	-204**	28	-107*
	B	dark/light	165 (3)	-92	-65
		light/dark	239**	119 (4)	253**
	C	dark/light	2 (2)	-10	-43**
		light/dark	23	35	49
	D	dark/light	-26	17	41
		light/dark	86 (7)	158	88
Light	A	dark/light	28	-15	-35
		light/dark	54	2	128*
	B	dark/light	-19	-5	-36
		light/dark	148*	83**	145**
	C	dark/light	-126**	56**	-169*
		light/dark	81	-75**	118
	D	dark/light	19	20	8
		light/dark	-55	-21	-52

*=$P<0.05$

**=$P<0.01$

Table 6. Additivity of adaptation for inter-line crosses. Values are for midparent subtracted from progeny. Probability values were obtained by Student's t-test with a null hypothesis prediction of all mean differences being zero. Degrees of freedom are 32 unless otherwise noted in parentheses.

Assay Environment	Cross	r	K	P_{10}
D	AxD	161****	369**** (31)	250****
	DxA	-101* (20)	-127* (24)	-54*
L	AxD	-5	-4	14
	DxA	17	7	6

*=*P*<0.05

****=*P*<0.0001

Table 7. Additivity of response by cross type for inter-line crosses. Values given are for midparent subtracted from progeny. Significance determined by t-test with the null hypothesis that mean differences are zero. Degrees of freedom are 8 unless otherwise noted in parentheses.

Assay Environment	Cross	Cross type	r	K	P_{10}
Dark	AxD	light/light	171*	436**** (7)	228****
		dark/light	81	530****	167****
		light/dark	196**	201****	347****
		dark/dark	196****	319****	259**
	DxA	light/light	-	-381**** (4)	-100****
		dark/light	38*	-38 (4)	116***
		light/dark	-430 (3)	-3	-120*
		dark/dark	-87*	-168**	-113**
Light	AxD	light/light	-46	-55	-63
		dark/light	23*	-25	32
		light/dark	-13	39***	33
		dark/dark	16	25	54*
	DxA	light/light	26	33****	5
		dark/light	13	21**	11
		light/dark	41*	-20	22
		dark/dark	-11	-7	-12

*=$P<0.05$

**=$P<0.01$

***=$P<0.001$

****=$P<0.0001$

Table 8. Comparison to better parent for AxD matings in dark assay environment. Values are for better parent subtracted from progeny. Significance determined by Student's t-test, with the null hypothesis that mean differences are zero. Degrees of freedom are 8 unless otherwise noted in parentheses.

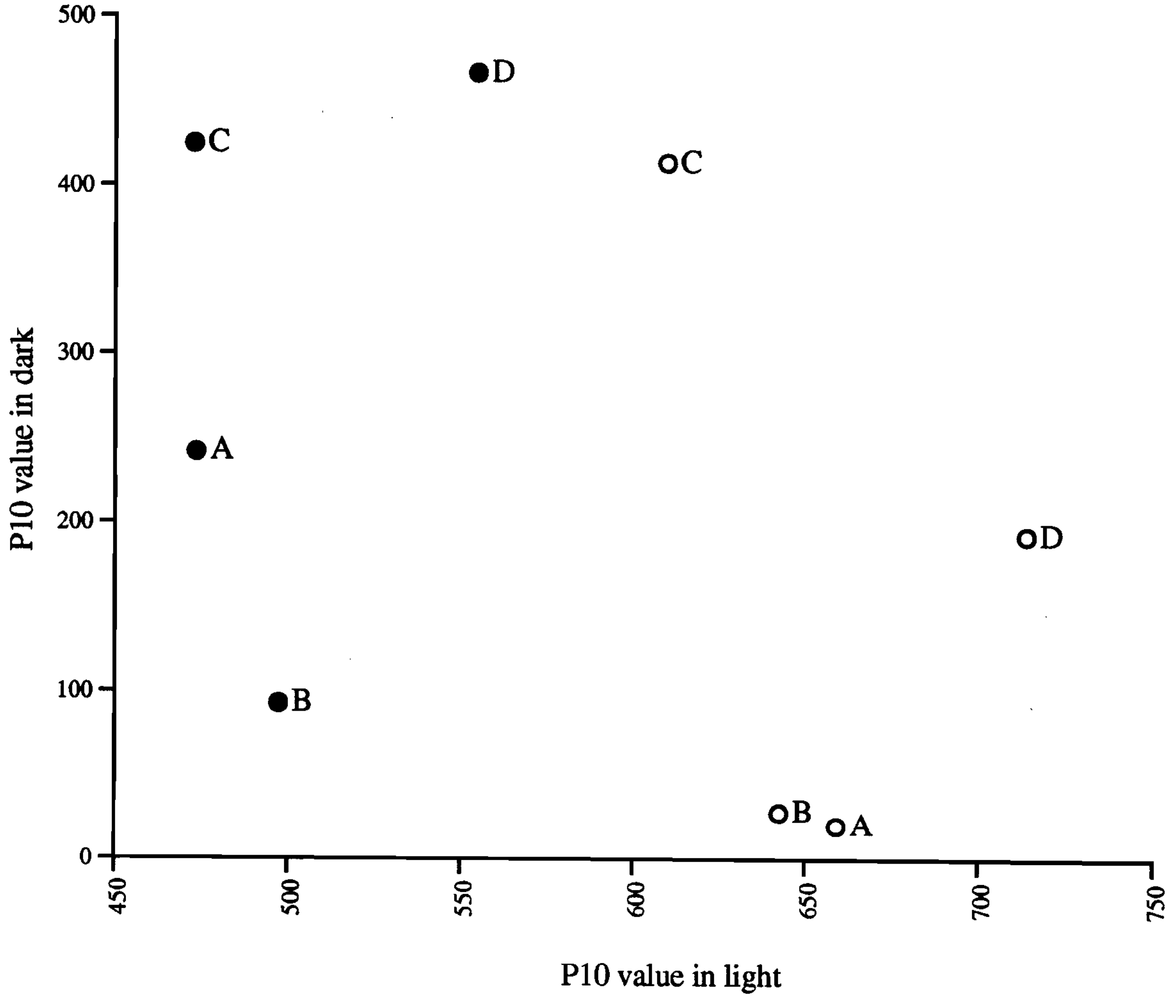
Cross type	r	K	P_{10}
light/light	141*	320* (7)	216***
dark/light	-1	383****	133***
light/dark	59	181****	213**
dark/dark	81*	268****	146

*=$P<0.05$
**=$P<0.01$
***=$P<0.001$
****=$P<0.0001$

Figures

Fig. 1. P_{10} values for parents in both assay environments. Open circles represent means for light-selected parents, closed circles represent means for dark-selected parents. Letters designate selection lines.

Fig. 2. P_{10} values for progeny in both assay environments. Open circles represent means for progeny whose parents were both light-selected, closed circles represent means for progeny whose parents were both dark-selected. Letters designate selection lines.



500
400
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200
100
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700
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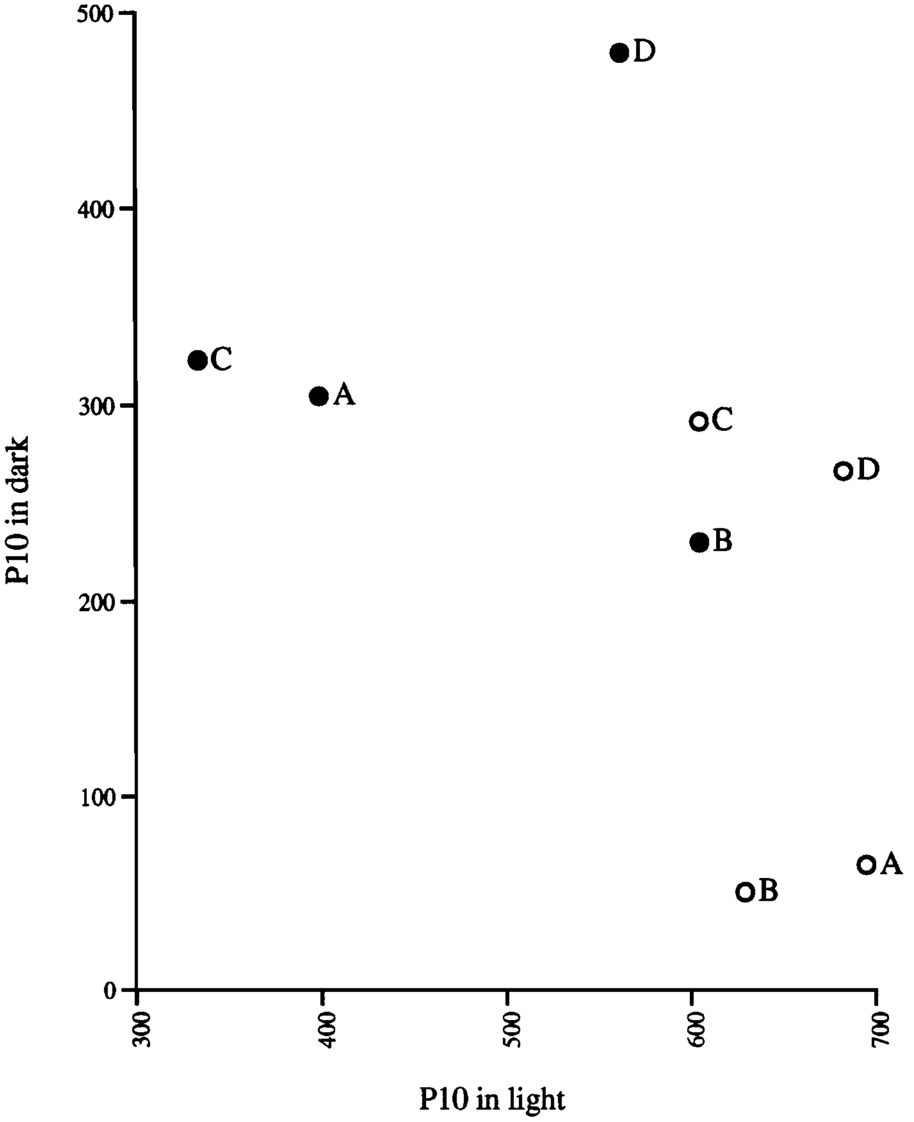
P10 value in dark
P10 value in light

Figure 1


500
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100
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P10 in dark
300
400
500
600
700
P10 in light
D
C
A
C
D
B
A
B

Figure 2

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Appendix

The following is the raw data obtained during the course of the experiment. The column titles are explained below:

Mating: Which selection lines were mated. The first letter is that of the mt^+ selection line, the second is for that of the mt^- selection line.

Cross: Corresponds to the table below of the mating scheme. Numbers indicate offspring of a particular $\text{mt}^+ \times \text{mt}^-$ parental cross. Alphanumeric labels indicate parents included in the assay, as follows: "U" "L" "D" and "D" labels indicate un-, light-, or dark-selected parents, respectively. Numbers for parents indicate replicate spores from identical selection lines. The "+" and "-" indicate parental mating type.

				mt^+		
		L1+	L2+	D1+	D2+	U+
	L1-	1	2	3	4	5
	L2-	6	7	8	9	10
mt^-	D1-	11	12	13	14	15
	D2-	16	17	18	19	20
	U-	21	22	23	24	25

Spore: Replicate offspring from a cross or replicate assay culture of parent.

Ass. Env.: Assay environment of culture. "L" and "D" indicate light and dark environments, respectively.

Rep.: Replicate culture.

Day *x*: Reading of culture *x* days after inoculation.

i, r, K: Values calculated from logistic equation.

P10: P10 value.

Mating	Cross	Spore	Ass.Env.	Rep.	Day																	i	r	K	P10
					1	2	3	4	5	6	8	10	12	13	14	16	18	20	22	25	29				
AxA	1	1	L	1	988	928	836	688	572	484	338	298	206	190	158	150	148	134	98	114	68	58.8	0.676	861	630
AxA	1	2	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	58.5	0.653	835	568
AxA	2	1	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
AxA	2	2	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	64.1	0.816	845	786
AxA	3	1	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	63.6	0.77	829	736
AxA	3	2	L	1	986	962	938	902	862	820	718	560	380	306	258	198	192	154	136	146	86	21.9	0.428	874	368
AxA	4	1	L	1	996	942	826	674	550	496	378	298	240	218	212	170	146	118	112	98	66	72.3	0.674	860	630
AxA	4	2	L	1	978	918	810	654	532	466	320	256	196	176	154	122	80	72	68	74	56	74.6	0.7	899	672
AxA	5	1	L	1	986	956	886	774	694	642	518	434	360	332	310	272	224	202	180	162	130	72.6	0.557	817	494
AxA	5	2	L	1	992	956	894	802	714	658	534	448	348	350	290	242	202	140	110	116	72	75	0.535	885	480
AxA	6	1	L	1	994	968	908	788	660	566	384	308	206	196	176	160	136	122	116	116	78	39.1	0.604	866	620
AxA	6	2	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	41.6	0.803	864	806
AxA	7	1	L	1	970	918	810	660	556	480	338	240	180	172	178	148	126	102	88	92	66	67.6	0.693	880	688
AxA	7	2	L	1	984	936	846	710	600	518	376	264	204	186	152	180	148	108	98	80	48	60.5	0.646	880	664
AxA	8	1	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	66.9	0.738	815	668
AxA	8	2	L	1	998	962	900	802	702	638	510	386	306	270	226	210	172	126	110	100	86	59.7	0.539	876	542
AxA	9	1	L	1	998	962	888	766	652	606	418	332	254	244	212	170	134	122	98	112	82	56.6	0.583	871	596
AxA	9	2	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	46.4	0.691	869	702
AxA	10	1	L	1	972	966	904	802	668	580	432	342	290	234	186	158	102	94	92	92	70	60.4	0.57	895	586
AxA	10	2	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	61.1	0.634	819	552
AxA	11	1	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	51	0.748	846	732
AxA	11	2	L	1	994	962	892	768	670	590	442	390	336	296	250	198	176	146	160	150	118	65.3	0.579	835	538
AxA	12	1	L	1	986	968	896	754	640	572	416	288	222	180	192	156	160	136	104	88	58	48.8	0.601	874	640
AxA	12	2	L	1	994	972	908	770	648	594	428	324	234	216	200	162	146	138	108	106	70	49.7	0.583	869	604
AxA	13	1	L	1	984	960	930	860	720	606	442	296	220	186	186	.	138	110	124	88	62	32.9	0.565	882	632
AxA	13	2	L	1	999	988	966	930	902	886	786	680	566	506	460	.	278	228	172	160	96	25.5	0.351	874	248
AxA	14	1	L	1	999	988	968	944	920	910	870	802	662	580	488	354	250	192	160	134	90	11.3	0.337	899	126
AxA	14	2	L	1	998	970	944	878	762	678	506	418	350	348	316	276	240	194	172	156	110	45.2	0.505	811	510
AxA	15	1	L	1	998	970	944	900	844	808	626	490	360	330	304	250	202	174	160	150	130	28.2	0.447	839	438
AxA	15	2	L	1	999	966	938	900	872	852	770	634	504	460	392	286	256	270	266	228	148	25.1	0.39	794	294
AxA	16	1	L	1	988	966	940	912	878	860	696	540	414	370	318	268	220	178	158	126	92	26.6	0.413	861	388
AxA	16	2	L	1	999	992	960	826	692	574	374	290	208	168	154	144	108	110	94	90	58	27.1	0.606	883	638
AxA	17	1	L	1	992	954	878	752	646	582	422	314	232	224	180	174	150	134	120	114	94	53.6	0.599	862	614
AxA	17	2	L	1	980	910	806	664	564	504	356	268	210	210	194	182	142	124	94	112	74	73.4	0.687	863	660
AxA	18	1	L	1	998	958	936	896	868	840	776	682	598	562	564	487	432	362	342	326	246	46	0.372	724	246
AxA	18	2	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	50.7	0.742	864	740

					Day																				
Mating	Cross	Spore	Ass.Env.	Rep.	1	2	3	4	5	6	8	10	12	13	14	16	18	20	22	25	29	i	r	K	P10
AxA	19	1	L	1	996	970	934	856	730	620	430	300	234	222	198	202	170	142	118	100	62	29	0.574	856	628
AxA	19	2	L	1	998	972	942	898	846	810	604	450	294	224	224	184	150	116	90	82	48	23.3	0.464	903	478
AxA	20	1	L	1	990	956	918	880	818	774	642	524	430	388	356	298	242	210	188	160	110	48.1	0.444	840	404
AxA	20	2	L	1	990	960	926	854	742	680	574	562	530	528	512	516	482	450	400	326	226	80.8	0.52	637	366
AxA	21	1	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	41.1	0.742	864	758
AxA	21	2	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	23.5	0.755	863	782
AxA	22	1	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
AxA	22	2	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	50.6	0.761	833	738
AxA	23	1	L	1	999	978	952	918	886	864	730	556	438	370	336	276	228	172	156	138	98	23.2	0.405	858	372
AxA	23	2	L	1	988	954	926	890	852	828	718	572	476	428	372	322	246	214	190	186	136	37.5	0.407	834	356
AxA	24	1	L	1	984	924	802	690	602	516	320	290	256	276	252	260	212	190	194	170	120	48.6	0.7	789	638
AxA	24	2	L	1	984	924	802	690	602	516	320	290	218	234	232	196	168	120	118	112	88	62.3	0.675	844	640
AxA	25	1	L	1	986	978	944	866	760	684	512	412	296	276	232	180	138	100	84	88	70	44.9	0.497	900	516
AxA	25	2	L	1	988	958	934	890	828	772	608	496	378	314	280	214	182	158	150	130	90	36.3	0.45	869	432
AxA	L1+	1	L	1	974	934	826	672	576	486	330	290	182	192	166	164	122	98	104	108	72	63.5	0.679	872	710
AxA	L1+	2	L	1	992	970	896	746	628	544	374	304	208	190	160	144	114	94	98	92	54	50.2	0.612	887	696
AxA	L2+	1	L	1	990	946	862	704	568	484	302	230	152	148	152	132	94	60	74	68	40	46.4	0.673	901	770
AxA	L2+	2	L	1	988	954	890	782	690	616	488	382	268	250	232	216	174	146	150	146	92	57.1	0.561	848	618
AxA	D1+	1	L	1	994	972	950	886	794	714	504	356	266	244	200	164	132	102	86	88	54	30.7	0.504	896	644
AxA	D1+	2	L	1	999	978	958	902	834	752	578	444	286	272	224	154	126	98	106	86	64	28	0.467	905	556
AxA	D2+	1	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	59.3	0.739	812	632
AxA	D2+	2	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	31.5	0.655	871	620
AxA	U+	1	L	1	974	936	848	718	620	558	428	390	302	250	194	166	136	108	104	110	74	89.1	0.63	888	610
AxA	U+	2	L	1	982	950	920	860	800	.	630	558	436	408	350	280	248	180	152	142	102	54.7	0.447	872	442
AxA	L1-	1	L	1	976	932	808	654	538	476	354	282	206	188	180	.	108	102	104	86	58	77.3	0.694	883	718
AxA	L1-	2	L	1	988	928	800	666	554	488	370	288	230	212	186	152	126	102	86	84	62	82.6	0.687	880	712
AxA	L2-	1	L	1	990	934	822	664	546	476	338	270	190	176	160	124	104	90	104	96	66	65.1	0.686	883	730
AxA	L2-	2	L	1	986	938	858	738	620	540	368	280	208	190	158	130	104	82	70	64	42	62.6	0.623	907	720
AxA	D1-	1	L	1	984	946	900	772	650	598	444	346	254	252	236	210	186	168	148	126	96	54.6	0.587	837	654
AxA	D1-	2	L	1	978	948	912	800	674	634	456	350	272	256	244	222	198	184	152	126	80	50.5	0.566	835	650
AxA	D2-	1	L	1	996	974	950	922	888	870	716	572	436	390	344	284	224	180	158	138	96	24.6	0.401	860	428
AxA	D2-	2	L	1	994	970	944	904	862	822	600	428	298	258	234	188	136	114	94	88	50	22.8	0.463	900	572
AxA	U-	1	L	1	972	914	802	664	580	518	396	316	222	200	166	132	92	76	74	66	56	96.4	0.681	914	684
AxA	U-	2	L	1	974	926	816	666	566	514	374	298	194	204	152	138	118	86	82	82	64	81.9	0.674	896	702
BxB	1	1	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	47.6	0.854	839	816
BxB	1	2	L	1	999	976	902	728	592	494	352	274	234	224	218	202	162	138	178	166	110	29.3	0.703	816	674

													Day												
Mating	Cross	Spore	Ass.Env.	Rep.	1	2	3	4	5	6	8	10	12	13	14	16	18	20	22	25	29	i	r	K	P10
BxB	2	1	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
BxB	2	2	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
BxB	3	1	L	1	994	952	860	644	572	494	348	280	158	152	120	90	72	48	50	46	28	70.4	0.659	931	668
BxB	3	2	L	1	990	948	874	694	594	548	418	308	234	190	156	122	82	96	84	70	46	73.7	0.626	912	640
BxB	4	1	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	55.3	0.818	916	846
BxB	4	2	L	1	986	928	816	672	600	572	414	306	232	220	168	132	110	90	80	76	40	87.7	0.649	912	642
BxB	5	1	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	58.2	0.922	816	804
BxB	5	2	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	27.5	0.72	878	758
BxB	6	1	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	71.1	0.721	692	560
BxB	6	2	L	1	994	972	906	752	638	558	388	316	222	186	174	134	102	84	94	102	84	50.4	0.601	887	632
BxB	7	1	L	1	980	932	806	670	588	538	390	322	246	204	188	154	118	108	128	136	110	79.6	0.665	865	626
BxB	7	2	L	1	988	944	868	706	606	536	442	312	194	194	174	128	128	110	118	102	72	66.3	0.624	885	636
BxB	8	1	L	1	978	938	884	766	660	606	460	408	294	280	260	224	202	178	166	152	100	68.8	0.585	831	540
BxB	8	2	L	1	992	956	916	830	734	688	600	494	356	344	282	304	260	252	240	234	194	47.7	0.507	766	454
BxB	9	1	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	64.2	0.709	727	576
BxB	9	2	L	1	986	948	896	796	700	646	514	426	310	302	246	256	214	198	182	184	154	55.8	0.549	808	522
BxB	10	1	L	1	998	962	886	752	606	562	386	306	232	240	190	206	224	196	178	168	106	37.9	0.648	810	642
BxB	10	2	L	1	982	938	842	696	582	518	390	322	284	262	258	248	248	228	220	192	130	49.2	0.687	771	626
BxB	11	1	L	1	990	954	884	814	740	664	554	440	368	332	262	232	188	170	144	132	88	65.4	0.521	865	508
BxB	11	2	L	1	990	958	900	768	680	602	458	322	256	228	210	226	192	178	178	184	148	41.1	0.594	813	626
BxB	12	1	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	95.7	0.906	894	824
BxB	12	2	L	1	994	970	914	790	688	622	494	348	272	238	212	168	126	100	78	70	40	59.3	0.546	910	600
BxB	13	1	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	88.9	0.718	854	594
BxB	13	2	L	1	990	954	870	702	560	482	344	272	218	174	150	122	84	64	52	52	38	64.6	0.654	910	676
BxB	14	1	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	83.8	0.699	842	540
BxB	14	2	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	39.9	0.778	692	678
BxB	15	1	L	1	988	952	866	740	636	560	416	348	242	230	192	168	140	136	128	150	84	61.5	0.61	858	600
BxB	15	2	L	1	986	952	852	668	528	458	310	234	202	246	208	204	178	142	152	130	90	35.4	0.748	824	714
BxB	16	1	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	53	0.827	818	802
BxB	16	2	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	26.8	0.575	763	512
BxB	17	1	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	80.9	0.876	831	792
BxB	17	2	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	62.2	0.724	804	676
BxB	18	1	L	1	986	938	844	668	560	496	334	330	264	270	296	272	254	272	282	270	242	30.1	0.787	727	618
BxB	18	2	L	1	992	950	880	734	608	558	412	356	296	272	292	256	254	222	270	270	194	37.5	0.673	741	592
BxB	19	1	L	1	992	954	890	786	702	648	584	480	346	360	266	266	248	202	208	234	220	60.4	0.536	781	468
BxB	19	2	L	1	992	934	834	666	554	506	370	330	242	248	238	230	232	210	200	232	164	47.3	0.715	774	618

					Day																				
Mating	Cross	Spore	Ass.Env.	Rep.	1	2	3	4	5	6	8	10	12	13	14	16	18	20	22	25	29	i	r	K	P10
BxB	20	1	L	1	992	940	820	630	508	438	314	272	224	212	232	222	206	198	198	164	96	37.7	0.784	798	676
BxB	20	2	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	30.1	0.806	754	752
BxB	21	1	L	1	994	950	824	650	514	436	306	234	180	184	184	190	130	140	120	130	100	40.8	0.749	844	714
BxB	21	2	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	62.7	0.661	835	604
BxB	22	1	L	1	974	892	780	676	592	548	388	328	292	266	244	210	188	154	142	136	90	96.9	0.693	838	620
BxB	22	2	L	1	988	922	776	632	480	396	276	212	178	190	146	134	142	138	118	132	96	46.5	0.78	854	736
BxB	23	1	L	1	994	966	928	816	718	676	550	470	354	300	228	196	154	116	92	86	50	61.9	0.505	916	478
BxB	23	2	L	1	986	940	874	724	660	600	478	360	254	242	176	142	104	92	82	70	48	75.9	0.588	920	588
BxB	24	1	L	1	996	954	890	746	694	656	536	410	286	282	214	164	122	110	90	84	46	70.1	0.545	918	538
BxB	24	2	L	1	982	938	870	686	636	604	466	366	236	218	172	.	120	102	84	72	38	80	0.605	919	582
BxB	25	1	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	58.7	0.708	748	614
BxB	25	2	L	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	69.2	0.861	808	776
BxB	L1+	1	L	1	996	970	868	706	578	506	362	298	288	260	258	266	236	262	270	282	214	24.1	0.774	737	702
BxB	L1+	2	L	1	984	928	824	722	618	554	460	370	312	294	292	300	304	292	318	314	296	46.5	0.684	697	630
BxB	L2+	1	L	1	992	952	822	664	518	444	310	246	192	204	208	186	166	168	138	158	120	37.5	0.757	824	754
BxB	L2+	2	L	1	990	950	824	636	490	408	260	208	188	184	194	174	182	156	136	148	110	30	0.815	832	792
BxB	D1+	1	L	1	984	948	876	736	632	572	430	392	288	294	276	260	228	202	236	248	212	49.3	0.633	756	608
BxB	D1+	2	L	1	976	920	810	682	578	538	434	376	356	322	330	314	224	312	318	330	320	50.3	0.726	684	624
BxB	D3+	1	L	1	966	898	780	640	514	456	340	314	220	222	226	226	202	186	194	222	198	58.4	0.76	784	686
BxB	D3+	2	L	1	978	916	808	666	538	460	290	256	222	212	212	198	194	156	196	178	198	41.5	0.756	802	744
BxB	U+	1	L	1	999	966	874	660	520	456	294	248	208	216	212	170	162	138	122	112	86	31.2	0.758	835	752
BxB	U+	2	L	1	999	972	884	734	608	564	386	336	288	280	290	292	276	252	246	246	192	28.1	0.705	735	664
BxB	L1-	1	L	1	999	968	916	756	698	624	466	358	252	238	194	166	128	104	88	70	48	58.2	0.554	904	642
BxB	L1-	2	L	1	982	940	874	744	702	642	496	386	284	274	250	212	178	154	138	132	78	68.9	0.567	861	614
BxB	L3-	1	L	1	984	958	902	802	710	650	530	438	312	258	234	212	180	150	146	124	84	59.4	0.532	866	562
BxB	L3-	2	L	1	988	954	896	778	654	590	490	398	250	236	214	166	138	134	130	122	82	63	0.57	875	602
BxB	D1-	1	L	1	999	960	948	904	852	804	774	686	594	578	556	554	532	488	442	360	228	64.5	0.399	705	314
BxB	D1-	2	L	1	996	990	960	844	804	736	622	552	514	548	536	546	510	426	348	314	204	80.2	0.478	699	448
BxB	D2-	1	L	1	990	974	954	904	856	820	730	676	576	520	476	434	428	370	316	286	192	45.6	0.387	742	324
BxB	D2-	2	L	1	996	980	948	850	784	758	674	546	438	410	374	344	312	310	262	204	156	47.1	0.449	769	454
BxB	U-	1	L	1	990	950	888	746	692	662	560	460	374	330	270	214	174	132	142	124	86	79.3	0.548	886	540
BxB	U-	2	L	1	992	952	896	732	620	568	436	348	240	180	146	128	92	76	62	60	138	64.7	0.596	907	652

					Day																		
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	8	10	12	15	18	20	22	24	29	I	r	K	P10
AxA	1	1	L	2	986	940	850	762	672	590	456	342	274	190	142	102	94	84	56	70.7	0.59	901	730
AxA	1	2	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	114	0.768	842	578
AxA	2	1	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
AxA	2	2	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	66.6	0.861	883	830
AxA	3	1	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	58.4	0.762	863	770
AxA	3	2	L	2	976	962	944	926	906	902	876	834	750	558	378	314	276	256	214	17.2	0.302	809	238
AxA	4	1	L	2	984	916	786	662	566	496	362	294	240	178	130	116	88	94	56	86.2	0.696	884	778
AxA	4	2	L	2	984	940	874	784	714	664	496	378	296	206	138	102	94	68	52	65.2	0.548	913	694
AxA	5	1	L	2	982	940	878	800	746	686	574	484	406	302	198	168	148	132	74	76.6	0.525	884	588
AxA	5	2	L	2	980	962	942	896	846	800	672	596	508	400	276	244	206	174	86	51.8	0.414	864	476
AxA	6	1	L	2	990	970	916	866	788	716	532	412	308	238	194	160	136	128	82	37.5	0.5	859	660
AxA	6	2	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	68.6	0.748	878	720
AxA	7	1	L	2	984	940	852	770	686	608	450	354	270	188	152	114	104	100	72	65.5	0.582	888	718
AxA	7	2	L	2	976	930	848	746	658	586	440	348	272	202	152	132	112	108	76	72.7	0.606	878	724
AxA	8	1	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	87.1	0.778	852	708
AxA	8	2	L	2	992	944	838	732	670	624	496	426	350	288	220	194	158	138	104	86.2	0.599	840	646
AxA	9	1	L	2	992	970	916	864	828	808	720	674	598	500	384	342	304	264	194	61.2	0.407	798	398
AxA	9	2	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	90.7	0.716	843	614
AxA	10	1	L	2	968	952	910	864	826	796	720	648	588	486	418	358	340	302	242	64.1	0.427	738	424
AxA	10	2	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	75.4	0.746	825	674
AxA	11	1	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	49.3	0.747	837	736
AxA	11	2	L	2	992	952	874	798	704	648	500	418	374	334	294	254	222	184	136	61	0.561	773	654
AxA	12	1	L	2	996	974	878	786	694	626	456	358	270	174	152	140	106	98	60	54.1	0.561	885	714
AxA	12	2	L	2	992	976	932	884	818	754	586	464	378	274	176	150	142	130	100	38.1	0.462	866	608
AxA	13	1	L	2	986	968	954	932	912	894	828	750	620	344	324	258	262	252	196	13.7	0.366	778	322
AxA	13	2	L	2	990	970	952	936	910	902	856	806	742	642	510	434	384	324	224	33	0.288	824	266
AxA	14	1	L	2	999	992	972	952	938	926	880	842	768	642	510	434	384	324	224	21.3	0.271	799	230
AxA	14	2	L	2	986	966	946	914	882	860	768	668	528	372	260	242	242	218	180	24.8	0.379	802	404
AxA	15	1	L	2	994	972	950	926	900	892	852	794	728	592	478	390	338	298	182	34	0.299	850	278
AxA	15	2	L	2	992	958	934	916	900	870	820	754	640	476	344	276	234	196	156	30.2	0.332	856	318
AxA	16	1	L	2	990	972	954	934	914	892	840	784	672	508	362	284	224	194	120	25.5	0.312	888	288
AxA	16	2	L	2	986	968	886	768	656	578	386	290	230	162	126	106	92	88	52	49.1	0.6	893	782

					Day																		
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	8	10	12	15	18	20	22	24	29	i	r	K	P10
AxA	17	1	L	2	996	968	918	822	766	692	538	428	340	236	170	136	130	110	66	51	0.503	883	644
AxA	17	2	L	2	972	928	834	750	678	612	460	368	292	200	154	108	116	88	68	78.9	0.598	895	704
AxA	18	1	L	2	984	958	938	924	898	890	848	838	808	782	754	704	696	660	608	50.2	0.298	422	234
AxA	18	2	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	56.6	0.648	870	642
AxA	19	1	L	2	982	960	936	900	886	870	806	714	648	508	430	366	322	284	196	43.6	0.348	796	358
AxA	19	2	L	2	994	976	956	926	902	882	820	758	676	532	392	322	318	314	254	25.4	0.327	746	314
AxA	20	1	L	2	990	960	934	910	874	856	778	692	592	450	338	266	226	182	114	41.4	0.359	879	380
AxA	20	2	L	2	984	954	924	846	802	756	586	464	460	466	438	418	386	352	284	27.7	0.539	613	608
AxA	21	1	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	62.6	0.769	858	746
AxA	21	2	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	47.6	0.729	848	724
AxA	22	1	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
AxA	22	2	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	74.3	0.715	806	616
AxA	23	1	L	2	988	962	938	914	888	868	782	702	596	402	260	200	166	142	96	30.3	0.351	905	370
AxA	23	2	L	2	994	974	944	932	912	888	842	778	684	486	336	278	218	184	110	24.6	0.314	892	294
AxA	24	1	L	2	976	948	894	768	696	614	450	328	220	202	170	160	158	158	122	45.4	0.586	842	744
AxA	24	2	L	2	980	954	880	788	708	662	522	448	326	268	234	226	220	238	176	55.5	0.552	781	624
AxA	25	1	L	2	988	966	924	882	828	790	674	602	538	420	368	316	296	256	192	53.1	0.427	756	470
AxA	25	2	L	2	978	958	932	906	890	870	812	764	638	460	308	256	228	176	112	32.2	0.334	892	751
AxA	L1+	1	L	2	988	952	850	756	646	568	406	284	230	166	136	104	94	90	52	58.1	0.609	894	716
AxA	L1+	2	L	2	998	966	904	824	722	644	476	358	284	206	166	140	114	104	72	46.5	0.542	874	642
AxA	L2+	1	L	2	976	944	846	760	684	614	484	402	350	250	196	160	140	124	82	81.3	0.589	862	598
AxA	L2+	2	L	2	980	948	854	782	706	644	494	394	322	236	166	120	110	116	88	70.2	0.561	882	606
AxA	D1+	1	L	2	994	982	966	956	936	918	874	842	742	552	390	318	270	230	164	14.8	0.298	838	158
AxA	D1+	2	L	2	999	988	982	960	940	922	850	830	756	594	408	326	270	234	136	17.5	0.286	874	170
AxA	D3+	1	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	64	0.68	854	590
AxA	D3+	2	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	66.6	0.67	853	630
AxA	U+	1	L	2	972	942	864	790	750	732	660	598	550	474	434	388	368	336	260	90.7	0.527	687	412
AxA	U+	2	L	2	982	940	860	770	710	676	640	578	490	434	388	334	304	284	206	97.9	0.561	738	422
AxA	L1-	1	L	2	980	934	834	728	644	576	440	348	278	200	140	118	92	86	48	82.4	0.62	899	652
AxA	L1-	2	L	2	980	916	778	686	602	542	422	340	272	182	130	102	92	82	46	101	0.677	906	660
AxA	L3-	1	L	2	988	940	842	772	718	684	572	534	434	350	290	254	214	180	118	93.3	0.561	827	466
AxA	L3-	2	L	2	978	934	828	750	686	642	524	468	380	326	238	202	166	146	74	100	0.602	859	532

					Day																		
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	8	10	12	15	18	20	22	24	29	i	r	K	P10
AxA	D1-	1	L	2	992	976	954	916	890	878	722	582	458	370	290	266	254	232	182	20.8	0.415	766	418
AxA	D1-	2	L	2	984	966	946	890	860	854	726	610	486	384	286	246	232	214	174	32.8	0.398	798	390
AxA	D2-	1	L	2	990	968	940	924	904	888	832	786	686	500	358	254	226	174	122	26.3	0.313	899	214
AxA	D2-	2	L	2	990	966	948	924	902	878	828	750	610	460	320	250	204	180	146	25.7	0.334	862	250
AxA	U-	1	L	2	978	942	866	800	706	656	508	414	338	230	174	168	164	166	162	61	0.552	834	586
AxA	U-	2	L	2	986	958	898	798	736	670	538	476	426	392	364	302	290	240	188	60.1	0.541	717	524
BxB	1	1	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	68.5	0.863	872	820
BxB	1	2	L	2	986	966	888	810	702	640	476	374	270	170	130	124	130	120	88	50.6	0.549	880	678
BxB	2	1	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
BxB	2	2	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
BxB	3	1	L	2	990	958	864	774	720	678	600	540	478	384	318	252	214	208	124	94.4	0.549	827	512
BxB	3	2	L	2	996	972	946	886	844	810	648	508	360	216	126	84	68	74	54	29.7	0.433	935	544
BxB	4	1	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	68.2	0.659	868	628
BxB	4	2	L	2	978	936	896	826	730	708	558	454	356	246	176	144	128	130	102	60.5	0.511	876	598
BxB	5	1	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	67.9	0.82	826	776
BxB	5	2	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	50.8	0.836	803	770
BxB	6	1	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	83.6	0.75	794	624
BxB	6	2	L	2	988	958	918	856	820	788	712	682	638	570	504	464	430	400	292	75.2	0.434	678	370
BxB	7	1	L	2	980	948	898	820	786	748	680	654	596	558	484	440	398	348	268	92.7	0.491	714	398
BxB	7	2	L	2	972	922	774	632	532	454	340	340	292	256	204	176	166	158	120	68.4	0.748	797	712
BxB	8	1	L	2	968	932	874	806	750	702	592	520	416	384	320	308	298	278	256	64.1	0.529	712	532
BxB	8	2	L	2	980	938	862	804	716	680	592	482	380	342	352	340	360	360	310	50.6	0.561	660	570
BxB	9	1	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	61.7	0.715	754	616
BxB	9	2	L	2	996	966	918	836	790	750	642	528	430	366	302	276	248	252	200	47.9	0.469	755	524
BxB	10	1	L	2	998	962	878	796	684	608	414	314	224	154	130	114	130	128	96	43.1	0.585	874	738
BxB	10	2	L	2	992	972	940	872	804	740	560	424	314	206	138	136	138	144	118	30.6	0.489	866	628
BxB	11	1	L	2	986	956	910	842	758	708	606	474	374	296	200	154	144	150	140	54.2	0.488	853	578
BxB	11	2	L	2	990	956	896	816	728	664	506	380	286	184	138	122	126	116	116	48.1	0.533	876	672
BxB	12	1	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	120	0.876	886	736
BxB	12	2	L	2	998	976	920	866	786	716	544	420	330	230	146	114	88	76	34	44.6	0.484	914	632
BxB	13	1	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	61.5	0.631	855	584
BxB	13	2	L	2	986	948	862	756	666	634	530	474	422	346	282	242	224	176	114	93.5	0.591	806	578

					Day																		
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	8	10	12	15	18	20	22	24	29	i	r	K	P10
BxB	14	1	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	69.9	0.707	808	658
BxB	14	2	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	55.4	0.756	795	714
BxB	15	1	L	2	986	966	910	828	774	716	608	580	520	434	360	308	262	194	112	87.6	0.502	842	472
BxB	15	2	L	2	982	940	844	776	698	634	498	392	304	218	160	146	132	126	100	69	0.569	869	660
BxB	16	1	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	70.7	0.796	846	744
BxB	16	2	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	42.2	0.601	790	548
BxB	17	1	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	78.2	0.953	828	800
BxB	17	2	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	58.5	0.738	856	728
BxB	18	1	L	2	994	962	914	844	780	716	602	528	412	314	246	242	206	198	174	48.6	0.484	800	524
BxB	18	2	L	2	988	944	862	764	704	654	566	522	462	324	256	220	218	216	196	81.7	0.558	796	530
BxB	19	1	L	2	980	928	834	710	636	568	440	394	300	212	154	120	120	120	98	86.7	0.635	877	658
BxB	19	2	L	2	982	930	832	720	634	570	470	414	282	216	172	156	148	146	140	81.4	0.628	847	638
BxB	20	1	L	2	982	942	832	754	644	572	432	324	240	190	172	160	160	158	136	58.5	0.624	840	728
BxB	20	2	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	48.5	0.728	748	660
BxB	21	1	L	2	982	924	808	684	566	496	346	252	212	162	140	130	126	114	86	65.2	0.693	868	800
BxB	21	2	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	54.3	0.757	832	748
BxB	22	1	L	2	982	916	782	694	582	522	376	258	200	138	106	66	80	62	40	82.2	0.677	922	794
BxB	22	2	L	2	980	940	862	790	700	632	474	364	304	224	198	460	148	144	118	49.5	0.587	789	688
BxB	23	1	L	2	992	966	928	890	822	806	638	530	402	264	178	134	112	110	88	33.8	0.441	896	522
BxB	23	2	L	2	978	946	886	840	768	744	594	458	332	212	118	96	84	90	74	47.3	0.486	924	594
BxB	24	1	L	2	986	966	938	880	842	810	690	570	474	348	246	192	160	138	96	40.7	0.419	875	482
BxB	24	2	L	2	988	950	914	876	816	784	624	536	408	328	282	258	234	226	190	36.4	0.465	773	516
BxB	25	1	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	66.5	0.795	789	.
BxB	25	2	L	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	61.2	0.762	812	724
BxB	L1+	3	L	2	980	964	910	802	722	640	460	322	224	160	134	130	132	136	130	37.1	0.57	868	678
BxB	L1+	4	L	2	984	954	896	824	748	676	514	396	292	196	140	128	116	126	104	45.7	0.528	881	604
BxB	L2+	3	L	2	990	960	912	852	798	744	614	494	402	258	160	130	102	92	58	48	0.465	918	506
BxB	L2+	4	L	2	992	958	886	804	718	644	462	318	210	150	154	184	160	155	120	35.5	0.58	851	682
BxB	D1+	3	L	2	986	968	918	842	766	686	554	506	380	290	224	162	178	180	158	50.2	0.5	827	494
BxB	D1+	4	L	2	980	930	818	714	648	588	496	470	376	262	224	216	208	198	194	90.6	0.633	795	530
BxB	D3+	3	L	2	972	922	848	762	678	638	524	514	404	326	234	178	172	154	120	97	0.595	855	486
BxB	D3+	4	L	2	966	882	758	646	590	514	382	322	238	182	146	126	124	130	98	100	0.722	869	678

					Day																		
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	8	10	12	15	18	20	22	24	29	i	r	K	P10
BxB	U+	3	L	2	974	952	888	822	756	692	530	430	340	214	144	110	110	100	68	55	0.515	905	570
BxB	U+	4	L	2	992	974	918	870	782	712	542	416	320	204	142	126	106	112	82	36.6	0.498	891	584
BxB	L1-	3	L	2	994	962	906	838	768	730	546	428	328	240	160	128	108	112	104	43.5	0.499	883	572
BxB	L1-	4	L	2	990	958	892	790	718	666	490	348	262	222	184	156	142	140	120	44.5	0.557	850	652
BxB	L3-	3	L	2	982	938	826	746	636	576	424	326	248	228	170	164	136	138	104	65.2	0.627	849	674
BxB	L3-	4	L	2	974	940	852	768	680	626	488	386	318	254	238	202	196	178	150	63.5	0.59	806	614
BxB	D1-	3	L	2	980	974	948	920	884	856	710	614	526	436	384	396	408	432	392	15.7	0.466	602	386
BxB	D1-	4	L	2	988	980	964	942	914	886	774	670	544	406	328	344	366	364	310	10.5	0.441	666	330
BxB	D2-	3	L	2	982	974	946	914	880	842	658	576	462	360	308	278	288	282	248	20.4	0.451	725	424
BxB	D2-	4	L	2	982	972	948	902	880	836	690	574	434	394	322	320	304	308	250	19.4	0.457	703	426
BxB	U-	3	L	2	982	962	922	866	818	782	628	480	360	238	154	116	90	96	76	35.6	0.458	910	520
BxB	U-	4	L	2	982	962	942	892	838	796	626	478	338	196	110	76	68	58	48	27.3	0.455	941	522

									Day											
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	9	10	13	15	20	i	r	K	P10
AxA	1	2	L	1	948	904	860	826	774	692	632	520	478	314	250	180	58.5	0.653	835	568
AxA	2	2	L	1	946	888	778	666	600	500	430	320	260	204	166	122	64.1	0.816	845	786
AxA	3	1	L	1	944	910	802	712	648	558	488	380	310	238	208	132	63.6	0.77	829	736
AxA	6	2	L	1	964	932	830	702	612	494	418	286	240	170	128	112	41.6	0.803	864	806
AxA	8	1	L	1	950	914	820	740	686	600	528	420	378	294	238	140	66.9	0.738	815	668
AxA	9	2	L	1	952	922	854	796	744	650	562	406	344	230	172	120	46.4	0.691	869	702
AxA	10	2	L	1	956	928	882	816	756	740	672	560	494	396	308	188	61.1	0.634	819	552
AxA	11	1	L	1	978	940	840	724	650	572	498	364	314	230	174	112	51	0.748	846	732
AxA	18	2	L	1	938	920	854	740	672	570	510	338	306	198	154	120	50.7	0.742	864	740
AxA	21	1	L	1	964	934	860	764	682	572	492	328	288	214	154	94	41.1	0.742	864	758
AxA	21	2	L	1	980	968	910	816	724	590	502	328	264	192	144	102	23.5	0.755	863	782
AxA	22	2	L	1	954	924	830	730	658	552	486	344	308	230	188	126	50.6	0.761	833	738
AxA	D2+	1	L	1	948	913	838	758	682	576	516	400	368	282	238	130	59.3	0.739	812	632
AxA	D2+	2	L	1	970	960	920	870	800	680	608	446	380	260	196	84	31.5	0.655	871	620
BxB	1	1	L	1	940	890	786	662	570	450	368	258	230	196	168	122	47.6	0.854	839	816
BxB	4	1	L	1	942	904	806	670	568	456	386	256	200	124	102	38	55.3	0.818	916	846
BxB	5	1	L	1	932	880	708	580	512	406	332	260	242	204	190	134	58.2	0.922	816	804
BxB	5	2	L	1	958	930	860	836	798	660	466	354	288	220	92	118	27.5	0.72	878	758
BxB	6	1	L	1	962	924	840	758	694	638	590	522	486	440	366	246	71.1	0.721	692	560
BxB	9	1	L	1	975	944	868	748	674	640	592	512	470	384	338	216	64.2	0.709	727	576
BxB	12	1	L	1	910	842	692	602	510	426	376	266	222	150	132	56	95.7	0.906	894	824
BxB	13	1	L	1	.	.	.	.	.	698	620	496	452	342	252	178	88.9	0.718	854	594
BxB	14	1	L	1	956	920	842	774	720	660	594	516	506	382	292	156	83.8	0.699	842	540
BxB	14	2	L	1	942	902	830	754	700	608	520	396	368	312	330	320	39.9	0.778	692	678
BxB	16	1	L	1	928	880	794	686	604	492	410	306	244	208	200	162	53	0.827	818	802
BxB	16	2	L	1	978	954	930	898	872	826	762	616	534	440	322	238	26.8	0.575	763	512
BxB	17	1	L	1	906	860	730	616	558	470	400	302	254	210	180	140	80.9	0.876	831	792
BxB	17	2	L	1	944	926	836	760	696	618	544	420	370	334	272	120	62.2	0.724	804	676

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	9	10	13	15	20	i	r	K	P10
BxB	20	2	L	1	978	960	844	744	650	558	492	354	294	272	270	210	30.1	0.806	754	752
BxB	21	2	L	1	944	922	860	812	766	694	626	506	442	364	276	148	62.7	0.661	835	604
BxB	25	1	L	1	946	926	850	774	718	640	578	470	432	352	310	208	58.7	0.708	748	614
BxB	25	2	L	1	934	864	762	638	544	474	418	322	270	232	208	142	69.2	0.861	808	776
CxC	1	1	L	1	966	954	918	770	702	560	450	396	334	254	196	140	29.1	0.612	795	640
CxC	1	2	L	1	984	962	880	812	752	674	602	464	392	370	284	202	34	0.537	741	582
CxC	2	1	L	1	960	950	916	840	788	690	598	462	418	354	260	178	32.6	0.517	770	556
CxC	2	2	L	1	984	962	908	850	792	730	642	506	406	342	254	136	33.9	0.485	817	568
CxC	3	1	L	1	990	990	964	940	918	892	862	790	756	544	464	186	20.1	0.318	954	218
CxC	3	2	L	1	976	968	942	914	894	872	840	754	676	494	380	176	24.9	0.346	915	298
CxC	4	1	L	1	972	968	936	896	848	770	682	516	418	280	248	144	19.2	0.487	822	556
CxC	4	2	L	1	988	978	948	922	896	864	784	602	490	366	256	144	14.7	0.442	832	484
CxC	5	1	L	1	956	928	896	830	796	714	650	476	396	322	250	146	38.1	0.495	819	578
CxC	5	2	L	1	956	862	776	696	658	594	536	472	414	334	274	170	96.5	0.641	792	560
CxC	6	1	L	1	974	954	918	846	790	674	582	410	350	264	232	148	22.3	0.552	803	624
CxC	6	2	L	1	950	930	874	776	714	628	552	412	400	320	238	174	47.3	0.559	780	574
CxC	7	1	L	1	962	944	888	772	692	670	566	366	314	222	180	124	36.9	0.554	850	660
CxC	7	2	L	1	966	942	794	682	608	516	446	352	308	242	190	150	50	0.652	799	666
CxC	8	1	L	1	958	944	904	796	766	636	578	448	372	294	224	134	40.5	0.53	819	602
CxC	8	2	L	1	976	966	940	904	840	736	640	488	388	248	186	84	21.6	0.49	878	586
CxC	9	1	L	1	990	976	944	918	896	870	826	700	620	456	342	184	21.5	0.374	850	354
CxC	9	2	L	1	980	976	946	918	880	810	724	578	484	352	284	166	18.8	0.452	802	490
CxC	10	1	L	1	968	950	900	836	780	728	678	582	476	384	314	190	47.8	0.468	796	498
CxC	10	2	L	1	994	980	940	916	872	784	700	486	380	314	242	194	9.25	0.56	773	594
CxC	11	1	L	1	966	952	884	832	768	670	572	480	410	334	260	180	38.3	0.523	775	564
CxC	11	2	L	1	964	952	868	780	678	580	536	442	380	310	258	172	44.8	0.578	764	594
CxC	12	1	L	1	960	942	866	778	690	596	514	418	332	290	192	136	44.9	0.572	814	642
CxC	12	2	L	1	984	980	942	920	900	872	836	730	654	470	368	368	12.8	0.413	668	320

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	9	10	13	15	20	i	r	K	P10
CxC	13	1	L	1	980	970	940	922	910	872	832	740	666	498	418	294	20	0.369	736	308
CxC	13	2	L	1	962	948	922	890	856	776	708	580	416	274	186	114	23.9	0.454	888	558
CxC	14	1	L	1	990	978	960	930	890	820	732	582	492	330	282	208	12.8	0.48	772	482
CxC	14	2	L	1	926	832	764	720	676	576	468	388	372	332	370	300	62.6	0.673	678	602
CxC	15	1	L	1	984	964	948	902	858	780	686	570	500	426	330	198	27.3	0.448	756	474
CxC	15	2	L	1	986	974	944	924	906	886	866	800	758	574	426	296	18.4	0.334	788	216
CxC	16	1	L	1	962	940	832	726	650	550	490	390	320	254	208	140	49.8	0.609	806	654
CxC	16	2	L	1	958	938	870	798	722	620	532	406	334	270	194	120	41.5	0.556	832	640
CxC	17	1	L	1	962	936	840	720	680	560	508	416	332	250	198	136	54.8	0.592	822	642
CxC	17	2	L	1	972	946	882	806	748	654	606	520	444	360	340	230	44.5	0.528	719	530
CxC	18	1	L	1	982	984	962	942	926	902	878	798	740	542	424	190	16.1	0.329	910	234
CxC	18	2	L	1	999	998	994	994	990	978	962	928	916	876	854	814	2.84	0.355	185	58
CxC	19	1	L	1	996	998	996	999	996	998	996	994	992	976	952	884	7.94	0.06	.	.
CxC	19	2	L	1	996	992	982	976	960	948	930	890	870	800	738	582	11.9	0.26	536	104
CxC	20	1	L	1	978	970	950	930	906	888	868	798	756	524	416	204	18.5	0.33	901	218
CxC	20	2	L	1	984	968	946	924	902	880	850	784	730	548	410	222	22.3	0.332	887	244
CxC	21	1	L	1	978	958	944	928	880	854	824	728	636	416	316	130	22.9	0.367	929	338
CxC	21	2	L	1	960	928	854	794	706	618	540	444	360	304	224	138	51	0.556	812	614
CxC	22	1	L	1	962	934	836	770	686	618	532	470	366	360	278	200	50.3	0.58	740	608
CxC	22	2	L	1	970	944	884	788	700	624	528	432	360	272	202	108	46.7	0.55	838	614
CxC	23	1	L	1	958	948	922	888	852	758	684	560	490	390	336	216	30.4	0.46	749	484
CxC	23	2	L	1	962	946	912	866	810	726	642	492	406	300	224	136	31.1	0.486	835	568
CxC	24	1	L	1	965	948	914	856	776	674	586	430	360	250	216	134	27.4	0.531	826	614
CxC	24	2	L	1	976	970	942	926	892	840	764	606	464	314	230	122	15.1	0.449	860	510
CxC	25	1	L	1	990	974	954	928	904	880	846	718	662	494	330	194	18.8	0.363	858	312
CxC	25	2	L	1	968	954	926	912	882	826	764	610	510	404	320	158	27	0.414	829	464
CxC	L1+	1	L	1	946	920	886	850	824	764	680	498	430	324	278	170	35	0.477	807	544
CxC	L2+	2	L	1	928	890	746	624	530	450	378	276	232	164	114	58	72.7	0.705	885	742

					Day																
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	9	10	13	15	20	i	r	K	P10
CxC	D1+	1	L	1	956	936	890	838	792	702	626	506	460	370	304	220	40.9	0.501	747	514
CxC	D2+	2	L	1	960	952	910	860	814	748	666	538	454	338	262	152	36.6	0.464	828	520
CxC	U+	1	L	1	934	926	900	868	830	778	708	492	400	282	166	78	31.7	0.461	917	574
CxC	L1-	1	L	1	942	922	814	726	684	598	532	422	388	344	284	170	63.8	0.599	759	586
CxC	L2-	2	L	1	936	930	876	806	752	640	580	400	348	304	240	160	37.5	0.55	794	626
CxC	D1-	1	L	1	924	932	886	864	816	786	720	562	508	426	326	184	50.5	0.448	825	466
CxC	D2-	2	L	1	976	958	934	910	874	818	738	606	512	420	316	152	30	0.414	836	462
CxC	U-	1	L	1	952	946	918	884	844	782	738	628	544	434	322	134	46.5	0.413	913	430
DxD	1	1	L	1	952	924	854	756	690	588	508	386	322	252	182	112	50.1	0.579	842	669
DxD	1	2	L	1	968	954	904	808	740	648	556	452	344	286	190	128	37.6	0.534	831	647
DxD	2	1	L	1	938	890	768	670	600	514	448	392	340	270	224	160	73.1	0.672	783	651
DxD	2	2	L	1	960	940	886	794	722	642	554	420	366	274	198	114	44.8	0.54	841	625
DxD	3	1	L	1	970	942	870	754	696	576	468	372	340	326	298	298	20.1	0.694	693	651
DxD	3	2	L	1	944	922	882	836	794	758	692	574	506	406	320	170	58.6	0.465	846	485
DxD	4	1	L	1	964	896	736	658	604	522	458	408	358	264	206	144	83.4	0.672	803	633
DxD	4	2	L	1	938	902	774	636	558	442	376	300	240	170	130	68	62.2	0.691	869	751
DxD	5	1	L	1	950	926	856	738	636	556	440	364	272	182	150	98	47.2	0.608	864	719
DxD	5	2	L	1	946	942	762	612	518	0	350	254	218	180	144	140	39.6	0.747	829	773
DxD	6	1	L	1	956	924	848	754	716	616	570	442	344	294	222	118	57.8	0.557	836	647
DxD	6	2	L	1	936	888	734	592	484	410	346	266	236	216	154	126	53.2	0.763	818	755
DxD	7	1	L	1	952	926	846	760	726	630	548	450	388	326	264	178	53.9	0.562	775	603
DxD	7	2	L	1	954	930	854	790	754	622	530	360	312	196	162	92	38.9	0.555	877	679
DxD	8	1	L	1	946	922	842	710	652	544	462	342	262	176	146	94	50.6	0.61	873	729
DxD	8	2	L	1	950	930	864	770	714	632	566	428	374	282	234	136	52.3	0.551	820	617
DxD	9	1	L	1	952	910	782	654	562	468	382	274	232	176	146	110	49.5	0.688	849	759
DxD	9	2	L	1	946	912	818	710	650	572	504	394	322	262	214	168	58.8	0.614	800	669
DxD	10	1	L	1	918	790	712	642	596	520	422	302	248	200	166	118	98.9	0.724	862	743
DxD	10	2	L	1	952	916	810	702	650	570	492	398	332	252	190	102	69.2	0.61	847	659

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	9	10	13	15	20	i	r	K	P10
DxD	11	1	L	1	944	834	750	668	600	520	464	380	300	260	178	92	97	0.688	856	691
DxD	11	2	L	1	956	932	842	778	732	658	608	544	448	400	340	234	63.3	0.541	726	543
DxD	12	1	L	1	966	940	868	788	768	678	596	550	520	444	382	296	52.6	0.529	656	471
DxD	12	2	L	1	944	922	878	840	810	746	640	496	362	282	202	114	36.9	0.487	870	629
DxD	13	1	L	1	966	948	908	852	770	708	622	510	428	344	330	200	34.1	0.507	745	563
DxD	13	2	L	1	958	936	870	792	700	604	532	418	334	280	220	108	45.9	0.561	826	657
DxD	14	1	L	1	948	850	736	662	566	480	430	364	324	250	246	206	69.2	0.714	757	667
DxD	14	2	L	1	968	946	916	880	832	784	716	574	494	350	274	144	34.5	0.437	852	497
DxD	15	1	L	1	942	936	862	772	716	640	576	478	432	358	306	190	58.4	0.552	755	559
DxD	15	2	L	1	932	826	752	700	602	532	454	346	302	212	188	98	89.5	0.676	860	689
DxD	16	1	L	1	956	928	822	750	688	620	556	452	368	302	230	160	61.9	0.571	807	623
DxD	16	2	L	1	938	898	790	672	618	520	512	394	336	264	204	154	76.4	0.648	808	655
DxD	17	1	L	1	968	962	922	884	840	774	708	614	570	458	420	326	31.7	0.449	651	421
DxD	17	2	L	1	970	958	932	906	870	808	746	676	612	544	450	338	35.2	0.404	661	379
DxD	18	1	L	1	968	974	944	914	870	828	768	664	616	524	456	370	24.8	0.416	617	375
DxD	18	2	L	1	976	966	924	890	860	760	670	562	460	392	332	208	24.9	0.472	741	531
DxD	19	1	L	1	970	946	882	816	778	692	606	506	460	360	328	230	40.9	0.515	727	531
DxD	19	2	L	1	936	854	760	706	624	540	490	444	390	342	258	186	91.7	0.672	759	601
DxD	20	1	L	1	980	970	940	902	874	814	752	648	610	502	482	326	29.2	0.414	643	381
DxD	20	2	L	1	984	974	940	930	894	862	828	766	722	640	588	526	23.1	0.375	479	269
DxD	21	1	L	1	940	902	804	670	600	482	412	354	288	230	196	142	54	0.672	803	703
DxD	21	2	L	1	932	848	670	546	482	416	366	290	250	182	166	136	81.5	0.789	820	741
DxD	22	1	L	1	954	936	858	724	670	546	450	382	316	266	190	140	43	0.617	802	675
DxD	22	2	L	1	954	930	832	738	672	534	472	374	318	236	200	108	50.3	0.607	828	673
DxD	23	1	L	1	964	944	844	736	692	606	560	462	410	370	334	234	48.3	0.591	697	581
DxD	23	2	L	1	954	900	756	648	544	472	392	312	258	176	132	74	67.7	0.685	867	733
DxD	24	1	L	1	964	948	888	836	816	720	640	524	438	360	320	206	36.4	0.493	753	553
DxD	24	2	L	1	970	934	868	776	708	604	520	448	384	310	254	184	44.3	0.572	764	607

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	9	10	13	15	20	i	r	K	P10
DxD	25	1	L	1	948	942	848	766	676	590	506	424	346	282	202	130	53	0.578	819	645
DxD	25	2	L	1	942	922	838	730	652	554	468	374	300	242	180	88	56	0.606	848	691
DxD	L1+	1	L	1	944	922	818	716	640	574	478	376	328	230	178	98	64	0.608	854	663
DxD	L2+	2	L	1	938	904	812	744	654	564	486	362	326	236	170	128	60.1	0.607	841	665
DxD	D1+	1	L	1	968	942	854	744	692	550	440	352	282	230	184	114	35.2	0.617	825	709
DxD	D2+	2	L	1	960	918	826	740	672	582	498	376	324	252	220	128	51.8	0.597	817	667
DxD	U+	1	L	1	928	914	806	680	574	496	400	326	280	210	158	114	55.7	0.666	834	711
DxD	L1-	1	L	1	950	934	854	736	666	562	472	350	248	210	168	100	42	0.604	853	743
DxD	L2-	2	L	1	968	928	792	624	528	446	358	240	216	154	132	72	43.3	0.709	866	775
DxD	D1-	1	L	1	978	968	928	876	828	726	646	506	396	290	198	128	25.4	0.486	846	595
DxD	D2-	2	L	1	980	966	928	896	864	792	742	648	578	490	466	350	27.1	0.437	619	413
DxD	U-	1	L	1	960	940	882	764	690	608	524	388	310	212	138	76	46.8	0.558	889	681

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	8	10	11	14	16	20	i	r	K	P10
AxA	1	2	L	2	936	900	780	690	636	598	560	480	450	326	248	162	114	0.768	842	578
AxA	2	2	L	2	952	892	740	610	486	440	354	232	198	166	142	78	66.6	0.861	883	830
AxA	3	1	L	2	960	928	814	702	626	542	466	314	258	204	172	118	58.4	0.762	863	770
AxA	6	2	L	2	974	936	800	708	622	544	474	344	308	208	172	80	68.6	0.748	878	720
AxA	8	1	L	2	950	904	784	682	584	528	498	376	320	258	196	104	87.1	0.778	852	708
AxA	9	2	L	2	932	902	820	748	678	618	574	456	414	310	258	144	90.7	0.716	843	614
AxA	10	2	L	2	940	908	802	716	680	546	500	380	354	278	226	138	75.4	0.746	825	674
AxA	11	1	L	2	968	948	838	724	674	576	478	326	292	234	206	130	49.3	0.747	837	736
AxA	18	2	L	2	9 2 8	918	884	818	768	684	596	446	386	264	216	126	56.6	0.648	870	642
AxA	21	1	L	2	958	924	816	696	608	524	452	326	282	214	176	104	62.6	0.769	858	746
AxA	21	2	L	2	974	956	878	762	658	574	508	352	304	232	196	108	47.6	0.729	848	724
AxA	22	2	L	2	940	914	846	760	660	600	536	434	412	300	238	178	74.3	0.715	806	616
AxA	D2+	4	L	2	958	944	864	766	700	634	574	432	370	276	222	122	64	0.68	854	590
AxA	D2+	2	L	2	968	944	860	770	704	644	584	454	410	286	202	148	66.6	0.67	853	630
BxB	1	1	L	2	934	896	740	596	480	496	322	240	208	164	150	112	68.5	0.863	872	820
BxB	4	1	L	2	958	926	860	778	746	646	604	478	400	276	236	126	68.2	0.659	868	628
BxB	5	1	L	2	926	894	764	662	572	496	426	300	252	210	186	192	67.9	0.82	826	776
BxB	5	2	L	2	944	928	796	670	566	490	418	296	258	204	260	176	50.8	0.836	803	770
BxB	6	1	L	2	940	912	822	718	624	562	528	426	404	308	270	158	83.6	0.75	794	624
BxB	9	1	L	2	956	942	862	752	668	608	544	442	412	340	304	190	61.7	0.715	754	616
BxB	12	1	L	2	906	854	708	602	538	490	422	344	292	208	162	80	120	0.876	886	736
BxB	13	1	L	2	976	946	888	818	742	680	622	522	444	310	238	150	61.5	0.631	855	584
BxB	14	1	L	2	954	918	842	750	670	630	540	450	370	296	254	170	69.9	0.707	808	658
BxB	14	2	L	2	942	912	830	742	650	564	490	364	314	242	242	204	55.4	0.756	795	714
BxB	16	1	L	2	922	902	780	686	590	510	428	308	284	208	192	130	70.7	0.796	846	744
BxB	16	2	L	2	962	944	912	874	822	764	698	522	480	358	300	206	42.2	0.601	790	548
BxB	17	1	L	2	902	850	674	544	438	378	330	254	228	206	172	156	78.2	0.953	828	800

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	8	10	11	14	16	20	i	r	K	P10
BxB	17	2	L	2	950	926	846	736	646	568	474	354	300	210	198	112	58.5	0.738	856	728
BxB	20	2	L	2	980	960	838	750	688	618	562	406	368	298	308	230	48.5	0.728	748	660
BxB	21	2	L	2	946	920	832	740	636	548	484	334	280	220	206	156	54.3	0.757	832	748
BxB	25	1	L	2	936	910	770	678	614	548	460	346	292	244	274	192	66.5	0.795	789	
BxB	25	2	L	2	942	920	812	714	642	548	478	370	304	228	208	198	61.2	0.762	812	724
CxC	1	1	L	2	972	960	914	840	800	640	546	420	384	336	272	156	22.3	0.572	756	642
CxC	1	2	L	2	960	940	904	850	816	754	696	524	474	358	324	166	38.6	0.464	798	552
CxC	2	1	L	2	964	950	926	862	812	696	648	502	422	346	300	186	28.4	0.503	761	604
CxC	2	2	L	2	980	960	920	890	864	836	784	684	602	456	362	218	31.8	0.389	814	424
CxC	3	1	L	2	990	980	950	930	902	886	850	754	676	564	476	268	24.7	0.34	793	350
CxC	3	2	L	2	992	984	962	950	934	910	896	812	738	506	372	190	9.49	0.365	858	288
CxC	4	1	L	2	986	980	964	938	928	908	886	834	806	610	510	244	17	0.303	912	220
CxC	4	2	L	2	974	956	922	882	846	768	676	496	432	300	278	172	20	0.497	789	594
CxC	5	1	L	2	950	952	866	758	710	618	554	416	378	304	236	140	48.3	0.56	802	648
CxC	5	2	L	2	916	846	720	588	520	474	440	354	346	306	292	204	74.7	0.771	719	680
CxC	6	1	L	2	956	950	886	796	732	656	590	480	444	372	288	174	51	0.528	769	582
CxC	6	2	L	2	956	934	876	806	744	630	570	438	372	284	230	150	41.6	0.542	809	654
CxC	7	1	L	2	944	936	844	754	710	622	578	420	388	294	230	156	55.2	0.559	810	638
CxC	7	2	L	2	954	930	826	708	616	532	466	370	324	260	218	172	45.8	0.642	779	702
CxC	8	1	L	2	950	924	822	696	626	566	486	386	340	260	212	156	57.4	0.621	798	686
CxC	8	2	L	2	982	972	942	920	870	780	668	490	414	270	208	128	14.4	0.509	836	612
CxC	9	1	L	2	990	980	962	944	930	912	900	830	770	632	484	262	15.4	0.312	857	256
CxC	9	2	L	2	984	978	954	922	888	836	734	546	470	332	270	174	12.1	0.492	788	556
CxC	10	1	L	2	964	948	888	788	720	658	600	498	420	314	260	162	50.6	0.524	803	606
CxC	10	2	L	2	982	970	948	922	908	874	836	706	638	428	340	212	16.4	0.389	809	388
CxC	11	1	L	2	960	952	860	808	724	636	520	382	366	270	230	132	35.6	0.565	806	660
CxC	11	2	L	2	950	928	862	786	750	666	604	516	464	390	332	200	61.4	0.53	754	562

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	8	10	11	14	16	20	i	r	K	P10
CxC	12	1	L	2	960	944	884	808	766	654	560	470	390	316	236	134	43.9	0.526	815	636
CxC	12	2	L	2	974	970	938	922	896	880	862	800	760	628	496	430	22.3	0.338	630	266
CxC	13	1	L	2	974	960	924	888	842	766	694	564	464	390	314	162	30.9	0.452	795	562
CxC	13	2	L	2	978	966	936	904	878	846	792	620	522	314	256	198	14.2	0.451	811	504
CxC	14	1	L	2	980	974	952	928	910	804	730	530	486	312	260	158	13.2	0.485	806	540
CxC	14	2	L	2	908	842	756	692	650	574	556	506	482	406	408	284	106	0.697	654	544
CxC	15	1	L	2	994	980	950	932	906	864	812	672	574	422	360	178	18.6	0.397	812	452
CxC	15	2	L	2	978	966	944	924	920	904	892	850	816	654	542	472	15.8	0.324	590	210
CxC	16	1	L	2	964	944	842	750	660	572	490	326	344	258	204	108	41.8	0.603	817	682
CxC	16	2	L	2	938	932	784	706	644	554	506	400	358	288	240	170	63.4	0.626	779	668
CxC	17	1	L	2	970	948	894	834	796	702	630	486	416	316	228	146	37.1	0.495	826	610
CxC	17	2	L	2	968	948	858	736	696	618	510	366	346	290	232	172	36.9	0.596	778	680
CxC	18	1	L	2	988	988	968	948	928	916	898	826	786	594	492	234	14.5	0.315	882	240
CxC	18	2	L	2	992	992	990	988	988	978	968	944	936	898	876	790	5.87	0.236	269	90
CxC	19	1	L	2	986	986	986	988	990	990	988	978	974	936	886	772	18.1	0.103		52
CxC	19	2	L	2	990	988	980	978	970	952	942	904	904	846	806	728	10.1	0.263	312	122
CxC	20	1	L	2	984	974	950	932	912	884	872	826	800	674	572	340	27.4	0.291	889	226
CxC	20	2	L	2	982	966	944	922	910	890	854	712	630	474	348	166	20	0.365	875	396
CxC	21	1	L	2	972	960	932	908	886	874	844	782	734	498	418	208	25.4	0.338	895	292
CxC	21	2	L	2	954	944	868	786	730	640	564	452	402	286	214	118	53.1	0.535	845	624
CxC	22	1	L	2	964	936	818	742	676	580	472	360	306	248	192	94	47.6	0.598	838	720
CxC	22	2	L	2	964	954	838	726	648	564	462	376	322	254	200	110	45.5	0.609	817	704
CxC	23	1	L	2	970	950	936	912	898	864	808	666	572	428	314	230	18.9	0.409	782	454
CxC	23	2	L	2	972	958	910	854	810	722	622	450	378	264	256	170	21.3	0.531	794	648
CxC	24	1	L	2	962	956	906	856	790	712	618	480	424	300	260	152	32.4	0.5	806	602
CxC	24	2	L	2	992	980	960	940	920	904	882	780	718	506	380	192	13.4	0.354	863	308
CxC	25	1	L	2	992	980	964	940	930	912	896	822	766	504	378	224	8.13	0.374	820	260

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	8	10	11	14	16	20	i	r	K	P10
CxC	25	2	L	2	982	960	942	926	918	880	856	794	740	594	486	350	22.1	0.334	717	286
CxC	L1+	1	L	2	950	942	900	886	862	844	842	788	748	576	468	264	44.1	0.342	965	278
CxC	L2+	2	L	2	934	898	816	718	626	556	498	380	310	220	160	104	68.1	0.615	865	716
CxC	D1+	2	L	2	974	966	910	852	772	680	586	426	366	278	250	196	20.8	0.563	771	634
CxC	D2+	1	L	2	950	934	870	802	762	702	614	452	392	294	280	240	34.5	0.536	753	660
CxC	U+	2	L	2	954	936	916	882	856	834	820	736	682	486	380	194	39	0.364	926	344
CxC	L1-	1	L	2	928	918	830	714	640	584	510	394	358	246	200	142	64.9	0.605	826	668
CxC	L2-	2	L	2	930	922	818	718	642	548	474	350	308	242	190	136	53.2	0.622	821	718
CxC	D1-	2	L	2	974	962	942	940	924	888	870	806	746	550	458	290	17.5	0.337	776	246
CxC	D2-	1	L	2	930	924	910	890	896	840	828	778	780	662	584	418	56	0.348	841	280
CxC	U-	2	L	2	952	948	924	898	850	798	760	602	532	428	334	172	36.4	0.416	830	494
DxD	1	1	L	2	950	930	810	684	584	506	432	358	304	218	184	130	52.1	0.654	815	705
DxD	1	2	L	2	958	930	838	734	650	556	484	352	330	264	186	126	47.3	0.609	816	679
DxD	2	1	L	2	966	924	794	670	550	458	386	316	254	166	116	58	53.3	0.669	874	755
DxD	2	2	L	2	964	936	850	710	624	522	442	316	278	206	152	104	40.5	0.634	844	731
DxD	3	1	L	2	960	938	822	692	580	502	450	380	386	342	346	304	22.7	0.788	655	623
DxD	3	2	L	2	956	936	852	764	682	598	524	432	374	326	250	114	56.3	0.573	803	635
DxD	4	1	L	2	956	890	732	610	560	460	426	420	382	266	218	170	74.8	0.718	755	627
DxD	4	2	L	2	950	926	838	724	650	552	478	382	326	242	188	108	55	0.605	835	683
DxD	5	1	L	2	954	932	838	718	626	536	476	372	306	210	164	120	52.1	0.613	842	703
DxD	5	2	L	2	948	920	800	668	568	492	414	310	266	230	238	168	40.1	0.699	782	743
DxD	6	1	L	2	950	916	780	678	574	496	438	322	302	210	152	88	63.3	0.657	851	707
DxD	6	2	L	2	956	924	766	586	462	372	316	244	242	170	124	108	34.3	0.794	833	767
DxD	7	1	L	2	950	926	798	718	642	536	466	414	376	300	240	148	60.8	0.628	775	633
DxD	7	2	L	2	950	934	826	742	642	566	506	386	340	270	198	132	54.6	0.601	816	669
DxD	8	1	L	2	954	930	866	780	712	632	554	414	360	262	200	112	49	0.549	847	649
DxD	8	2	L	2	960	930	804	666	546	446	352	212	190	144	112	76	35.2	0.705	882	819

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	8	10	11	14	16	20	i	r	K	P10
DxD	9	1	L	2	944	926	836	728	658	572	492	326	272	208	180	116	44.6	0.606	846	737
DxD	9	2	L	2	946	930	848	756	682	608	528	396	330	248	210	142	48.1	0.577	822	679
DxD	10	1	L	2	910	808	642	502	402	406	340	290	262	232	184	130	82	0.86	790	747
DxD	10	2	L	2	950	926	850	750	674	590	520	376	316	208	172	98	50.9	0.577	866	693
DxD	11	1	L	2	942	862	760	740	706	606	550	480	410	338	292	190	88.9	0.618	780	599
DxD	11	2	L	2	968	942	860	752	700	604	498	406	340	254	182	100	48.2	0.569	847	669
DxD	12	1	L	2	962	934	868	774	706	646	568	446	386	318	270	136	51.4	0.548	798	623
DxD	12	2	L	2	960	940	886	838	794	730	678	576	490	410	368	270	42.8	0.482	706	519
DxD	13	1	L	2	956	946	904	854	808	710	612	468	382	268	200	148	28.5	0.508	834	627
DxD	13	2	L	2	952	952	904	854	802	730	658	498	400	286	242	144	30.8	0.489	829	609
DxD	14	1	L	2	948	888	734	646	570	504	414	396	396	294	290	228	57.9	0.725	705	613
DxD	14	2	L	2	956	948	890	834	782	664	574	424	332	234	162	76	33.8	0.522	885	677
DxD	15	1	L	2	946	940	874	820	758	660	580	458	384	296	210	150	42.7	0.525	824	625
DxD	15	2	L	2	904	832	750	664	594	538	480	390	340	244	218	116	107	0.705	844	669
DxD	16	1	L	2	948	920	752	652	578	500	452	344	320	242	182	98	72	0.669	829	689
DxD	16	2	L	2	946	926	828	726	658	578	538	398	344	282	232	158	56.3	0.598	795	665
DxD	17	1	L	2	972	960	936	904	866	832	794	718	664	600	534	340	43.7	0.368	719	345
DxD	17	2	L	2	984	960	940	910	890	854	810	736	690	588	528	400	30.3	0.366	620	319
DxD	18	1	L	2	986	970	942	900	862	786	722	624	566	500	444	360	21.6	0.465	601	443
DxD	18	2	L	2	982	968	938	900	868	804	746	660	608	510	480	348	28.8	0.421	623	401
DxD	19	1	L	2	956	952	862	768	734	624	506	424	356	300	272	154	38.2	0.575	773	653
DxD	19	2	L	2	938	868	782	724	722	584	542	468	460	394	332	212	88.3	0.625	730	549
DxD	20	1	L	2	986	972	954	928	908	864	822	748	680	580	488	384	22.1	0.367	633	329
DxD	20	2	L	2	958	952	932	900	892	818	760	666	604	506	448	366	26.5	0.42	627	405
DxD	21	1	L	2	946	926	798	678	584	484	430	310	292	230	204	112	48	0.671	811	717
DxD	21	2	L	2	954	936	870	784	714	630	560	456	386	300	264	162	47.9	0.551	788	623
DxD	22	1	L	2	964	950	860	808	726	632	566	468	408	348	294	200	41.8	0.553	741	601

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	8	10	11	14	16	20	i	r	K	P10
DxD	22	2	L	2	942	918	760	654	570	492	444	314	270	206	152	78	67.8	0.667	860	739
DxD	23	1	L	2	958	940	822	710	648	586	560	446	386	326	310	220	55.2	0.608	723	623
DxD	23	2	L	2	958	936	818	706	618	558	454	352	328	216	170	94	56.4	0.617	848	681
DxD	24	1	L	2	966	944	908	868	830	786	714	620	580	498	470	338	39.7	0.447	630	429
DxD	24	2	L	2	948	924	838	750	670	560	490	386	358	270	228	152	48.8	0.603	791	651
DxD	25	1	L	2	946	936	866	778	702	600	502	426	360	280	208	128	48.6	0.568	819	649
DxD	25	2	L	2	960	950	890	822	774	680	582	446	390	296	238	134	36.7	0.521	816	619
DxD	L1+	1	L	2	934	884	718	596	488	410	342	260	224	146	108	50	69.3	0.736	883	785
DxD	L2+	2	L	2	932	894	780	698	618	552	480	330	310	258	248	140	61.3	0.646	797	699
DxD	D1+	1	L	2	962	944	856	784	740	676	644	588	578	500	446	264	82.3	0.528	710	431
DxD	D2+	2	L	2	942	932	846	786	718	630	542	410	402	360	340	224	37.8	0.591	704	607
DxD	U+	2	L	2	930	922	804	722	660	580	526	434	386	294	254	448	43.5	0.651	664	623
DxD	L1-	1	L	2	932	908	788	698	620	560	496	370	340	294	248	188	60.8	0.643	765	711
DxD	L2-	2	L	2	966	948	852	742	642	578	494	360	298	232	220	168	36.2	0.617	796	669
DxD	D1-	1	L	2	970	958	904	840	782	666	584	446	364	252	202	114	31	0.521	845	645
DxD	D2-	2	L	2	984	970	940	900	880	808	758	680	638	600	528	420	29.1	31.06	547	371
DxD	U-	2	L	2	964	944	904	848	802	732	646	510	406	308	224	98	38.1	0.476	872	603

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	8	10	12	14	18	22	i	r	K	P10
AxD	1	1	L	1	988	926	838	706	602	524	410	280	212	168	124	106	45.7	0.611	856	720
AxD	1	2	L	1	990	984	974	916	850	694	440	224	166	140	92	84	5.54	0.669	888	776
AxD	2	1	L	1	990	964	904	780	690	570	368	232	178	136	94	90	21.1	0.615	882	768
AxD	2	2	L	1	990	922	824	712	630	548	444	308	254	208	162	148	48.2	0.601	820	692
AxD	3	1	L	1	990	930	812	660	590	490	368	264	194	156	120	108	42.7	0.645	853	736
AxD	3	2	L	1	996	972	912	752	654	540	346	224	182	150	96	82	19.6	0.649	872	776
AxD	4	1	L	1	992	932	866	748	654	564	404	278	250	228	158	144	30.5	0.612	813	722
AxD	4	2	L	1	990	948	864	724	628	544	402	278	244	232	170	134	30.2	0.63	807	722
AxD	5	1	L	1	986	892	772	650	566	492	354	248	196	152	142	132	48.7	0.665	844	752
AxD	5	2	L	1	986	908	792	658	588	502	368	364	204	144	106	104	63.6	0.633	865	636
AxD	6	1	L	1	974	916	844	716	622	524	356	232	196	162	124	110	34.8	0.631	858	768
AxD	6	2	L	1	986	944	844	680	592	502	332	214	156	124	80	86	33.6	0.646	888	786
AxD	7	1	L	1	980	902	800	640	548	442	282	194	164	140	90	78	35.4	0.697	877	806
AxD	7	2	L	1	992	960	932	880	870	824	762	666	636	576	502	420	35.6	0.377	569	334
AxD	8	1	L	1	980	904	824	698	606	512	376	260	212	168	124	108	44.7	0.627	854	740
AxD	8	2	L	1	988	942	850	720	644	544	402	256	206	168	114	104	37.8	0.601	864	744
AxD	9	1	L	1	990	936	842	694	606	488	338	234	180	140	100	90	32.4	0.649	870	766
AxD	9	2	L	1	976	920	848	740	668	590	434	290	234	176	142	108	44.7	0.573	860	710
AxD	10	1	L	1	992	928	860	748	668	572	438	290	234	186	146	110	40	0.576	850	710
AxD	10	2	L	1	998	996	999	992	988	0	0	0	0	0	0	0	.	.	.	1
AxD	11	1	L	1	978	924	866	766	682	580	430	290	194	130	84	86	41.9	0.559	904	710
AxD	11	2	L	1	988	916	878	792	744	694	550	398	328	264	160	118	49.9	0.497	863	602
AxD	12	1	L	1	992	934	854	726	642	560	442	300	206	156	116	86	47.6	0.575	882	700
AxD	12	2	L	1	988	930	864	774	700	634	510	374	288	234	140	102	53.1	0.526	870	626
AxD	13	1	L	1	994	954	924	854	772	674	470	316	208	140	84	58	24.3	0.519	917	684
AxD	13	2	L	1	992	952	904	818	772	666	498	346	254	194	130	120	29.4	0.516	864	654
AxD	14	1	L	1	999	950	894	810	754	700	492	374	286	216	132	98	36.2	0.501	874	626

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	8	10	12	14	18	22	i	r	K	P10
AxD	14	2	L	1	990	954	916	840	790	710	538	354	244	170	96	62	28.5	0.486	920	646
AxD	15	1	L	1	988	920	830	700	652	566	440	290	232	184	102	68	57.5	0.58	891	710
AxD	15	2	L	1	986	962	886	732	652	572	436	304	224	152	100	78	43	0.564	888	696
AxD	16	1	L	1	970	900	816	718	678	590	470	336	224	150	124	92	62.2	0.569	896	664
AxD	16	2	L	1	990	916	842	724	630	540	390	248	164	108	108	100	40.2	0.602	890	752
AxD	17	1	L	1	986	954	882	766	674	612	436	288	184	134	94	80	36.3	0.554	902	712
AxD	17	2	L	1	984	936	856	758	684	644	464	334	272	184	116	84	50.4	0.538	889	666
AxD	18	1	L	1	992	938	880	806	740	664	538	414	328	252	180	146	45	0.502	833	586
AxD	18	2	L	1	986	908	806	732	640	542	440	290	196	156	118	96	53.9	0.589	882	710
AxD	19	1	L	1	986	972	912	800	734	682	578	410	300	244	154	114	41.1	0.485	867	590
AxD	19	2	L	1	998	992	978	908	824	752	612	398	268	168	106	76	16.5	0.476	911	602
AxD	20	1	L	1	974	876	816	754	708	654	518	366	250	192	116	90	63	0.539	909	634
AxD	20	2	L	1	982	906	802	662	588	466	368	222	154	118	82	86	48.3	0.642	893	778
AxD	21	1	L	1	986	956	900	800	726	684	590	408	320	272	192	108	45.4	0.487	853	592
AxD	21	2	L	1	990	950	894	786	726	676	564	418	316	216	148	120	46.8	0.493	874	582
AxD	22	1	L	1	992	954	876	760	700	664	476	334	254	184	124	106	40.5	0.53	875	666
AxD	22	2	L	1	996	940	868	808	752	698	550	412	342	292	180	130	46.6	0.491	840	588
AxD	23	1	L	1	999	980	910	764	694	638	520	360	228	176	112	94	39.9	0.517	892	640
AxD	23	2	L	1	996	916	874	762	670	574	430	274	196	162	130	92	37	0.574	873	726
AxD	24	1	L	1	994	990	990	986	0	0	0	0	0	0	0	0	.	.	.	1
AxD	24	2	L	1	992	936	874	768	676	612	486	336	234	162	100	74	48.5	0.535	906	664
AxD	25	1	L	1	990	990	990	990	0	0	0	0	0	0	0	0	.	.	.	1
AxD	25	2	L	1	996	992	988	0	0	0	0	0	0	0	0	0	.	.	.	1
AxD	L1+	1	L	1	994	924	812	662	570	456	300	222	176	142	100	98	30.4	0.692	862	778
AxD	L2+	1	L	1	999	972	894	726	624	492	346	204	162	146	114	84	20.4	0.674	868	796
AxD	D1+	1	L	1	984	958	948	920	886	798	640	498	382	312	240	204	16.3	0.456	778	502
AxD	D2+	1	L	1	998	940	862	726	670	570	406	374	258	182	132	90	50	0.568	860	626

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	8	10	12	14	18	22	i	r	K	P10
AxD	U+	1	L	1	986	952	934	834	740	616	446	278	214	150	98	64	24.8	0.548	895	722
AxD	L1-	1	L	1	988	946	844	672	608	514	386	264	200	144	84	68	46.8	0.611	887	736
AxD	L2-	1	L	1	986	952	902	752	656	524	378	242	184	132	82	68	29	0.606	890	758
AxD	D1-	1	L	1	994	962	940	892	864	786	576	474	334	274	198	152	20.4	0.461	823	526
AxD	D2-	1	L	1	984	948	922	886	870	820	630	450	338	238	140	98	21.8	0.439	893	550
AxD	U-	1	L	1	982	900	825	760	694	624	506	362	292	224	152	128	58.4	0.546	855	638
DxA	1	1	L	1	966	872	760	662	584	516	444	320	234	180	138	108	81.9	0.648	862	680
DxA	1	2	L	1	986	906	810	714	668	592	500	386	308	218	150	116	73.4	0.573	864	614
DxA	2	1	L	1	984	960	936	892	848	756	548	392	274	200	144	86	19.1	0.485	880	608
DxA	2	2	L	1	996	914	836	736	650	542	416	258	190	154	90	90	44.2	0.587	888	742
DxA	3	1	L	1	988	932	828	700	610	558	438	318	256	258	192	148	45	0.613	793	682
DxA	3	2	L	1	964	888	778	620	540	460	358	242	234	204	154	96	50.1	0.69	826	758
DxA	4	1	L	1	982	950	866	738	662	648	514	374	294	252	176	146	52	0.541	826	626
DxA	4	2	L	1	990	908	840	766	710	672	508	350	296	230	144	116	53.1	0.528	865	650
DxA	5	1	L	1	986	944	856	744	672	622	512	376	302	250	168	102	58.5	0.541	853	624
DxA	5	2	L	1	999	924	806	652	576	488	382	248	184	156	100	70	49.5	0.637	876	752
DxA	6	1	L	1	986	908	816	712	660	592	476	328	260	206	124	98	64.2	0.573	876	672
DxA	6	2	L	1	996	964	892	724	640	498	336	234	172	116	80	86	23.4	0.65	881	766
DxA	7	1	L	1	988	906	780	634	572	490	404	282	192	154	104	84	64.6	0.643	876	718
DxA	7	2	L	1	988	916	814	640	576	490	368	266	198	154	94	64	53.3	0.639	878	734
DxA	8	1	L	1	994	930	854	746	686	616	490	362	280	234	166	122	51.5	0.547	840	638
DxA	8	2	L	1	982	874	778	664	566	490	400	290	216	166	144	108	63.1	0.65	848	710
DxA	9	1	L	1	994	942	836	722	670	566	466	354	304	280	206	130	48.7	0.58	791	646
DxA	9	2	L	1	984	920	830	772	720	658	512	364	264	262	182	146	48	0.533	829	636
DxA	10	1	L	1	986	922	838	690	606	550	392	286	232	178	128	74	50.2	0.605	863	714
DxA	10	2	L	1	990	900	776	634	574	504	394	268	216	136	108	90	64	0.643	875	732
DxA	11	1	L	1	986	932	880	756	672	602	440	306	250	198	138	114	39.6	0.564	849	694

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	8	10	12	14	18	22	i	r	K	P10
DxA	11	2	L	1	992	920	832	720	660	604	470	330	266	188	126	90	59.3	0.563	880	670
DxA	12	1	L	1	982	926	876	740	666	584	420	314	272	260	208	154	32.5	0.604	784	686
DxA	12	2	L	1	990	920	852	694	618	546	402	280	228	174	136	116	43.4	0.609	846	720
DxA	13	1	L	1	992	940	860	704	606	558	396	354	206	156	98	84	52.4	0.587	881	646
DxA	13	2	L	1	990	954	924	808	710	612	466	334	270	212	146	134	29.8	0.549	832	666
DxA	14	1	L	1	996	972	934	840	762	702	560	420	352	260	218	168	30	0.489	799	580
DxA	14	2	L	1	996	962	914	782	708	632	492	340	268	224	166	122	33.7	0.537	835	660
DxA	15	1	L	1	990	970	950	926	902	844	628	446	356	284	200	160	11.6	0.479	810	554
DxA	15	2	L	1	986	914	862	742	640	566	408	314	278	262	208	138	34.7	0.614	785	686
DxA	16	1	L	1	980	890	766	642	604	554	422	288	218	188	108	74	76.2	0.63	887	712
DxA	16	2	L	1	992	920	794	646	588	514	436	290	222	174	118	98	63.3	0.625	864	710
DxA	17	1	L	1	992	906	800	664	586	488	372	260	202	142	90	82	53.1	0.635	878	740
DxA	17	2	L	1	974	936	838	738	678	608	438	314	226	174	100	72	51.7	0.556	899	686
DxA	18	1	L	1	994	922	824	700	608	536	410	294	216	202	124	100	19.4	0.608	852	706
DxA	18	2	L	1	996	968	904	736	660	542	398	248	204	154	84	62	30.0	0.593	886	752
DxA	19	1	L	1	998	920	824	754	700	612	442	354	312	272	198	144	46.2	0.566	796	646
DxA	19	2	L	1	980	918	832	728	660	600	438	318	250	216	164	126	49	0.577	835	682
DxA	20	1	L	1	988	944	866	696	638	594	404	274	222	170	106	76	44.2	0.581	880	726
DxA	20	2	L	1	992	956	860	684	614	518	372	214	186	138	88	80	34.6	0.625	883	786
DxA	21	1	L	1	986	958	876	720	664	582	392	284	230	192	140	114	32.4	0.598	840	716
DxA	21	2	L	1	998	946	846	718	648	566	446	314	250	184	126	96	49.3	0.574	863	686
DxA	22	1	L	1	964	908	810	640	552	456	338	232	174	134	86	82	47	0.665	878	768
DxA	22	2	L	1	999	964	866	674	636	516	344	224	168	120	78	68	31.6	0.628	893	776
DxA	23	1	L	1	992	952	936	906	882	856	722	496	414	290	202	150	16.5	0.423	841	504
DxA	23	2	L	1	999	966	938	900	880	844	708	434	310	196	120	78	12.3	0.457	912	566
DxA	24	1	L	1	982	938	896	772	702	622	466	378	320	310	230	164	35.7	0.56	763	622
DxA	24	2	L	1	990	948	928	896	874	834	648	434	328	232	200	180	13	0.48	819	566

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	8	10	12	14	18	22	i	r	K	P10
DxA	25	1	L	1	988	936	926	890	864	814	642	514	390	332	344	336	14.7	0.491	676	486
DxA	25	2	L	1	990	964	944	918	904	878	782	594	526	414	306	184	19.9	0.372	800	406
DxA	L1+	1	L	1	992	966	902	758	704	600	482	366	264	210	152	124	39.8	0.54	842	634
DxA	L2+	1	L	1	999	960	894	726	658	552	394	276	194	170	98	70	33.3	0.591	877	724
DxA	D1+	1	L	1	976	930	866	750	684	628	498	374	294	280	232	188	44	0.558	774	626
DxA	D2+	1	L	1	996	924	814	724	662	570	440	344	262	250	236	204	39.2	0.61	765	656
DxA	U+	1	L	1	996	914	852	746	692	604	518	390	302	242	180	112	60.3	0.544	847	610
DxA	L1-	1	L	1	992	930	862	712	620	528	354	240	198	162	136	108	29.8	0.64	850	760
DxA	L2-	1	L	1	988	922	834	726	642	560	454	326	254	222	160	118	51.9	0.584	834	674
DxA	D1-	1	L	1	990	926	832	712	624	504	348	232	138	114	74	76	37.6	0.621	903	768
DxA	D2-	1	L	1	978	896	828	718	628	528	420	288	188	128	94	78	56.4	0.594	902	712
DxA	U-	1	L	1	990	940	864	754	680	594	464	346	250	180	120	98	48.6	0.548	876	654

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	9	11	13	16	21	i	r	K	P10
AxD	1	1	L	2	972	890	770	660	556	468	394	304	236	204	150	152	28.4	0.618	816	696
AxD	1	2	L	2	988	980	952	884	768	670	570	394	270	206	142	102	12.1	0.513	863	606
AxD	2	1	L	2	962	888	780	674	564	482	430	308	250	218	178	148	31.5	0.601	808	692
AxD	2	2	L	2	982	902	816	716	626	538	472	342	274	230	178	152	30.7	0.557	811	658
AxD	3	1	L	2	962	888	780	680	584	518	430	308	250	190	148	142	36.3	0.577	834	692
AxD	3	2	L	2	968	930	842	736	640	550	496	328	282	204	150	116	30.6	0.535	845	672
AxD	4	1	L	2	956	912	814	722	612	526	440	292	260	220	202	156	23	0.593	802	708
AxD	4	2	L	2	974	928	798	720	626	528	446	344	292	246	228	184	22.6	0.595	769	656
AxD	5	1	L	2	960	864	766	676	588	510	410	288	212	190	138	138	37	0.584	846	712
AxD	5	2	L	2	960	860	762	664	556	476	378	258	196	142	102	70	39.3	0.59	890	742
AxD	6	1	L	2	970	888	786	698	586	510	428	318	264	238	186	182	27.8	0.599	790	682
AxD	6	2	L	2	964	898	776	682	590	504	418	278	220	180	134	122	32.1	0.583	851	722
AxD	7	1	L	2	964	900	750	666	552	474	390	240	196	144	110	100	31.8	0.601	874	760
AxD	7	2	L	2	974	954	940	904	886	864	856	792	742	706	642	596	26	0.32	421	208
AxD	8	1	L	2	972	926	828	756	654	592	526	330	260	208	134	142	30	0.522	851	670
AxD	8	2	L	2	970	906	786	696	618	512	412	292	228	184	126	114	30.2	0.574	854	708
AxD	9	1	L	2	970	876	748	638	540	440	380	276	214	172	110	112	34.3	0.616	852	724
AxD	9	2	L	2	970	896	770	656	550	456	354	236	182	138	96	90	27	0.617	879	764
AxD	10	1	L	2	966	866	764	672	596	510	420	320	272	222	160	130	41.6	0.579	824	680
AxD	10	2	L	2	984	990	990	.	.	.	.	.	.	.	.	.	.	.	.	1
AxD	11	1	L	2	970	906	806	714	618	518	440	312	222	206	126	112	30.9	0.562	853	688
AxD	11	2	L	2	962	914	818	732	624	518	450	310	224	164	122	100	30.3	0.553	871	690
AxD	12	1	L	2	970	914	826	758	694	584	516	390	296	238	190	142	34.6	0.513	825	610
AxD	12	2	L	2	956	936	902	862	776	670	568	376	242	184	100	82	17.8	0.486	907	624
AxD	13	1	L	2	966	912	818	722	656	566	480	330	258	206	142	98	35.9	0.53	863	670
AxD	13	2	L	2	970	930	872	800	702	596	506	352	230	194	108	78	25.4	0.507	892	648
AxD	14	1	L	2	982	920	820	730	626	498	416	292	218	160	116	110	22.6	0.582	861	708

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	9	11	13	16	21	i	r	K	P10
AxD	14	2	L	2	978	944	876	788	704	576	500	362	262	206	148	114	22.4	0.524	849	638
AxD	15	1	L	2	986	960	872	768	636	518	438	266	208	152	102	72	15.4	0.592	879	734
AxD	15	2	L	2	974	954	882	800	730	650	598	494	408	320	242	176	37.4	0.458	796	506
AxD	16	1	L	2	950	864	740	666	594	470	370	240	166	120	86	74	39.1	0.587	908	760
AxD	16	2	L	2	956	876	788	690	610	524	454	324	226	168	126	98	44.5	0.553	878	676
AxD	17	1	L	2	960	918	842	742	642	526	452	316	224	182	126	108	26.4	0.553	861	684
AxD	17	2	L	2	978	924	872	800	670	544	464	290	178	116	76	62	19.8	0.546	918	710
AxD	18	1	L	2	966	868	794	696	584	460	352	282	198	182	142	122	23.6	0.622	841	718
AxD	18	2	L	2	954	868	758	656	554	466	394	282	210	140	110	104	40.6	0.593	873	718
AxD	19	1	L	2	978	948	862	768	658	522	418	246	184	126	96	72	14.6	0.597	893	754
AxD	19	2	L	2	986	980	956	918	830	702	620	426	272	182	124	92	9.87	0.499	890	574
AxD	20	1	L	2	952	854	732	606	516	414	312	192	134	98	68	50	35.7	0.629	920	808
AxD	20	2	L	2	964	890	782	672	610	472	364	282	210	148	140	132	26.3	0.607	848	718
AxD	21	1	L	2	966	918	824	738	662	620	510	372	270	200	138	100	39.5	0.506	880	628
AxD	21	2	L	2	970	934	852	748	658	560	462	360	252	194	108	100	30.7	0.525	872	640
AxD	22	1	L	2	974	940	898	812	720	634	594	426	330	250	178	92	32.2	0.464	870	574
AxD	22	2	L	2	976	928	844	750	724	594	530	432	302	210	132	96	41	0.485	891	568
AxD	23	1	L	2	982	968	936	916	874	840	804	606	462	342	204	124	12.7	0.39	882	394
AxD	23	2	L	2	972	942	868	788	670	564	512	340	226	160	110	98	24.4	0.522	886	660
AxD	24	1	L	2	994	998	994	992	.	.	.	.	.	.	.	.	.	.	.	1
AxD	24	2	L	2	978	932	854	744	688	640	528	432	320	246	162	88	43.7	0.484	880	568
AxD	25	1	L	2	990	992	992	.	.	.	.	.	.	.	.	.	.	.	.	1
AxD	25	2	L	2	966	996	999	.	.	.	.	.	.	.	.	.	.	.	.	1
AxD	L1+	1	L	2	956	782	684	596	514	416	412	300	232	204	192	144	55.4	0.651	810	700
AxD	L2+	1	L	2	978	944	832	702	650	572	518	378	296	256	222	154	31.7	0.536	793	622
AxD	D1+	1	L	2	994	962	944	912	826	698	594	360	254	192	150	98	7.23	0.552	863	640
AxD	D2+	1	L	2	964	874	734	614	512	420	336	216	160	118	78	64	33.7	0.628	900	784

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	9	11	13	16	21	i	r	K	P10
AxD	U+	1	L	2	982	952	854	726	598	504	422	308	222	166	106	78	26.3	0.535	888	692
AxD	L1-	1	L	2	978	952	860	756	632	544	452	310	220	168	114	98	21	0.56	868	764
AxD	L2-	1	L	2	958	850	694	580	480	398	344	236	170	130	84	54	44.2	0.641	893	690
AxD	D1-	1	L	2	954	896	790	688	608	546	452	324	274	240	212	150	34.6	0.571	799	676
AxD	D2-	1	L	2	968	946	920	898	860	798	716	474	318	218	140	90	10.9	0.454	902	526
AxD	U-	1	L	2	956	922	844	730	686	566	484	288	210	152	128	88	21.7	0.579	867	712
DxA	1	1	L	2	932	796	722	642	562	478	436	362	254	192	118	100	81.6	0.62	881	638
DxA	1	2	L	2	958	854	752	664	578	536	466	366	310	262	170	118	64.5	0.578	830	634
DxA	2	1	L	2	996	948	902	818	688	612	504	358	270	202	144	120	18	0.531	846	642
DxA	2	2	L	2	984	860	726	652	574	478	426	312	212	172	114	90	49.5	0.583	875	688
DxA	3	1	L	2	954	834	732	626	554	460	414	330	290	244	192	132	48.7	0.617	796	670
DxA	3	2	L	2	952	860	756	658	610	514	472	288	316	268	244	210	37.6	0.597	758	712
DxA	4	1	L	2	964	870	776	680	648	550	480	396	350	290	248	214	44.2	0.564	746	604
DxA	4	2	L	2	948	866	768	672	670	556	480	370	326	276	216	150	55.1	0.554	801	630
DxA	5	1	L	2	956	890	804	704	668	600	526	428	356	268	191	132	60.7	0.522	842	572
DxA	5	2	L	2	958	874	762	666	590	502	452	370	266	212	160	94	56.2	0.569	852	630
DxA	6	1	L	2	960	840	708	648	554	496	442	352	284	212	156	100	68.5	0.601	849	648
DxA	6	2	L	2	974	906	736	630	506	404	342	250	164	112	78	84	27.9	0.639	886	750
DxA	7	1	L	2	960	840	738	672	570	484	398	322	228	150	112	96	52.3	0.585	879	678
DxA	7	2	L	2	972	904	812	734	640	552	490	382	310	244	158	90	47.7	0.524	857	618
DxA	8	1	L	2	966	838	728	622	530	438	386	314	242	236	174	100	41.6	0.628	814	686
DxA	8	2	L	2	940	800	676	594	528	434	422	334	308	260	230	164	56.5	0.658	763	666
DxA	9	1	L	2	968	866	748	676	584	500	414	318	256	212	164	104	43.2	0.582	836	682
DxA	9	2	L	2	970	888	780	680	628	530	446	346	286	224	182	170	37	0.568	803	654
DxA	10	1	L	2	976	926	830	712	616	530	434	320	256	186	110	80	31.9	0.549	870	680
DxA	10	2	L	2	958	878	746	664	596	512	440	360	284	228	168	138	50.3	0.576	820	640
DxA	11	1	L	2	968	932	844	730	654	528	452	356	328	294	254	178	17.2	0.613	742	644

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	9	11	13	16	21	i	r	K	P10
DxA	11	2	L	2	966	850	724	630	536	450	388	272	194	142	110	68	47.5	0.604	887	728
DxA	12	1	L	2	952	894	798	704	660	606	512	336	274	232	190	172	38.5	0.533	818	664
DxA	12	2	L	2	968	906	764	664	562	486	414	298	240	234	202	146	27	0.619	797	702
DxA	13	1	L	2	980	934	840	752	658	606	526	400	332	306	294	212	24.1	0.549	729	600
DxA	13	2	L	2	974	942	866	776	672	582	490	364	334	308	254	194	16.1	0.586	739	636
DxA	14	1	L	2	954	926	866	780	680	624	560	434	362	300	246	210	32.9	0.502	761	566
DxA	14	2	L	2	990	960	898	810	714	640	560	392	322	290	246	170	17.4	0.526	771	608
DxA	15	1	L	2	974	968	946	918	876	800	698	522	382	304	206	162	10.7	0.448	824	478
DxA	15	2	L	2	970	922	826	738	660	560	474	354	330	300	256	190	22	0.579	744	646
DxA	16	1	L	2	954	820	662	556	460	368	304	214	162	120	68	54	45.5	0.665	898	786
DxA	16	2	L	2	970	824	712	622	528	440	380	318	248	182	132	94	52.3	0.62	847	682
DxA	17	1	L	2	968	900	786	712	624	530	452	336	296	228	148	192	32.9	0.566	803	664
DxA	17	2	L	2	978	908	784	674	546	450	380	298	220	146	92	68	31.1	0.596	875	702
DxA	18	1	L	2	972	890	796	690	614	520	454	348	308	240	206	156	34.5	0.572	789	652
DxA	18	2	L	2	974	902	756	664	606	490	412	318	262	202	134	100	39.2	0.576	845	682
DxA	19	1	L	2	982	912	794	700	638	520	426	316	256	208	150	96	31.3	0.563	844	684
DxA	19	2	L	2	962	856	772	672	624	572	506	400	308	262	230	180	55.5	0.557	789	600
DxA	20	1	L	2	986	830	810	732	676	604	520	380	286	220	132	134	49.1	0.515	870	620
DxA	20	2	L	2	964	908	808	732	684	570	468	342	272	218	168	130	32.9	0.534	836	658
DxA	21	1	L	2	976	908	746	638	524	454	418	270	214	174	140	126	31.3	0.618	839	730
DxA	21	2	L	2	984	910	796	714	620	550	480	358	284	230	160	102	41.6	0.537	844	642
DxA	22	1	L	2	976	930	844	738	630	552	470	336	250	184	134	90	30.3	0.536	866	664
DxA	22	2	L	2	972	882	780	692	596	528	448	338	262	190	130	98	46.3	0.554	865	662
DxA	23	1	L	2	974	944	914	894	860	818	780	614	466	328	336	274	12.6	0.421	730	386
DxA	23	2	L	2	962	936	916	892	856	826	770	546	406	280	192	142	24.6	0.206	.	454
DxA	24	1	L	2	954	849	718	622	594	472	392	254	186	150	106	88	48.5	0.595	889	746
DxA	24	2	L	2	978	946	894	800	704	632	600	408	302	224	184	138	25.9	0.484	841	592

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	9	11	13	16	21	i	r	K	P10
DxA	25	1	L	2	966	946	918	884	832	738	662	452	324	336	350	364	5.38	0.595	667	548
DxA	25	2	L	2	994	974	946	930	908	864	800	492	394	308	222	132	12.1	.	.	508
DxA	L1+	1	L	2	998	968	862	786	716	602	532	380	308	240	160	112	25.5	0.501	842	620
DxA	L2+	1	L	2	976	914	786	704	614	552	466	362	310	222	146	116	44.9	0.541	843	638
DxA	D1+	1	L	2	978	900	796	704	646	576	546	452	408	382	302	202	51	0.538	715	548
DxA	D2+	1	L	2	970	888	774	710	670	546	458	348	316	252	226	214	31.5	0.568	765	652
DxA	U+	1	L	2	956	872	768	664	586	480	416	298	226	156	122	92	51.5	0.557	889	702
DxA	L1-	1	L	2	974	896	796	716	630	550	476	384	338	282	206	196	36.2	0.556	765	616
DxA	L2-	1	L	2	956	894	798	698	614	550	462	292	236	178	166	158	32.3	0.563	836	708
DxA	D1-	1	L	2	974	922	850	750	646	526	464	312	230	172	122	96	25.4	0.549	868	688
DxA	D2-	1	L	2	970	922	842	742	654	538	476	368	268	198	134	108	33.7	0.528	858	632
DxA	U-	1	L	2	962	880	772	666	600	530	442	340	236	166	114	84	43.1	0.577	873	660

					Day																									
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	8	10	11	13	15	16	17	18	19	21	23	25	29	32	39	i	r	K	P10
AxA	1	1	D	1	992	990	980	986	984	982	974	966	940	922	880	796	736	678	628	598	554	524	478	.	.	.	1.824	0.22	529	66
AxA	1	2	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	16.53	0.34	542	100
AxA	2	1	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
AxA	2	2	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	12.61	0.25	402	64
AxA	3	1	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	20.35	0.53	614	274
AxA	3	2	D	1	984	988	974	966	954	946	934	914	822	762	676	662	652	618	610	590	578	568	552	.	.	.	7.326	0.33	430	184
AxA	4	1	D	1	988	990	986	990	996	990	990	992	996	994	996	990	990	992	990	990	984	972	938	784	696	500	21.89	0.25	.	10
AxA	4	2	D	1	990	990	982	988	990	990	990	990	988	990	992	990	990	990	990	984	980	972	940	788	694	560	22.27	0.25	.	18
AxA	5	1	D	1	990	984	980	982	982	986	986	986	986	984	984	982	978	974	968	958	880	768	650	494	438	384	0.029	0.24	597	20
AxA	5	2	D	1	999	998	986	988	984	974	958	938	864	820	706	628	608	572	536	516	478	452	458	.	.	.	4.44	0.28	545	142
AxA	6	1	D	1	999	998	988	996	996	990	986	978	964	952	910	840	804	722	646	612	554	528	494	.	.	.	0.391	0.27	512	42
AxA	6	2	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1.246	0.19	519	84
AxA	7	1	D	1	990	992	986	988	984	986	974	968	950	944	930	904	890	864	838	818	768	736	674	566	544	.	7.143	0.14	545	56
AxA	7	2	D	1	986	986	980	980	982	980	962	960	944	936	926	910	892	878	854	836	790	730	670	598	556	.	8.44	0.15	548	62
AxA	8	1	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	12	12
AxA	8	2	D	1	998	996	990	992	994	994	994	998	992	994	999	994	996	994	992	990	986	976	950	890	854	740	11.1	0.06	.	14
AxA	9	1	D	1	994	988	978	976	960	912	872	842	790	768	714	678	658	642	626	604	566	548	522	478	484	.	26.82	0.53	505	216
AxA	9	2	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	32.3	0.48	.	12
AxA	10	1	D	1	999	999	988	986	984	976	960	944	884	838	736	654	626	590	556	536	502	472	456	.	.	.	4.313	0.27	537	122
AxA	10	2	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	6	6
AxA	11	1	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1.639	0.16	771	74
AxA	11	2	D	1	978	976	970	970	964	958	942	928	878	818	728	622	578	550	522	490	452	432	.	.	.	.	6.108	0.28	585	128
AxA	12	1	D	1	988	984	982	986	984	984	986	984	986	984	984	978	964	966	952	944	898	856	796	668	566	558	0.286	0.12	467	20
AxA	12	2	D	1	998	994	982	992	988	988	984	978	966	960	952	940	930	922	914	914	894	876	866	834	820	770	8.98	0.13	243	40
AxA	13	1	D	1	988	992	980	972	952	926	896	852	764	720	658	624	632	622	614	576	578	566	518	526	520	.	13.05	0.4	449	242
AxA	13	2	D	1	996	986	966	964	960	950	942	936	928	926	906	898	894	882	870	862	832	794	754	668	576	522	19.01	0.28	618	78
AxA	14	1	D	1	999	994	980	972	938	870	786	746	700	684	668	644	656	624	624	642	590	550	544	522	474	.	22.58	0.57	429	306
AxA	14	2	D	1	992	988	978	970	946	916	814	762	720	696	664	636	620	574	570	560	512	482	474	.	.	.	24.85	0.56	493	286
AxA	15	1	D	1	996	990	980	958	924	856	774	722	684	654	664	610	620	614	618	618	608	600	586	502	478	.	10.59	0.52	412	322
AxA	15	2	D	1	998	984	964	936	884	806	754	730	694	696	700	672	686	672	668	664	630	604	572	502	508	.	36.38	0.78	396	312
AxA	16	1	D	1	999	990	978	944	890	792	756	726	690	666	630	614	622	616	620	620	614	606	578	502	460	.	17.63	0.59	415	316
AxA	16	2	D	1	986	984	980	982	984	980	978	976	972	970	946	892	858	.	738	680	612	568	528	466	.	.	0.765	0.2	530	34
AxA	17	1	D	1	996	992	984	994	992	992	992	990	986	990	992	974	968	958	952	936	904	874	838	774	704	526	3.08	0.05	607	20
AxA	17	2	D	1	984	986	980	984	974	976	964	950	932	918	884	858	806	774	742	704	664	634	590	532	.	.	7.834	0.2	496	74
AxA	18	1	D	1	992	984	956	918	870	810	746	678	634	618	538	494	530	448	480	436	420	384	416	410	404	374	36.44	0.78	587	372
AxA	18	2	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	19.13	0.63	605	328
AxA	19	1	D	1	995	992	978	966	934	904	752	712	668	654	598	604	602	570	564	570	538	526	516	516	.	.	8.146	0.51	443	338
AxA	19	2	D	1	996	988	968	938	886	784	706	688	664	626	594	562	596	588	562	598	598	604	604	584	516	.	7.768	0.62	414	342
AxA	20	1	D	1	996	988	968	944	880	794	750	734	702	682	678	670	684	670	640	662	640	636	624	592	526	.	10.97	0.6	360	304
AxA	20	2	D	1	994	986	966	942	856	774	678	644	604	586	562	560	578	568	540	570	568	566	566	546	496	.	5.189	0.68	441	402
AxA	21	1	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	8.424	0.2	.	94
AxA	21	2	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	26
AxA	22	1	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.

Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	8	10	11	13	15	16	17	18	19	21	23	25	29	32	39	i	r	K	P10
AxA	22	2	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	23.57	0.45	337	86
AxA	23	1	D	1	999	992	976	978	978	966	954	930	894	870	770	640	598	544	518	510	462	414	372	296	294	.	8.077	0.26	681	112
AxA	23	2	D	1	999	996	984	980	972	964	946	940	894	864	768	.	614	556	536	520	480	430	400	338	306	.	8.246	0.26	659	112
AxA	24	1	D	1	988	980	958	952	940	924	910	898	870	856	814	792	770	720	684	670	616	568	496	390	378	.	29.56	0.5	735	136
AxA	24	2	D	1	988	992	982	980	972	960	942	940	918	904	868	836	818	760	716	678	582	476	446	414	.	.	6.979	0.19	671	88
AxA	25	1	D	1	990	990	978	974	966	952	914	868	740	712	630	586	540	522	486	476	432	426	.	.	.	.	10.06	0.36	562	266
AxA	25	2	D	1	994	990	978	974	970	958	950	936	910	894	836	764	706	648	588	568	490	446	414	338	304	.	8.54	0.23	691	96
AxA	L1+	1	D	1	994	994	986	992	988	984	974	964	934	914	882	778	704	648	612	580	530	504	478	.	.	.	1.393	0.24	530	66
AxA	L1+	2	D	1	999	992	982	992	992	992	986	978	974	962	938	892	858	798	736	692	614	566	520	480	.	.	0.707	0.21	524	26
AxA	L2+	1	D	1	988	994	982	990	990	990	986	978	968	958	946	930	924	910	900	894	870	840	822	770	724	578	12.21	0.16	585	32
AxA	L2+	2	D	1	999	999	998	999	999	998	999	999	996	992	976	950	934	910	896	882	842	820	786	702	662	572	3.35	0.08	438	4
AxA	D1+	1	D	1	996	994	984	980	972	962	960	948	932	924	890	830	796	742	702	676	664	650	630	574	578	.	5.054	0.2	420	68
AxA	D1+	2	D	1	988	992	986	982	972	956	940	926	900	880	824	756	710	674	634	626	624	612	578	552	.	.	6.564	0.25	436	100
AxA	D3+	1	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	8.971	0.3	588	170
AxA	D3+	2	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	10.72	0.31	593	170
AxA	U+	1	D	1	999	994	978	966	940	910	854	830	772	754	672	662	658	608	572	592	550	516	516	484	450	400	32.24	0.61	543	228
AxA	U+	2	D	1	988	994	988	982	968	948	908	884	832	786	702	672	648	600	570	560	510	496	448	438	414	398	18.01	0.39	580	168
AxA	L1-	1	D	1	999	999	994	998	996	999	998	998	999	998	998	996	996	996	992	992	974	942	848	666	574	448	0.019	0.2	551	2
AxA	L1-	2	D	1	996	992	984	994	996	994	992	992	994	998	992	994	996	990	988	986	958	900	810	676	622	568	0.013	0.24	422	6
AxA	L3-	1	D	1	998	996	990	994	994	996	996	994	998	996	996	994	994	990	988	986	962	930	886	788	722	544	0.285	0.08	508	2
AxA	L3-	2	D	1	974	986	974	974	980	976	982	974	970	988	990	982	970	964	960	962	932	912	882	782	712	542	26.92	.	.	30
AxA	D1-	1	D	1	990	980	960	924	860	796	776	762	728	716	684	668	666	648	646	640	640	626	620	592	570	470	45.93	0.89	405	272
AxA	D1-	2	D	1	990	978	958	934	910	856	720	666	606	602	578	578	568	498	474	512	486	476	486	484	494	.	13.57	0.57	493	394
AxA	D2-	1	D	1	996	982	964	948	900	832	696	664	614	606	542	534	518	502	498	468	512	504	528	540	498	.	9.703	0.57	486	386
AxA	D2-	2	D	1	999	992	974	938	868	772	740	732	692	670	634	628	640	620	624	600	594	578	558	518	470	.	24.92	0.67	420	308
AxA	U-	1	D	1	996	992	988	994	990	992	994	992	992	994	992	984	980	972	958	936	838	720	590	456	394	288	0.075	0.21	669	8
AxA	U-	2	D	1	998	994	994	996	994	996	994	994	994	998	996	988	984	978	962	932	792	638	550	450	406	304	0.011	0.31	628	6
BxB	1	1	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	0.445	0.25	574	120
BxB	1	2	D	1	996	990	986	988	990	984	982	976	956	936	860	798	738	696	666	646	614	.	.	.	.	.	0.854	0.27	414	39
BxB	2	1	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
BxB	2	2	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
BxB	3	1	D	1	996	982	962	942	894	838	748	706	644	600	562	552	560	532	490	494	478	450	436	428	416	390	31.68	0.71	547	351
BxB	3	2	D	1	999	998	992	998	996	994	998	998	994	998	999	998	996	996	996	994	994	998	998	996	994	986	0	24.6	4.23	1
BxB	4	1	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	18.62	0.18	176	14
BxB	4	2	D	1	980	984	972	980	980	974	976	978	982	980	980	982	978	978	978	980	976	980	978	960	924	806	17.22	.	.	13
BxB	5	1	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1.514	0.44	491	278
BxB	5	2	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1	0.44	551	246
BxB	6	1	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	12	12
BxB	6	2	D	1	996	999	984	990	984	968	962	960	980	974	960	954	928	930	898	894	884	854	832	776	756	694	7.929	0.12	340	15
BxB	7	1	D	1	992	992	980	982	978	980	976	974	960	960	950	936	930	924	914	908	898	884	874	840	824	786	11.96	0.16	237	35
BxB	7	2	D	1	972	984	974	970	964	974	966	964	954	950	944	920	916	908	890	872	854	836	810	764	742	682	14.75	0.21	363	41
BxB	8	1	D	1	994	990	986	992	992	992	990	990	992	994	994	994	994	994	992	994	994	992	990	994	992	982	.	.	3	3
BxB	8	2	D	1	988	988	976	988	988	986	988	984	988	986	990	988	986	986	988	992	988	990	990	986	988	992	.	.	7	7
BxB	9	1	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	28.75	.	4	4

Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	8	10	11	13	15	16	17	18	19	21	23	25	29	32	39	i	r	K	P10
BxB	9	2	D	1	999	999	998	998	999	999	999	999	999	999	999	999	999	999	999	999	999	999	999	999	999	999	.	.	1	1
BxB	10	1	D	1	999	990	984	978	976	966	932	896	762	712	642	594	632	718	734	736	746	754	748	714	698	686	0.074	.	300	233
BxB	10	2	D	1	992	994	984	988	982	978	956	938	812	756	658	.	624	700	722	730	758	746	760	720	696	.	0.032	.	288	183
BxB	11	1	D	1	974	984	976	946	904	814	648	496	370	324	324	310	318	292	302	288	276	278	300	330	.	.	2.002	0.71	699	625
BxB	11	2	D	1	992	992	984	988	984	980	976	970	944	924	850	792	738	690	650	618	568	.	.	.	.	.	2.139	0.22	494	51
BxB	12	1	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	22.15	0.65	530	286
BxB	12	2	D	1	996	996	986	988	986	978	958	934	802	714	534	460	468	466	436	440	424	414	.	.	.	.	0.368	0.52	566	193
BxB	13	1	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	18.12	0.36	929	152
BxB	13	2	D	1	996	990	978	950	886	854	798	764	702	670	622	610	610	576	572	590	586	572	560	568	566	.	15.3	0.53	423	293
BxB	14	1	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	52.54	.	.	200
BxB	14	2	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	57.52	.	.	196
BxB	15	1	D	1	986	986	978	978	968	952	918	884	840	814	760	754	724	688	680	664	658	636	642	656	666	652	10.59	0.34	350	155
BxB	15	2	D	1	982	976	966	968	958	942	906	854	768	722	634	600	674	692	688	724	720	726	708	700	702	692	1.082	0.56	312	227
BxB	16	1	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1.539	0.28	604	174
BxB	16	2	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1	0.58	833	552
BxB	17	1	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	2.657	0.26	675	154
BxB	17	2	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	3.899	0.39	692	334
BxB	18	1	D	1	988	986	972	952	926	882	854	834	782	770	754	.	736	716	702	674	674	652	638	600	.	.	29.77	0.6	357	213
BxB	18	2	D	1	996	986	972	956	918	882	856	818	794	770	750	728	728	704	698	700	668	642	646	620	630	.	29.66	0.6	354	201
BxB	19	1	D	1	996	988	964	936	900	864	934	810	752	738	714	732	740	716	674	700	672	680	632	642	632	628	24.31	0.56	341	243
BxB	19	2	D	1	994	984	966	956	914	880	844	812	756	768	722	726	734	710	680	690	648	634	638	632	622	616	30.9	0.63	360	239
BxB	20	1	D	1	999	994	984	988	980	968	944	912	806	764	656	614	612	696	710	740	754	762	772	748	712	706	0.136	0.71	292	189
BxB	20	2	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1	0.42	569	158
BxB	21	1	D	1	996	992	988	988	986	974	948	924	844	802	724	682	706	730	734	744	748	732	730	706	710	.	0.376	0.55	279	151
BxB	21	2	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	5.946	0.22	472	88
BxB	22	1	D	1	996	990	982	962	918	860	818	772	668	646	640	710	748	746	746	748	762	758	770	788	792	798	0.942	0.84	262	327
BxB	22	2	D	1	992	988	984	982	978	976	972	962	934	900	822	770	752	732	722	722	682	706	706	.	.	.	1.503	0.29	304	61
BxB	23	1	D	1	999	999	996	998	999	998	998	998	998	998	999	998	998	996	998	996	998	999	999	996	998	999	.	.	1	1
BxB	23	2	D	1	982	984	982	982	980	986	984	986	980	984	986	984	986	982	982	988	986	984	986	990	986	988	.	.	15	15
BxB	24	1	D	1	990	988	978	986	984	988	990	986	984	984	988	992	984	984	988	982	984	984	986	990	990	992	.	.	11	11
BxB	24	2	D	1	994	988	982	988	988	988	988	990	988	988	994	990	990	988	988	988	988	994	992	992	994	998	.	.	7	7
BxB	25	1	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1.961	0.37	524	234
BxB	25	2	D	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	3.196	0.37	565	254
BxB	L1+	1	D	1	994	984	976	980	980	976	968	960	944	924	852	804	746	734	710	676	634	.	.	.	.	.	3.562	0.21	417	56
BxB	L1+	2	D	1	998	999	996	998	992	992	986	974	940	918	838	754	748	680	652	636	600	.	.	.	.	.	1.217	0.26	421	60
BxB	L2+	1	D	1	990	988	984	988	982	984	982	976	960	946	878	812	752	708	672	700	650	654	.	.	.	.	0.402	0.31	358	40
BxB	L2+	2	D	1	992	990	980	978	970	974	974	962	946	924	856	790	734	694	632	622	634	.	.	.	.	.	1.292	0.26	420	54
BxB	D1+	1	D	1	996	986	968	954	920	878	846	830	778	764	722	738	726	714	676	696	702	680	670	656	656	.	18.41	0.51	318	222
BxB	D1+	2	D	1	996	988	974	970	948	906	880	846	818	798	760	764	768	742	714	716	722	694	690	686	682	682	19.06	0.46	303	182
BxB	D3+	1	D	1	968	956	926	890	852	818	786	762	724	704	680	674	692	686	666	688	670	640	630	618	632	598	38.59	0.84	352	276
BxB	D3+	2	D	1	976	966	930	898	862	828	798	772	738	706	700	696	702	696	684	666	668	640	616	612	612	612	43.23	0.87	358	262
BxB	U+	1	D	1	994	988	980	982	982	974	966	946	864	812	712	614	618	682	718	746	760	768	768	760	734	766	0.036	0.76	280	136
BxB	U+	2	D	1	998	996	988	990	992	988	976	962	888	832	724	650	638	704	738	750	764	768	776	740	716	724	0.006	.	277	112
BxB	L1-	1	D	1	980	994	984	994	994	994	994	988	992	994	996	994	994	990	990	994	990	992	992	999	994	996	.	.	8	8

Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	8	10	11	13	15	16	17	18	19	21	23	25	29	32	39	i	r	K	P10
BxB	L1-	2	D	1	986	996	986	992	992	994	994	994	988	994	996	.	990	992	992	990	988	992	996	994	992	994	.	.	12	12
BxB	L3-	1	D	1	984	996	988	998	998	998	996	992	994	996	998	996	996	996	996	999	996	998	998	996	996	998	108	.	3.36	6
BxB	L3-	2	D	1	984	988	980	988	986	988	988	984	986	988	988	988	988	988	986	990	986	988	990	988	990	992	11.88	.	11.9	14
BxB	D1-	1	D	1	988	998	990	999	996	996	998	998	998	996	994	996	994	994	996	998	994	990	984	904	724	326	21.25	.	.	2
BxB	D1-	2	D	1	980	996	992	996	990	992	994	992	994	990	994	994	990	992	992	994	992	988	982	956	910	616	14.35	.	.	6
BxB	D2-	1	D	1	994	992	988	990	992	990	992	990	990	990	988	984	980	974	966	944	872	780	658	470	402	318	0.083	0.19	667	10
BxB	D2-	2	D	1	996	986	980	986	986	986	984	986	982	984	982	978	972	966	982	958	910	848	700	544	472	390	0.071	0.19	600	18
BxB	U-	1	D	1	994	990	984	990	986	992	990	992	988	990	994	990	990	990	988	992	992	990	992	990	988	982	0.586	.	10.5	12
BxB	U-	2	D	1	992	990	982	990	990	992	990	986	990	990	990	992	990	990	988	990	990	990	992	990	990	988	1.346	.	10.5	10

					Day																									
Mating	Cross	Spore Rep.	Ass. Env.	Rep.	1	2	3	4	5	6	7	8	10	11	12	13	14	15	16	18	19	22	24	26	29	32	39	I	r	K	P10
AxA	1	1	D	2	992	990	992	992	990	988	988	984	970	962	956	932	912	888	854	740	678	562	510	498	.	.	.	0.46	0.2303	533	24
AxA	1	2	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	22.2	0.4108	305	99
AxA	2	1	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
AxA	2	2	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	12.5	0.288	200	83
AxA	3	1	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	12.1	0.4532	507	305
AxA	3	2	D	2	984	982	978	968	952	930	904	894	862	842	816	804	786	764	750	700	682	636	596	566	510	446	.	31.9	0.5423	570	132
AxA	4	1	D	2	988	994	992	990	990	992	990	990	990	992	990	990	988	992	992	990	988	980	948	874	624	540	374	0	0.266	613	4
AxA	4	2	D	2	984	982	984	986	990	988	990	988	986	988	988	984	988	986	984	978	978	928	824	724	596	526	412	0.08	0.1685	578	8
AxA	5	1	D	2	986	992	988	982	990	990	988	988	990	986	986	992	988	988	990	984	982	962	918	840	636	554	386	0.02	0.1882	614	4
AxA	5	2	D	2	982	986	984	974	972	960	940	910	828	772	732	652	604	578	534	472	432	386	366	.	.	.	.	6.82	0.3055	632	166
AxA	6	1	D	2	986	988	988	984	982	982	974	970	948	938	906	882	832	802	732	590	554	490	458	466	.	.	.	0.67	0.2671	554	46
AxA	6	2	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	26.9	.	.	89
AxA	7	1	D	2	994	996	996	994	994	990	988	984	966	944	914	884	828	774	720	656	640	610	578	560	.	.	.	0.39	0.3145	423	28
AxA	7	2	D	2	968	970	970	974	968	964	954	944	932	924	910	896	886	850	842	780	732	646	622	626	552	.	.	9.75	0.206	496	62
AxA	8	1	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	49	49
AxA	8	2	D	2	992	992	992	990	990	990	990	990	992	994	992	992	992	994	994	990	990	982	960	926	824	728	516	20.4	.	.	2
AxA	9	1	D	2	996	994	998	990	974	950	890	854	782	758	722	700	670	652	640	590	588	556	538	514	482	484	.	14.8	0.3891	485	212
AxA	9	2	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	25	25
AxA	10	1	D	2	990	988	986	980	974	968	956	942	884	852	802	710	670	634	592	516	474	418	396	.	.	.	.	4.2	0.2666	609	110
AxA	10	2	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1	3.6559	97.3	33
AxA	11	1	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	3.03	0.1786	813	69
AxA	11	2	D	2	978	986	986	982	982	968	958	938	880	822	774	746	636	602	566	496	456	434	462	554	636	.	.	0.9	0.3678	498	114
AxA	12	1	D	2	984	988	988	988	990	990	990	988	976	968	958	938	922	910	894	816	804	686	640	624	554	548	.	1.72	0.1432	467	18
AxA	12	2	D	2	978	988	988	986	988	990	990	990	984	988	978	970	966	956	946	934	922	886	852	796	704	620	518	2.19	0.0624	533	10
AxA	13	1	D	2	984	982	978	966	944	924	890	872	776	744	672	664	630	626	612	592	576	574	548	504	524	502	.	12.4	0.3949	464	218
AxA	13	2	D	2	988	986	970	950	912	860	798	764	718	710	708	680	678	650	638	586	542	480	426	426	392	360	.	52.3	0.9169	637	276
AxA	14	1	D	2	998	999	998	984	974	942	892	778	654	636	626	612	620	618	628	610	604	578	562	558	516	478	.	1.32	0.5639	422	340
AxA	14	2	D	2	994	992	986	964	940	904	778	714	642	602	590	578	564	552	540	494	470	444	440	432	.	.	.	15.2	0.5065	527	352
AxA	15	1	D	2	999	999	996	980	966	946	896	744	632	578	586	580	558	554	570	540	540	550	578	562	532	488	478	0.64	0.6624	456	362
AxA	15	2	D	2	988	986	980	960	930	916	812	708	612	600	580	582	590	590	590	570	598	568	562	536	518	484	470	2.93	0.5647	447	382
AxA	16	1	D	2	998	994	986	960	922	882	710	652	622	606	602	580	582	552	526	490	494	460	418	462	468	458	.	19.2	0.5777	518	372
AxA	16	2	D	2	984	994	996	994	996	996	998	996	984	976	968	950	914	888	854	700	632	542	496	486	.	.	.	0.08	0.3396	518	10
AxA	17	1	D	2	999	998	998	998	999	998	999	998	990	988	982	966	958	938	932	888	878	828	784	746	664	590	480	3.56	0.0819	549	4
AxA	17	2	D	2	988	984	986	988	990	984	978	970	932	900	880	840	812	762	734	690	676	632	576	560	.	.	.	3.85	0.2166	434	62
AxA	18	1	D	2	990	976	964	920	898	834	784	756	698	692	634	618	584	564	576	518	500	498	472	454	432	390	376	43.1	0.8233	570	296
AxA	18	2	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	18.1	0.614	517	347
AxA	19	1	D	2	988	990	982	964	924	890	744	668	636	610	598	586	584	584	598	576	564	546	500	518	488	474	.	5.9	0.5486	452	358
AxA	19	2	D	2	999	996	988	970	944	904	800	676	598	574	590	564	582	566	590	566	548	546	546	540	488	484	440	1.72	0.6357	460	396
AxA	20	1	D	2	984	986	980	946	912	880	722	654	610	598	592	538	552	544	538	510	504	526	512	542	498	462	456	8.82	0.5474	484	384
AxA	20	2	D	2	992	980	966	928	862	764	658	630	602	576	554	562	554	524	520	512	508	460	442	470	450	.	.	16.7	0.6503	499	392
AxA	21	1	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	16.3	0.3077	794	111
AxA	21	2	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	24.6	.	.	53
AxA	22	1	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
AxA	22	2	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	22.5	0.3857	594	99
AxA	23	1	D	2	988	984	986	974	970	956	942	936	902	874	848	822	780	734	692	560	536	448	404	386	314	324	.	7.87	0.2375	685	92

					Day																						
Mating	Cross	Spore Rep.	Ass. Env.	Rep.	1	2	3	4	5	6	7	8	10	11	12	13	14	15	16	18	19	22	24	26	29	32	39	I	r	K	P10
AxA	23	2	D	2	988	986	982	976	970	952	948	948	924	918	902	856	880	872	856	820	806	766	728	700	648	596	440	26.8	0.4082	667	70
AxA	24	1	D	2	988	986	986	968	962	942	914	908	884	880	858	854	834	800	790	750	712	670	638	614	552	426	366	31.9	0.5144	688	110
AxA	24	2	D	2	992	986	986	982	976	958	942	926	912	900	874	864	836	814	788	728	726	658	594	530	442	354	.	21.4	0.3543	779	82
AxA	25	1	D	2	980	980	978	974	962	948	926	886	776	722	676	620	592	562	530	462	446	400	410	.	.	.	.	8.57	0.3445	594	218
AxA	25	2	D	2	998	994	988	980	976	966	946	928	922	930	924	926	922	918	918	900	886	830	756	684	538	486	408	7.18	0.1244	675	72
AxA	L1+	1	D	2	999	999	999	998	996	998	994	992	980	978	954	936	900	878	810	700	618	508	492	484	.	.	.	0.15	0.3136	530	20
AxA	L1+	2	D	2	992	996	996	992	994	990	986	986	970	962	944	928	916	898	842	788	668	548	512	506	458	.	.	0.53	0.219	545	30
AxA	L2+	1	D	2	980	980	982	980	982	978	978	972	956	952	928	922	902	892	882	828	822	780	736	712	634	584	496	12.5	0.1993	540	44
AxA	L2+	2	D	2	998	990	992	990	990	988	988	988	976	964	942	930	904	896	854	804	774	714	650	604	528	486	.	4.61	0.1358	546	24
AxA	D1+	1	D	2	992	992	990	982	974	952	932	926	882	864	834	814	786	752	732	638	620	580	574	568	558	.	.	8.36	0.26	454	118
AxA	D1+	2	D	2	994	994	992	984	978	966	946	934	914	908	886	868	834	806	776	708	654	620	582	580	544	544	.	6.66	0.2112	464	86
AxA	D3+	1	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	11.5	0.3392	448	116
AxA	D3+	2	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	3.72	0.2637	492	156
AxA	U+	1	D	2	986	992	988	970	946	932	898	880	870	850	838	840	826	824	808	774	760	690	636	624	538	468	380	37.5	0.5991	700	130
AxA	U+	2	D	2	986	992	986	974	954	926	880	856	824	798	766	766	740	722	710	672	642	574	536	522	462	398	350	39.9	0.6783	637	176
AxA	L1-	1	D	2	988	988	986	982	986	988	986	990	988	990	986	986	986	986	986	978	974	920	826	754	634	570	472	0.11	0.1525	523	12
AxA	L1-	2	D	2	992	996	992	990	990	994	992	990	990	990	988	990	986	990	988	982	982	952	888	784	622	528	410	0.03	0.1932	588	10
AxA	L3-	1	D	2	992	990	992	990	992	994	998	996	992	992	990	994	992	984	986	974	968	888	792	714	636	568	422	0.35	0.1133	569	8
AxA	L3-	2	D	2	986	990	994	990	992	992	990	994	992	996	992	990	992	992	990	986	980	948	900	856	754	700	610	0.1	0.1312	395	8
AxA	D1-	1	D	2	990	986	984	970	942	908	840	720	566	528	528	540	550	548	544	486	520	486	460	464	438	422	428	2.5	0.5535	515	434
AxA	D1-	2	D	2	992	982	970	936	872	804	724	708	676	650	646	640	606	618	622	592	608	580	544	528	490	448	440	43.7	0.874	474	324
AxA	D2-	1	D	2	994	990	984	946	888	804	704	680	626	612	596	594	590	568	576	546	570	516	492	478	424	392	.	26.6	0.678	496	374
AxA	D2-	2	D	2	999	998	996	978	954	912	854	668	604	584	580	566	540	538	552	526	548	536	522	514	478	418	.	1.79	0.5971	477	396
AxA	U-	1	D	2	982	988	988	984	986	990	988	986	986	988	984	986	984	984	980	964	952	850	674	558	462	364	274	0.07	0.2023	698	14
AxA	U-	2	D	2	996	999	998	996	998	998	996	998	996	998	996	998	992	994	990	962	932	754	560	494	412	350	276	0.01	0.3008	672	4
BxB	1	1	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	4.36	0.2944	478	147
BxB	1	2	D	2	984	990	984	984	980	978	978	976	962	954	930	894	858	828	790	720	708	654	654	.	.	.	.	0.89	0.2448	362	44
BxB	2	1	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
BxB	2	2	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
BxB	3	1	D	2	998	994	980	956	924	860	774	746	660	630	604	576	576	542	554	518	498	474	456	446	402	388	.	25.8	0.6073	549	346
BxB	3	2	D	2	996	996	996	998	999	999	999	998	998	999	999	996	998	999	999	998	999	999	999	999	998	998	986	2.88	.	1.9	8
BxB	4	1	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	35
BxB	4	2	D	2	986	988	984	982	980	984	984	984	988	988	986	986	982	986	982	984	988	988	982	988	986	984	974	11.1	.	15.7	18
BxB	5	1	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	7.66	0.447	430	275
BxB	5	2	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	2.86	0.4516	442	267
BxB	6	1	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	25
BxB	6	2	D	2	988	998	994	986	990	988	986	986	982	978	976	976	972	970	968	954	950	924	904	878	828	780	686	3.45	0.0414	390	24
BxB	7	1	D	2	990	990	986	982	980	974	974	966	952	950	944	934	928	918	914	870	872	810	780	764	708	660	590	10.5	0.1624	445	54
BxB	7	2	D	2	978	986	984	980	976	972	966	962	952	948	942	930	918	914	916	894	884	850	820	808	754	730	672	14.3	0.2061	372	54
BxB	8	1	D	2	972	982	980	976	982	984	982	982	984	980	984	990	984	984	984	984	984	986	982	986	984	984	980	31.9	0.6888	16	22
BxB	8	2	D	2	984	988	990	986	988	990	992	990	988	988	990	990	988	988	990	986	988	992	990	990	988	990	990	.	.	18	18
BxB	9	1	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	29
BxB	9	2	D	2	999	994	992	988	992	990	992	992	992	988	992	992	992	992	994	990	992	994	994	996	992	994	988	0.09	.	8.2	14
BxB	10	1	D	2	990	988	986	978	970	962	942	898	784	744	700	678	652	678	680	706	734	768	766	758	702	650	660	0.17	0.7072	299	222
BxB	10	2	D	2	994	994	990	984	986	978	964	946	844	786	742	698	660	652	648	658	714	744	750	756	714	660	660	0.05	0.7333	308	162

					Day																						
Mating	Cross	Spore Rep.	Ass. Env.	Rep.	1	2	3	4	5	6	7	8	10	11	12	13	14	15	16	18	19	22	24	26	29	32	39	I	r	K	P10
BxB	11	1	D	2	984	986	984	966	948	888	786	654	460	390	334	294	302	288	306	270	302	306	312	.	.	.	400	1.76	0.6091	694	546
BxB	11	2	D	2	992	986	986	982	982	978	978	974	964	952	928	888	852	816	770	690	696	648	650	640	.	.	.	0.49	0.2906	362	42
BxB	12	1	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	15.8	0.5764	475	323
BxB	12	2	D	2	998	990	980	974	980	972	968	944	850	776	650	542	482	446	388	388	404	374	372	.	.	.	.	0.23	0.523	622	156
BxB	13	1	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	11.3	0.4182	538	263
BxB	13	2	D	2	999	998	994	964	926	876	824	778	718	692	672	644	634	618	616	620	622	634	634	636	628	604	.	7.18	0.4851	376	288
BxB	14	1	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	19	0.4951	459	221
BxB	14	2	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	11.1	0.4758	332	203
BxB	15	1	D	2	988	988	986	968	972	956	932	894	856	848	830	836	804	780	782	724	718	706	676	644	626	598	580	22.6	0.4158	400	150
BxB	15	2	D	2	990	988	990	986	982	970	962	934	828	774	720	676	640	620	626	696	730	750	746	770	768	760	696	0.03	0.8275	294	178
BxB	16	1	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	4.91	0.291	392	133
BxB	16	2	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1.49	0.5335	801	513
BxB	17	1	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	6.76	0.2573	482	115
BxB	17	2	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	4.07	0.3846	573	265
BxB	18	1	D	2	992	994	992	982	962	910	884	858	802	776	770	768	758	746	746	690	702	692	654	660	596	.	.	18.7	0.439	344	204
BxB	18	2	D	2	996	992	992	980	958	912	882	850	768	776	754	760	750	730	732	696	702	686	672	662	610	616	.	17.1	0.4377	341	238
BxB	19	1	D	2	988	986	972	942	904	864	824	792	712	690	674	670	670	640	638	608	596	552	558	550	.	.	.	24.2	0.5812	425	294
BxB	19	2	D	2	992	986	972	956	922	882	848	824	778	764	762	740	738	730	734	694	696	672	658	632	584	574	.	36	0.6766	381	228
BxB	20	1	D	2	988	990	986	982	980	972	962	946	854	816	760	710	704	718	750	752	760	780	794	784	772	744	724	0.04	0.7694	251	152
BxB	20	2	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	0.54	0.3814	458	163
BxB	21	1	D	2	992	988	988	980	980	970	946	918	840	808	774	738	700	692	710	708	728	752	730	716	704	.	.	0.74	0.479	286	166
BxB	21	2	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	9.99	0.3005	438	127
BxB	22	1	D	2	984	974	966	946	904	840	804	756	656	632	618	636	666	692	701	708	728	752	730	716	704	.	.	3.04	0.6795	312	350
BxB	22	2	D	2	990	986	988	982	978	972	966	960	920	890	854	818	786	780	742	742	702	622	.	.	.	.	.	5.63	0.2341	378	86
BxB	23	1	D	2	994	996	996	992	994	994	994	994	994	998	994	994	994	996	996	996	996	996	992	994	996	996	988	.	.	12	12
BxB	23	2	D	2	982	988	988	984	986	988	988	986	988	988	988	994	990	990	990	988	990	990	988	992	988	990	876	9.82	.	.	18
BxB	24	1	D	2	998	994	996	996	996	994	999	998	994	996	998	996	996	994	996	994	998	998	996	996	996	998	998	.	.	12	12
BxB	24	2	D	2	992	990	992	990	996	994	996	994	992	992	994	988	992	992	992	992	992	992	994	994	992	994	996	10.1	0.4844	7.11	14
BxB	25	1	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1	0.6652	389	.
BxB	25	2	D	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	5.25	0.444	435	267
BxB	L1+	1	D	2	992	992	990	986	988	984	978	980	966	950	926	882	834	806	772	726	700	636	630	.	.	.	.	1.05	0.243	378	34
BxB	L1+	2	D	2	999	996	998	996	994	994	986	984	964	946	912	862	804	754	724	654	626	584	.	.	.	.	.	0.31	0.3404	415	36
BxB	L2+	1	D	2	982	980	982	980	984	976	978	978	960	950	936	896	860	820	768	702	714	654	.	.	.	.	.	0.59	0.2739	359	40
BxB	L2+	2	D	2	994	988	990	990	992	984	982	976	956	942	912	856	812	770	722	660	636	582	.	.	.		.	0.64	0.2897	425	44
BxB	D1+	1	D	2	984	986	984	972	948	896	874	858	826	798	778	772	754	746	724	712	708	702	672	658	642	630	.	22.6	0.4847	340	174
BxB	D1+	2	D	2	988	986	982	970	948	888	874	850	796	788	760	750	728	720	726	674	686	682	656	640	614	624	.	21	0.4797	355	204
BxB	D3+	1	D	2	950	962	934	904	868	832	794	756	744	718	708	692	692	704	668	654	668	652	630	606	578	584	.	50.5	0.9599	382	56
BxB	D3+	2	D	2	972	966	948	914	878	834	806	780	744	746	710	696	700	694	696	658	684	640	628	620	580	578	.	45.7	0.8725	382	56
BxB	U+	1	D	2	982	992	990	986	988	984	976	968	918	882	826	754	710	682	654	610	644	742	760	758	748	688	626	0.02	0.714	310	82
BxB	U+	2	D	2	996	996	994	990	986	990	980	972	934	898	856	806	778	762	756	742	758	752	762	784	772	764	746	0.05	0.6016	242	66
BxB	L1-	1	D	2	986	992	992	986	990	990	990	990	986	994	990	992	990	992	990	988	994	990	988	990	994	994	990	.	.	14	14
BxB	L1-	2	D	2	984	992	988	988	986	986	990	984	986	982	980	986	984	984	994	984	986	988	984	988	982	984	968	11.8	0.0408	175	14
BxB	L3-	1	D	2	996	996	996	992	994	996	994	994	994	994	992	998	996	996	996	994	996	998	994	998	994	996	996	2.8	.	4.85	6
BxB	L3-	2	D	2	986	980	982	986	986	984	984	984	984	984	984	986	974	988	988	984	986	988	984	984	984	984	988	16.4	0.1128	6.9	16
BxB	D1-	1	D	2	999	999	999	998	998	998	996	998	998	999	996	998	998	999	999	998	996	998	990	982	932	790	370	17	0.1578	.	2

					Day																										
Mating	Cross	Spore Rep.	Ass. Env.	Rep.	1	2	3	4	5	6	7	8	10	11	12	13	14	15	16	18	19	22	24	26	29	32	39	l	r	K	P10
BxB	D1-	2	D	2	999	999	999	999	999	999	999	999	999	999	999	999	999	999	999	999	999	999	999	992	968	934	684	8.19	0.0037	.	2
BxB	D2-	1	D	2	994	999	999	998	999	999	999	999	996	996	996	998	994	990	998	978	968	898	790	682	544	496	378	0.05	0.194	598	4
BxB	D2-	2	D	2	998	998	996	994	994	996	994	996	996	996	994	994	992	990	992	980	980	912	824	690	556	474	340	0.07	0.1753	646	4
BxB	U-	1	D	2	990	990	988	990	990	988	988	992	988	994	990	990	988	990	992	992	990	992	988	988	992	992	994	.	.	12	12
BxB	U-	2	D	2	996	992	992	992	992	992	990	992	992	994	992	992	990	996	996	990	992	996	990	990	988	992	998	.	.	8	8

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	8	9	12	14	19	i	r	K	P10
AxA	1	2	D	1	964	960	956	952	944	936	926	912	890	820	820	714	16.5	0.337	542	100
AxA	2	2	D	1	972	976	970	966	962	952	946	936	926	896	886	826	12.6	0.247	402	64
AxA	3	1	D	1	952	954	926	912	884	854	794	734	716	670	626	522	20.3	0.531	614	274
AxA	6	2	D	1	976	980	980	978	970	966	952	926	906	844	770	678	1.25	0.189	519	84
AxA	8	1	D	1	972	972	978	978	978	978	978	976	978	978	982	974	.	.	12	12
AxA	9	2	D	1	970	976	976	976	974	980	982	980	978	974	374	958	32.3	0.483	.	12
AxA	10	2	D	1	976	982	982	980	984	980	986	984	984	984	988	978	.	.	6	6
AxA	11	1	D	1	986	986	988	982	974	966	958	936	916	840	782	566	1.64	0.161	771	74
AxA	18	2	D	1	956	944	908	848	796	736	690	670	662	614	576	494	19.1	0.627	605	328
AxA	21	1	D	1	980	984	980	972	966	954	942	924	896	856	802	562	8.42	0.202	.	94
AxA	21	2	D	1	986	990	984	984	982	982	978	972	964	936	920	788	.	.	.	26
AxA	22	2	D	1	960	958	948	938	944	926	920	902	904	878	860	836	23.6	0.454	337	86
AxA	D2+	1	D	1	982	980	970	956	946	920	890	856	830	756	710	594	8.97	0.303	588	170
AxA	D2+	3	D	1	972	978	970	960	948	916	900	860	830	772	726	602	10.7	0.312	593	170
BxB	1	1	D	1	964	970	968	966	954	948	932	908	870	734	674	600	0.45	0.247	574	120
BxB	4	1	D	1	960	976	980	982	976	982	978	976	976	972	980	984	18.6	0.18	176	14
BxB	5	1	D	1	966	966	950	924	908	854	794	768	712	692	656	680	1.51	0.44	491	278
BxB	5	2	D	1	980	982	970	954	942	906	844	780	744	640	608	738	1	0.442	551	246
BxB	6	1	D	1	978	976	980	982	982	978	982	976	978	978	984	986	.	.	12	12
BxB	9	1	D	1	980	988	988	986	984	986	986	984	986	986	990	992	28.8	.	4	4
BxB	12	1	D	1	946	932	902	836	818	784	754	716	704	636	632	612	22.1	0.655	530	286
BxB	13	1	D	1	974	982	972	958	946	918	894	866	838	790	760	736	18.1	0.365	929	152
BxB	14	1	D	1	964	956	920	898	880	852	828	814	790	754	716	746	52.5	.	.	200
BxB	14	2	D	1	972	960	930	892	866	840	824	802	792	774	742	754	57.5	.	.	196
BxB	16	1	D	1	962	972	964	958	948	934	910	874	816	678	636	606	1.54	0.28	604	174
BxB	16	2	D	1	962	960	946	908	854	764	652	504	438	348	316	290	1	0.582	833	552
BxB	17	1	D	1	962	972	964	960	950	938	918	888	836	692	630	644	2.66	0.257	675	154

					Day														
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	8	9	12	14	19	i	r	K	P10
BxB	17	2	D	1	940	956	948	936	902	852	810	722	656	538	488	442	3.9	0.395	692	334
BxB	20	2	D	1	986	986	986	982	974	962	940	896	832	688	620	712	1	0.423	569	158
BxB	21	2	D	1	964	970	968	962	964	950	946	932	902	818	750	658	5.95	0.223	472	88
BxB	25	1	D	1	966	964	958	946	930	894	840	778	756	684	664	668	1.96	0.372	524	234
BxB	25	2	D	1	976	968	954	940	920	872	830	794	736	640	634	728	3.2	0.371	565	254
CxC	1	1	D	1	968	978	958	936	930	886	830	746	634	462	410	398	2.93	0.445	609	358
CxC	1	2	D	1	976	980	974	972	962	944	914	888	832	538	438	306	1.68	0.36	704	160
CxC	2	1	D	1	972	974	956	952	926	888	840	768	664	366	340	334	1.94	0.455	690	328
CxC	2	2	D	1	976	984	970	942	924	890	854	812	750	480	336	254	5.24	0.357	774	242
CxC	3	1	D	1	978	986	978	956	926	872	782	600	552	524	476	424	0.3	0.761	530	440
CxC	3	2	D	1	990	986	978	966	934	878	786	606	524	514	526	420	0.09	.	519	468
CxC	4	1	D	1	978	984	976	966	922	850	708	616	600	580	532	458	0.37	0.779	474	392
CxC	4	2	D	1	986	988	972	926	858	710	616	582	544	518	482	400	1.31	0.713	524	448
CxC	5	1	D	1	968	972	952	938	908	840	782	692	606	434	374	338	5.81	0.439	659	386
CxC	5	2	D	1	962	964	940	904	866	784	690	568	484	410	394	292	5.07	0.522	654	508
CxC	6	1	D	1	972	972	952	934	906	844	764	664	578	428	372	318	5.3	0.454	664	414
CxC	6	2	D	1	978	976	952	926	884	822	752	610	530	406	378	340	3.45	0.507	643	462
CxC	7	1	D	1	972	982	968	968	958	928	896	828	690	422	384	290	1.3	0.446	694	302
CxC	7	2	D	1	988	988	980	976	964	948	926	898	846	566	420	282	1.38	0.359	734	146
CxC	8	1	D	1	966	958	924	876	834	706	624	528	470	380	346	322	7.14	0.555	661	522
CxC	8	2	D	1	984	978	974	926	894	790	688	596	582	544	512	448	1.38	0.652	499	410
CxC	9	1	D	1	992	988	976	966	946	904	804	678	504	350	316	328	0.3	0.696	682	488
CxC	9	2	D	1	990	988	978	966	924	838	704	632	602	612	586	530	2.15	0.552	522	390
CxC	10	1	D	1	980	972	952	946	914	820	722	600	486	362	330	276	1.63	0.576	669	506
CxC	10	2	D	1	978	986	978	972	956	946	928	914	876	538	432	334	1.12	0.367	756	116
CxC	11	1	D	1	976	966	948	906	846	716	580	438	412	370	336	254	1.56	0.688	672	580
CxC	11	2	D	1	974	970	934	886	802	652	556	508	488	416	354	284	8.75	0.574	678	504

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	8	9	12	14	19	i	r	K	P10
CxC	12	1	D	1	974	960	942	928	830	654	512	404	358	312	298	218	0.88	0.791	698	634
CxC	12	2	D	1	982	992	980	968	946	888	780	648	546	420	380	288	0.46	0.67	609	446
CxC	13	1	D	1	982	984	966	946	906	828	710	620	594	532	486	396	7.31	0.467	606	398
CxC	13	2	D	1	980	980	956	906	838	660	522	426	412	396	364	284	0.4	.	619	580
CxC	14	1	D	1	980	982	974	966	916	820	662	594	584	564	526	448	0.62	0.73	513	408
CxC	14	2	D	1	952	942	902	796	692	550	522	468	454	454	418	356	3.78	0.765	572	538
CxC	15	1	D	1	988	990	982	972	946	908	836	720	658	576	536	398	2.92	0.44	533	334
CxC	15	2	D	1	978	976	968	950	930	870	772	724	644	546	502	396	2.43	0.498	494	348
CxC	16	1	D	1	980	992	990	994	988	990	990	988	990	992	992	992	.	.	2	2
CxC	16	2	D	1	986	988	984	992	988	994	992	994	986	986	992	992	.	.	6	6
CxC	17	1	D	1	972	978	942	908	784	620	560	526	488	406	358	264	6.64	0.589	654	504
CxC	17	2	D	1	972	978	968	952	932	870	762	676	580	500	456	362	2.35	0.505	581	412
CxC	18	1	D	1	976	990	990	978	966	940	884	816	624	396	386	370	0.1	0.737	628	368
CxC	18	2	D	1	986	994	996	996	996	992	992	994	992	988	988	974	5.06	.	464	10
CxC	19	1	D	1	984	996	996	966	992	994	994	996	996	996	996	986	23	0.389	6.62	.
CxC	19	2	D	1	992	996	994	992	990	988	988	982	982	946	918	852	1.11	0.17	185	10
CxC	20	1	D	1	990	994	996	990	978	952	900	832	716	572	516	424	1.3	0.436	544	276
CxC	20	2	D	1	976	982	970	952	922	844	724	612	516	422	378	266	2.06	0.539	663	476
CxC	21	1	D	1	988	994	980	970	950	900	842	768	664	512	470	374	2.93	0.42	594	328
CxC	21	2	D	1	966	956	936	914	878	762	636	506	410	364	332	256	2.38	0.599	694	582
CxC	22	1	D	1	968	970	946	926	898	862	812	738	648	464	430	300	11	0.423	694	344
CxC	22	2	D	1	974	972	958	942	922	874	814	738	594	444	398	294	5.26	0.418	680	398
CxC	23	1	D	1	978	974	950	936	906	884	866	806	764	684	616	516	16.5	0.424	502	228
CxC	23	2	D	1	966	960	906	818	666	550	514	498	450	426	424	340	3.73	0.756	587	542
CxC	24	1	D	1	968	940	892	778	640	558	506	452	450	414	438	370	4.5	0.769	584	542
CxC	24	2	D	1	986	982	962	940	874	756	604	560	512	494	434	416	0.79	0.757	548	480
CxC	25	1	D	1	999	999	990	982	970	954	922	876	806	428	346	306	0.26	0.543	699	186

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	8	9	12	14	19	i	r	K	P10
CxC	25	2	D	1	988	984	988	986	984	984	990	976	982	984	980	986	9.96	0.303	17.4	10
CxC	L1+	1	D	1	962	958	916	898	836	736	632	536	464	338	288	252	8.63	0.529	729	528
CxC	L2+	2	D	1	974	976	976	976	976	978	980	976	978	976	980	982	.	.	14	14
CxC	D1+	1	D	1	948	922	876	698	590	520	536	488	528	462	396	340	8.27	0.789	564	464
CxC	D2+	2	D	1	980	970	944	922	808	730	572	584	542	528	496	468	1.18	0.767	497	450
CxC	U+	1	D	1	962	960	940	890	838	744	662	630	600	532	482	386	13.2	0.545	554	392
CxC	L1-	1	D	1	954	952	926	894	800	698	602	538	468	388	348	342	7.45	0.566	648	524
CxC	L2-	2	D	1	952	950	910	858	782	654	556	496	426	370	352	338	6.87	0.607	651	566
CxC	D1-	1	D	1	954	948	878	792	730	632	594	568	540	470	426	326	26.5	0.749	605	452
CxC	D2-	2	D	1	984	982	970	956	940	892	806	710	646	566	516	406	3.63	0.443	537	346
CxC	U-	1	D	1	962	952	920	874	818	702	624	600	564	492	464	362	13.3	0.576	574	428
DxD	1	1	D	1	982	974	948	920	860	726	592	520	470	360	320	296	3.41	0.581	677	514
DxD	1	2	D	1	978	990	988	986	986	988	988	988	988	988	982	966	10.4	0.028	147	10
DxD	2	1	D	1	976	972	954	926	900	838	760	690	642	588	514	520	4.67	0.486	473	342
DxD	2	2	D	1	974	972	950	940	924	878	810	722	640	468	398	350	5.37	0.417	646	344
DxD	3	1	D	1	978	976	958	944	922	876	818	718	620	376	328	304	2.99	0.445	705	364
DxD	3	2	D	1	974	966	932	886	804	636	522	460	426	392	366	380	1.43	0.767	616	558
DxD	4	1	D	1	976	966	946	904	846	750	696	644	624	558	514	436	9.84	0.523	511	360
DxD	4	2	D	1	972	962	938	900	794	620	496	432	394	322	314	336	1.65	0.742	673	590
DxD	5	1	D	1	980	974	950	936	884	772	664	546	482	410	402	322	1.35	0.655	599	502
DxD	5	2	D	1	990	976	958	936	866	738	608	474	410	320	284	302	1.42	0.664	700	574
DxD	6	1	D	1	988	999	999	999	998	999	998	996	999	999	999	992	.	.	0	0
DxD	6	2	D	1	972	966	934	890	822	692	604	544	514	446	420	356	3.64	0.625	563	470
DxD	7	1	D	1	974	966	974	962	952	920	862	766	646	450	382	364	3.36	0.401	707	338
DxD	7	2	D	1	978	982	982	984	984	986	984	982	986	984	988	978	.	.	0	0
DxD	8	1	D	1	982	980	952	934	912	828	748	630	524	344	296	272	3.05	0.497	715	460
DxD	8	2	D	1	976	972	950	928	908	824	732	604	516	340	302	284	3.08	0.508	708	468

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	8	9	12	14	19	i	r	K	P10
DxD	9	1	D	1	982	978	960	938	912	842	754	660	544	356	288	334	3.54	0.472	726	440
DxD	9	2	D	1	984	980	956	944	910	828	734	618	496	338	304	314	2.32	0.526	713	488
DxD	10	1	D	1	972	962	924	888	836	724	638	512	438	312	276	274	6.32	0.541	727	546
DxD	10	2	D	1	976	974	954	922	906	862	788	682	578	356	290	274	4.43	0.443	742	406
DxD	11	1	D	1	960	944	896	818	714	616	550	518	528	456	412	326	12.7	0.656	590	456
DxD	11	2	D	1	976	968	942	930	880	778	672	570	520	410	400	264	5.62	0.508	665	464
DxD	12	1	D	1	968	962	956	942	912	888	856	804	756	532	422	342	11.6	0.373	810	228
DxD	12	2	D	1	966	954	922	896	834	702	562	454	442	366	324	256	5.06	0.58	707	542
DxD	13	1	D	1	982	972	948	910	838	672	580	516	486	358	316	240	3.97	0.594	654	498
DxD	13	2	D	1	978	958	944	890	824	676	556	478	452	350	294	210	6.11	0.571	716	532
DxD	14	1	D	1	972	952	914	864	792	674	630	550	538	478	466	350	6.08	0.617	527	446
DxD	14	2	D	1	972	950	912	838	760	626	536	470	436	328	292	224	11.7	0.607	722	548
DxD	15	1	D	1	980	980	984	986	986	986	984	984	984	986	942	716	11.4	0.064	374	14
DxD	15	2	D	1	948	924	842	718	578	514	464	438	420	348	310	232	12.1	0.762	644	564
DxD	16	1	D	1	980	986	986	980	984	984	984	984	984	984	994	994	.	.	0	0
DxD	16	2	D	1	976	988	986	990	986	986	984	984	988	984	990	992	15.9	0.102	13.3	16
DxD	17	1	D	1	980	984	970	948	908	850	760	614	476	368	330	234	1.62	0.553	709	508
DxD	17	2	D	1	986	978	964	954	932	860	758	588	496	406	370	308	0.67	0.656	647	488
DxD	18	1	D	1	976	982	978	962	930	894	816	700	564	328	266	258	1.27	0.52	745	420
DxD	18	2	D	1	994	992	982	970	954	904	848	726	554	428	390	310	0.44	0.628	641	430
DxD	19	1	D	1	972	956	910	844	762	716	668	634	612	544	522	440	18.7	0.633	507	372
DxD	19	2	D	1	962	962	928	884	816	700	560	434	384	328	300	282	3.02	0.633	702	600
DxD	20	1	D	1	984	982	966	954	934	874	780	608	480	334	300	254	0.68	0.631	717	504
DxD	20	2	D	1	966	976	968	960	944	912	836	738	624	282	234	256	0.21	0.698	636	360
DxD	21	1	D	1	986	988	994	998	994	994	996	992	992	968	884	580	10.5	0.009	.	0
DxD	21	2	D	1	984	984	984	984	984	984	984	986	984	980	976	674	12.9	0.078	104	18
DxD	22	1	D	1	986	994	994	994	992	990	996	994	996	992	999	998	.	.	0	0

					Day															
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	8	9	12	14	19	i	r	K	P10
DxD	22	2	D	1	964	952	938	918	910	894	872	840	826	770	740	652	47.6	0.65	.	158
DxD	23	1	D	1	976	972	958	934	910	864	822	778	660	410	390	354	5.25	0.403	689	324
DxD	23	2	D	1	984	988	980	970	962	952	938	918	880	682	550	490	2.76	0.282	717	104
DxD	24	1	D	1	974	958	926	884	848	782	694	598	554	494	454	332	7.1	0.529	552	430
DxD	24	2	D	1	962	950	904	848	774	710	670	624	614	556	518	434	12.4	0.615	461	370
DxD	25	1	D	1	972	974	976	976	976	976	974	978	970	966	960	900	36.4	0.457	.	14
DxD	25	2	D	1	980	984	978	968	966	958	940	920	886	722	586	336	2.01	0.3	549	98
DxD	L1+	1	D	1	966	968	970	982	976	980	984	978	980	978	978	964	.	.	4	4
DxD	L2+	2	D	1	970	976	974	974	974	968	972	974	974	976	974	988	.	.	10	10
DxD	D1+	1	D	1	974	962	930	890	824	730	592	522	486	414	388	350	4.51	0.587	619	498
DxD	D2+	2	D	1	960	942	890	818	742	668	638	578	564	498	466	350	43.1	0.913	661	420
DxD	U+	1	D	1	974	974	970	964	960	954	940	914	876	658	560	478	2.66	0.295	645	108
DxD	L1-	1	D	1	988	986	964	948	938	888	818	730	626	362	302	290	1.9	0.472	710	358
DxD	L2-	2	D	1	984	986	962	960	950	904	842	750	620	360	330	310	1.12	0.508	700	364
DxD	D1-	1	D	1	982	974	948	906	840	720	598	512	466	392	336	258	3.59	0.589	657	518
DxD	D2-	2	D	1	998	990	974	956	932	864	766	646	518	404	350	310	0.82	0.615	638	466
DxD	U-	1	D	1	982	984	976	978	974	968	964	958	938	892	836	596	17.9	0.136	.	46

					Day															
Mating	Cross	Spore	Ass.Env.	Rep.	1	2	3	4	5	6	7	8	9	12	14	19	i	r	K	P10
AxA	1	2	D	2	970	968	958	952	936	940	926	918	920	890	856	822	22.2	0.41	305	99
AxA	2	2	D	2	978	974	972	968	964	956	952	948	936	918	904	892	12.5	0.29	200	83
AxA	3	1	D	2	974	964	950	924	906	878	836	758	714	668	652	540	12.1	0.45	507	305
AxA	6	2	D	2	982	982	974	970	966	968	950	946	930	882	844	604	26.9	.	.	89
AxA	8	1	D	2	972	972	968	968	968	972	972	974	970	970	974	966	.	.	49	49
AxA	9	2	D	2	992	996	994	994	990	990	992	996	994	992	994	988	.	.	25	25
AxA	10	2	D	2	980	978	980	980	976	986	974	978	986	986	984	.	1	3.66	97.3	33
AxA	11	1	D	2	992	990	988	988	982	974	972	962	950	882	836	590	3.03	0.18	813	69
AxA	18	2	D	2	962	936	916	872	820	770	722	690	672	608	566	552	18.1	0.61	517	347
AxA	21	1	D	2	978	974	970	962	958	948	934	924	908	860	836	680	16.3	0.31	794	111
AxA	21	2	D	2	984	990	986	984	978	980	972	972	966	934	884	624	24.6	.	.	53
AxA	22	2	D	2	966	966	958	954	950	944	930	922	920	892	842	764	22.5	0.39	594	99
AxA	D2+	2	D	2	972	974	962	958	952	936	914	874	844	788	750	656	11.5	0.31	448	116
AxA	D2+	4	D	2	992	988	984	976	968	966	948	922	884	788	746	616	3.72	0.26	492	156
BxB	1	1	D	2	972	970	966	962	958	946	936	912	872	760	694	624	4.36	0.29	478	147
BxB	4	1	D	2	972	986	976	974	982	982	980	984	984	980	986	982	.	.	.	35
BxB	5	1	D	2	966	960	948	932	914	868	836	790	744	684	666	.	7.66	0.45	430	275
BxB	5	2	D	2	978	966	966	952	932	896	838	794	752	650	660	.	2.86	0.45	442	267
BxB	6	1	D	2	992	992	990	990	990	990	990	994	994	992	994	988	.	.	.	25
BxB	9	1	D	2	990	990	990	986	992	990	986	990	990	992	992	998	.	.	.	29
BxB	12	1	D	2	952	946	926	886	844	792	760	718	696	640	616	596	15.8	0.58	475	323
BxB	13	1	D	2	972	976	970	942	922	876	832	794	756	660	630	530	11.3	0.42	538	263
BxB	14	1	D	2	980	964	948	920	898	868	834	810	798	720	692	618	19	0.5	459	221
BxB	14	2	D	2	972	964	950	920	894	876	848	824	816	758	750	754	11.1	0.48	332	203
BxB	16	1	D	2	976	974	964	962	960	952	930	920	886	796	748	706	4.91	0.29	392	133
BxB	16	2	D	2	974	972	954	928	890	850	774	640	506	308	292	296	1.49	0.53	801	513

					Day																
Mating	Cross	Spore	Ass.Env.	Rep.	1	2	3	4	5	6	7	8	9	12	14	19	i	r	K	P10
BxB	17	1	D	2	966	974	970	966	960	950	942	932	904	840	746	658	6.76	0.26	482	115
BxB	17	2	D	2	966	960	958	946	938	914	878	826	754	600	554	516	4.07	0.38	573	265
BxB	20	2	D	2	988	980	984	978	976	968	942	914	856	716	680	618	0.54	0.38	458	163
BxB	21	2	D	2	960	964	960	956	954	946	930	916	892	816	752	688	9.99	0.3	438	127
BxB	25	1	D	2	996	996	994	984	978	962	942	898	830	696	714	686	1	0.67	389	.
BxB	25	2	D	2	968	966	952	938	922	886	830	778	752	670	660	.	5.25	0.44	435	267
CxC	1	1	D	2	974	974	960	942	930	896	860	812	714	466	372	364	2.9	0.4	662	294
CxC	1	2	D	2	986	988	980	976	974	960	934	904	870	594	482	340	1.08	0.37	668	138
CxC	2	1	D	2	974	970	956	930	918	878	824	740	634	436	396	340	4.42	0.42	658	374
CxC	2	2	D	2	990	982	976	968	954	934	922	906	868	630	406	254	1.61	0.34	779	140
CxC	3	1	D	2	992	990	984	968	946	916	846	752	594	318	296	.	0.53	0.59	729	414
CxC	3	2	D	2	999	996	986	970	954	914	850	770	592	282	272	.	0.37	0.61	759	416
CxC	4	1	D	2	999	994	986	968	944	900	812	640	540	512	490	442	0.07	.	523	468
CxC	4	2	D	2	990	980	970	948	890	776	628	510	488	482	490	410	0.17	.	541	520
CxC	5	1	D	2	968	964	950	934	922	872	824	780	726	490	398	324	8.16	0.39	697	282
CxC	5	2	D	2	978	962	944	910	884	826	736	634	548	430	390	294	7.54	0.47	668	460
CxC	6	1	D	2	978	974	960	930	912	864	792	700	594	420	394	326	4.18	0.45	658	414
CxC	6	2	D	2	968	966	948	934	894	862	800	738	640	334	314	318	3.65	0.44	718	368
CxC	7	1	D	2	982	970	954	944	934	906	840	780	658	398	364	290	2.74	0.42	707	350
CxC	7	2	D	2	986	982	982	972	960	950	922	886	836	588	480	352	1.9	0.35	659	172
CxC	8	1	D	2	974	960	940	908	876	788	708	610	526	408	382	332	6.11	0.5	648	482
CxC	8	2	D	2	980	972	956	932	906	802	680	552	492	488	472	396	0.58	0.76	554	516
CxC	9	1	D	2	986	990	974	964	952	908	838	730	584	480	476	.	0.25	0.71	533	424
CxC	9	2	D	2	992	990	978	958	928	878	760	618	550	502	506	500	0.16	0.83	501	458
CxC	10	1	D	2	984	964	938	930	916	858	816	756	652	342	328	264	4.34	0.42	748	356
CxC	10	2	D	2	996	998	990	982	972	962	950	934	922	676	486	362	0.36	0.42	653	86

					Day															
Mating	Cross	Spore	Ass.Env.	Rep.	1	2	3	4	5	6	7	8	9	12	14	19	i	r	K	P10
CxC	11	1	D	2	980	970	944	912	880	784	618	486	418	368	338	260	1.45	0.66	685	590
CxC	11	2	D	2	978	964	952	914	870	766	620	498	442	372	356	268	2.09	0.62	674	566
CxC	12	1	D	2	980	966	950	912	878	776	592	480	448	386	342	268	1.58	0.66	671	560
CxC	12	2	D	2	990	990	982	970	950	908	834	708	530	262	240	220	0.37	0.65	778	478
CxC	13	1	D	2	984	986	970	952	932	874	770	680	604	488	480	384	2.05	0.52	567	404
CxC	13	2	D	2	998	988	962	932	868	742	546	428	358	254	.	.	0.71	0.77	736	650
CxC	14	1	D	2	994	986	978	962	934	868	728	570	478	372	366	330	0.32	0.76	647	530
CxC	14	2	D	2	968	938	884	814	678	552	468	380	332	312	296	326	5.05	0.71	692	676
CxC	15	1	D	2	999	994	986	974	966	934	866	800	704	572	522	452	1.56	0.45	520	304
CxC	15	2	D	2	984	976	968	954	940	910	846	750	652	516	478	380	3.26	0.42	588	356
CxC	16	1	D	2	982	980	970	978	980	976	972	986	984	982	980	984	0.21	.	20.7	24
CxC	16	2	D	2	999	999	996	996	996	999	992	999	999	996	998	999	.	.	8	8
CxC	17	1	D	2	986	976	958	918	866	748	592	492	486	400	352	266	2.43	0.61	661	522
CxC	17	2	D	2	984	982	976	966	940	898	834	728	620	342	346	262	1.42	0.49	718	388
CxC	18	1	D	2	996	990	988	984	974	964	932	886	794	352	302	308	0.03	0.78	708	214
CxC	18	2	D	2	998	998	994	996	992	990	992	996	994	992	990	934	3.56	.	.	14
CxC	19	1	D	2	982	982	982	986	980	982	978	988	992	980	980	990	.	.	16	16
CxC	19	2	D	2	999	994	994	982	984	980	976	980	974	948	902	824	2.51	0.14	258	34
CxC	20	1	D	2	998	994	994	988	984	974	962	932	880	604	566	436	0.34	0.46	547	128
CxC	20	2	D	2	976	984	974	968	956	930	862	758	642	402	346	280	1.26	0.48	702	366
CxC	21	1	D	2	994	992	980	960	940	912	838	766	652	430	408	310	2.2	0.44	665	356
CxC	21	2	D	2	976	970	948	910	882	788	656	532	450	374	360	276	2.4	0.59	674	558
CxC	22	1	D	2	976	969	952	924	890	840	778	694	580	432	390	266	9.25	0.44	707	428
CxC	22	2	D	2	978	968	954	928	904	852	774	674	564	406	388	288	5.03	0.45	680	444
CxC	23	1	D	2	974	954	936	910	886	824	770	698	658	566	532	456	12.7	0.48	521	350
CxC	23	2	D	2	976	954	914	810	690	582	528	444	444	376	408	400	3.86	0.73	599	564

					Day															
Mating	Cross	Spore	Ass.Env.	Rep.	1	2	3	4	5	6	7	8	9	12	14	19	i	r	K	P10
CxC	24	1	D	2	972	954	916	822	676	570	526	444	418	416	400	362	3.36	0.75	603	590
CxC	24	2	D	2	990	984	962	950	934	876	762	626	504	262	250	.	1.09	0.57	770	504
CxC	25	1	D	2	984	988	978	968	964	942	916	878	826	464	366	346	0.33	0.52	670	182
CxC	25	2	D	2	990	988	984	980	980	982	978	982	980	976	974	970	10.4	0.16	31.8	28
CxC	L1+	1	D	2	968	952	924	908	870	774	660	530	442	336	310	270	4.08	0.54	710	566
CxC	L2+	2	D	2	974	968	972	974	976	974	976	974	976	972	976	982	.	.	32	32
CxC	D1+	1	D	2	960	940	900	788	660	576	572	534	552	488	458	388	7.37	0.72	531	456
CxC	D2+	2	D	2	986	970	946	912	820	666	608	578	562	536	536	454	0.89	0.83	480	446
CxC	U+	2	D	2	960	942	938	904	870	780	682	584	538	470	418	330	7.04	0.49	580	412
CxC	L1-	1	D	2	948	944	912	878	832	752	668	570	492	384	378	356	9.23	0.54	645	516
CxC	L2-	2	D	2	954	936	930	876	816	702	606	532	456	362	338	346	7.38	0.57	660	552
CxC	D1-	1	D	2	968	946	918	846	792	710	650	604	586	502	460	372	19.9	0.63	578	422
CxC	D2-	2	D	2	988	980	968	950	932	892	810	734	650	542	522	380	5.65	20	571	358
CxC	U-	2	D	2	980	966	952	924	866	808	704	636	596	482	460	380	8.12	0.51	619	470
DxD	1	1	D	2	984	980	960	934	884	802	676	530	456	338	306	250	2.08	0.58	713	560
DxD	1	2	D	2	988	990	992	992	990	990	992	994	992	986	984	970	7.63	.	578	24
DxD	2	1	D	2	978	970	956	924	892	818	732	638	572	460	420	330	6.3	0.47	628	444
DxD	2	2	D	2	956	956	936	924	906	866	798	706	634	450	392	348	7.47	0.43	658	382
DxD	3	1	D	2	988	980	960	954	940	914	862	810	724	478	384	316	3.33	0.38	693	292
DxD	3	2	D	2	980	966	932	882	794	648	532	458	434	366	390	368	1.87	0.73	622	582
DxD	4	1	D	2	984	964	958	950	924	856	766	658	600	546	510	428	2.04	0.54	519	416
DxD	4	2	D	2	976	962	942	910	836	716	568	454	426	330	316	.	1.98	0.66	676	590
DxD	5	1	D	2	982	968	946	926	884	800	680	548	478	390	380	336	1.93	0.6	639	538
DxD	5	2	D	2	986	976	950	912	862	752	668	510	416	316	284	290	2.52	0.59	713	600
DxD	6	1	D	2	992	994	990	986	984	988	984	990	990	992	992	992	2.37	0.81	11.1	26
DxD	6	2	D	2	984	972	948	898	838	710	600	522	490	444	418	360	2.53	0.64	592	526

					Day											
Mating	Cross	Spore	Ass.Env.	Rep.	1	2	3	4	5	6	7	8	9	12	14	19	i	r	K	P10
DxD	7	1	D	2	986	984	980	976	972	962	928	874	758	418	352	360	0.1	0.67	654	258
DxD	7	2	D	2	984	984	980	984	986	984	988	990	990	982	990	988	.	.	26	26
DxD	8	1	D	2	986	984	966	958	940	902	824	724	620	390	332	302	1.81	0.48	696	396
DxD	8	2	D	2	980	976	956	940	930	902	840	772	670	414	334	244	4.33	0.39	759	346
DxD	9	1	D	2	970	964	942	918	884	822	748	646	566	344	300	280	6.31	0.46	731	450
DxD	9	2	D	2	986	986	980	952	930	896	822	740	634	402	324	266	3.04	0.43	729	382
DxD	10	1	D	2	968	962	944	914	870	790	692	596	504	342	302	.	5.69	0.5	713	512
DxD	10	2	D	2	984	982	964	954	946	920	874	800	708	410	334	304	1.45	0.45	708	308
DxD	11	1	D	2	974	958	936	902	818	690	562	456	434	354	346	286	2.93	0.64	671	582
DxD	11	2	D	2	982	966	948	926	888	822	730	644	584	414	392	320	6.72	0.47	658	432
DxD	12	1	D	2	978	962	966	950	928	910	888	856	804	660	546	390	10.4	0.34	664	212
DxD	12	2	D	2	978	960	954	934	884	820	738	608	458	338	304	278	2.48	0.54	713	558
DxD	13	1	D	2	984	970	944	888	850	754	600	494	438	344	306	256	3.77	0.57	707	578
DxD	13	2	D	2	976	968	940	906	840	718	624	496	468	358	312	268	4.59	0.56	698	548
DxD	14	1	D	2	976	954	918	850	788	702	634	578	560	498	460	408	11.2	0.59	550	456
DxD	14	2	D	2	968	950	920	858	786	652	542	450	430	358	298	280	6.39	0.61	691	586
DxD	15	1	D	2	976	978	980	976	976	978	976	978	980	968	954	840	20.1	0.21	.	36
DxD	15	2	D	2	966	936	902	824	752	616	528	456	436	330	328	278	10.3	0.62	689	580
DxD	16	1	D	2	990	988	992	992	990	992	994	996	992	990	990	990	.	.	24	24
DxD	16	2	D	2	968	970	966	964	966	968	964	968	970	968	970	.	.	.	46	46
DxD	17	1	D	2	996	994	984	976	958	920	860	760	616	404	346	286	0.88	0.53	690	400
DxD	17	2	D	2	998	988	980	968	954	916	840	740	566	398	350	284	0.65	0.58	681	450
DxD	18	1	D	2	982	992	984	980	972	948	916	850	716	314	280	272	0.08	0.71	738	300
DxD	18	2	D	2	988	980	972	968	956	930	886	802	660	294	244	.	0.45	0.56	796	356
DxD	19	1	D	2	980	960	936	878	808	732	688	614	594	536	490	440	10.4	0.55	521	422
DxD	19	2	D	2	982	974	964	934	888	818	702	572	452	362	340	320	1.44	0.61	669	564

					Day															
Mating	Cross	Spore	Ass.Env.	Rep.	1	2	3	4	5	6	7	8	9	12	14	19	i	r	K	P10
DxD	20	1	D	2	992	984	974	964	948	888	798	688	538	332	320	242	1	0.56	725	478
DxD	20	2	D	2	986	982	976	970	956	928	892	816	720	308	262	.	0.49	0.53	796	296
DxD	21	1	D	2	992	988	980	980	986	984	980	992	986	978	952	688	22.2	0.21	.	30
DxD	21	2	D	2	980	980	980	980	978	976	978	984	982	980	980	898	13.7	0.06	.	34
DxD	22	1	D	2	984	986	980	984	986	988	982	990	992	990	990	996	.	.	24	24
DxD	22	2	D	2	972	954	948	928	910	876	834	810	770	680	622	510	20.7	0.48	515	246
DxD	23	1	D	2	982	962	952	934	906	864	814	750	664	452	436	388	5.49	0.42	619	352
DxD	23	2	D	2	988	990	980	978	978	978	968	968	958	912	834	604	3.65	0.16	795	58
DxD	24	1	D	2	986	972	952	912	864	798	728	648	596	506	484	392	7.76	0.49	563	420
DxD	24	2	D	2	970	952	926	878	782	714	680	600	584	530	500	414	12.7	0.58	529	432
DxD	25	1	D	2	984	984	984	982	976	986	980	982	982	980	976	946	12.2	0.04	.	34
DxD	25	2	D	2	978	982	972	970	960	962	952	942	922	798	676	364	4.08	0.22	818	94
DxD	L1+	1	D	2	970	976	976	976	976	974	978	980	978	974	978	972	24.3	0.25	.	38
DxD	L2+	2	D	2	978	980	984	980	982	984	982	984	984	982	982	982	18	0.14	.	32
DxD	D1+	1	D	2	992	974	960	940	904	816	718	614	568	488	466	368	2.72	0.54	571	448
DxD	D2+	2	D	2	972	952	928	876	780	696	650	582	564	490	462	396	11.2	0.58	557	452
DxD	U+	2	D	2	976	966	964	958	952	948	942	926	904	774	624	508	3.58	0.26	540	112
DxD	L1-	1	D	2	980	972	952	946	926	880	818	738	640	378	304	300	2.96	0.44	721	376
DxD	L2-	2	D	2	986	982	970	962	946	906	854	778	666	394	316	294	1.59	0.46	716	350
DxD	D1-	1	D	2	990	980	958	936	890	814	694	546	466	370	314	284	1.79	0.59	688	550
DxD	D2-	2	D	2	998	992	974	962	942	908	856	772	642	342	286	252	1.12	0.49	752	374
DxD	U-	2	D	2	992	992	988	984	986	984	978	976	968	932	880	700	18	0.14	.	48

					Day																			
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	9	11	12	13	16	18	20	24	27	i	r	K	P10
AxD	1	1	D	1	994	984	978	964	944	920	872	640	350	270	220	200	.	.	.	.	0.456	0.556	824.1	360
AxD	1	2	D	1	990	986	990	988	972	972	968	878	700	530	380	220	208	.	.	.	0.052	0.5905	803.7	122
AxD	2	1	D	1	990	972	970	976	956	940	908	716	450	370	302	232	218	.	.	.	0.53	0.5028	784.1	284
AxD	2	2	D	1	986	984	984	976	954	934	894	700	420	368	294	230	216	.	.	.	0.577	0.5057	784	300
AxD	3	1	D	1	980	970	966	964	938	906	864	620	400	326	254	222	.	.	.	.	1.171	0.477	799.4	380
AxD	3	2	D	1	990	984	984	974	958	950	930	820	662	602	490	394	266	244	.	.	2.817	0.3134	756.8	180
AxD	4	1	D	1	974	970	978	976	952	950	922	788	502	440	322	226	.	.	.	.	36.63	0.4607	.	212
AxD	4	2	D	1	970	968	970	960	948	922	882	660	442	366	300	232	218	.	.	.	1.245	0.4523	785.9	340
AxD	5	1	D	1	984	974	970	960	932	912	860	652	446	386	312	264	228	238	230	.	1.844	0.4314	767.2	348
AxD	5	2	D	1	978	976	970	970	960	956	932	862	752	674	574	394	300	242	236	.	3.086	0.2784	782.7	138
AxD	6	1	D	1	984	982	974	966	946	924	858	660	402	310	230	212	.	.	.	.	0.819	0.4939	819.5	340
AxD	6	2	D	1	978	976	974	970	946	950	922	806	606	466	370	238	220	.	.	.	.	.	.	194
AxD	7	1	D	1	970	968	972	964	936	908	868	606	342	266	230	206	.	.	.	.	.	.	.	394
AxD	7	2	D	1	968	956	960	954	922	902	866	664	430	348	306	240	200	.	.	.	2.062	0.4235	797.5	336
AxD	8	1	D	1	990	986	986	976	962	948	920	738	438	338	280	212	.	.	.	.	0.226	0.5713	799.9	262
AxD	8	2	D	1	998	984	986	980	966	952	912	746	482	388	304	230	214	.	.	.	0.41	0.5088	788.8	254
AxD	9	1	D	1	986	984	984	978	954	948	914	758	484	388	322	232	222	.	.	.	0.433	0.5023	783.2	242
AxD	9	2	D	1	978	974	974	964	954	954	916	810	610	496	400	268	254	232	242	.	.	.	.	190
AxD	10	1	D	1	990	980	974	960	944	914	856	548	326	244	214	214	.	.	.	.	0.387	0.6064	804.8	452
AxD	10	2	D	1	992	986	990	984	984	990	986	986	990	996	982	984	980	968	964	988	.	.	1	1
AxD	11	1	D	1	986	974	962	942	888	810	690	352	308	300	260	238	242	.	.	.	0.698	0.6727	745.6	648
AxD	11	2	D	1	980	972	958	940	894	816	728	390	322	316	274	230	.	.	.	.	1.107	0.6032	741.4	610
AxD	12	1	D	1	982	972	964	952	910	852	752	392	310	296	264	216	220	.	.	.	0.651	0.639	760.8	608
AxD	12	2	D	1	980	978	962	950	916	880	822	534	354	344	284	216	.	.	.	.	1.825	0.4802	773.4	466
AxD	13	1	D	1	976	968	960	942	902	836	760	474	324	322	276	240	246	.	.	.	1.941	0.5176	753.9	526
AxD	13	2	D	1	990	976	958	936	860	754	626	402	324	300	248	214	.	.	.	.	2.793	0.5536	754.8	598
AxD	14	1	D	1	988	976	972	950	902	836	726	470	400	364	338	242	220	.	.	.	3.877	0.4672	742.6	530
AxD	14	2	D	1	994	996	988	978	960	930	860	558	366	342	302	226	222	.	.	.	0.508	0.5707	758.2	442
AxD	15	1	D	1	992	990	988	984	980	978	970	942	904	870	814	634	566	504	412	386	2.023	0.2051	623	58
AxD	15	2	D	1	986	984	982	984	978	976	966	950	904	868	812	616	558	524	502	452	0.716	0.2682	527.8	50
AxD	16	1	D	1	980	966	938	884	778	648	462	332	284	292	278	284	.	.	.	.	1.391	0.7361	718.7	668
AxD	16	2	D	1	982	976	960	942	900	842	770	578	320	246	218	.	.	.	.	.	4.462	0.4224	910.9	422
AxD	17	1	D	1	984	986	980	968	934	892	814	514	280	260	240	246	.	.	.	.	0.377	0.6408	775.4	486
AxD	17	2	D	1	986	976	968	954	920	868	794	584	338	242	216	200	.	.	.	.	1.822	0.4732	835.2	416

					Day																			
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	9	11	12	13	16	18	20	24	27	i	r	K	P10
AxD	18	1	D	1	982	976	962	944	910	858	776	550	260	240	232	.	.	.	.	.	36.98	0.4778	801.4	450
AxD	18	2	D	1	986	970	948	916	842	744	648	370	264	260	232	.	.	.	.	.	2.767	0.5594	780.4	630
AxD	19	1	D	1	990	982	970	958	930	884	796	550	290	254	246	248	266	276	.	.	0.507	0.6125	756.2	450
AxD	19	2	D	1	950	960	968	952	946	948	932	882	724	570	410	254	260	248	.	.	.	.	.	118
AxD	20	1	D	1	966	948	924	868	766	646	484	280	240	270	232	258	304	310	.	.	2.039	0.6936	737.9	720
AxD	20	2	D	1	986	980	968	970	920	870	782	550	288	230	194	210	260	262	322	.	0.541	0.6132	762.5	450
AxD	21	1	D	1	990	982	980	978	974	976	962	954	938	912	906	858	800	700	512	418	.	.	.	46
AxD	21	2	D	1	990	988	990	992	978	988	984	976	970	958	938	894	842	742	608	470	.	.	.	24
AxD	22	1	D	1	986	980	978	978	970	982	972	958	972	964	954	950	922	884	816	706	.	.	.	42
AxD	22	2	D	1	974	978	976	976	972	972	978	970	966	962	954	942	920	872	784	686	.	.	.	30
AxD	23	1	D	1	952	952	948	936	972	980	970	976	966	968	952	938	898	812	680	542	.	.	.	24
AxD	23	2	D	1	990	984	984	982	980	984	980	974	980	974	966	954	932	886	762	672	.	.	.	26
AxD	24	1	D	1	982	978	978	980	972	988	976	972	982	978	974	974	982	974	962	.	.	.	.	1
AxD	24	2	D	1	972	970	974	970	960	972	970	952	948	944	942	882	826	734	568	444	.	.	.	48
AxD	25	1	D	1	972	970	974	976	960	964	970	960	946	968	956	970	970	968	972	962	.	.	1	1
AxD	25	2	D	1	980	980	978	976	972	980	980	972	978	982	982	976	968	970	974	.	.	.	1	1
AxD	L1+	1	D	1	978	970	968	974	960	960	950	932	902	882	844	700	616	570	502	448	4.701	0.186	579.3	68
AxD	L2+	1	D	1	980	972	974	980	976	972	978	974	968	966	950	946	918	882	838	824	.	.	.	26
AxD	D1+	1	D	1	982	978	974	966	958	944	926	910	876	860	846	796	756	732	758	688	11.72	0.2644	299.6	90
AxD	D2+	1	D	1	986	980	978	976	968	968	952	918	836	794	750	670	636	588	510	504	6.866	0.2329	501.3	82
AxD	U+	1	D	1	982	980	984	980	976	976	968	946	926	904	864	710	606	568	524	526	0.744	0.2392	490.1	54
AxD	L1-	1	D	1	982	980	982	968	978	978	976	982	982	986	980	986	982	972	964	950	6.431	0.7859	24.07	18
AxD	L2-	1	D	1	992	990	994	990	980	984	986	982	990	984	980	986	982	972	970	980	8.389	0.0606	31.42	18
AxD	D1-	1	D	1	986	986	978	968	932	880	812	694	636	612	588	530	508	506	504	482	6.147	0.3853	494.5	306
AxD	D2-	1	D	1	976	960	940	906	816	692	646	610	568	578	550	470	454	442	.	.	9.918	0.5475	502	390
AxD	U-	1	D	1	980	974	964	962	942	948	920	860	758	704	624	374	316	302	280	.	3.023	0.2764	746.5	140
DxA	1	1	D	1	982	982	982	984	976	980	986	980	986	988	980	988	986	982	960	988	.	.	20	20
DxA	1	2	D	1	994	990	988	990	978	990	988	988	982	998	982	994	986	980	972	988	0.796	0.9256	20.24	12
DxA	2	1	D	1	990	980	986	990	980	992	988	984	988	982	984	988	988	986	970	.	8.006	0.1503	696.6	16
DxA	2	2	D	1	994	984	988	986	982	986	980	992	990	988	986	986	992	994	986	988	0.06	.	11.96	8
DxA	3	1	D	1	976	962	956	940	916	896	820	586	368	304	270	258	254	250	.	.	1.327	0.6165	757.9	414
DxA	3	2	D	1	976	962	952	928	870	790	686	416	322	300	260	250	240	.	.	.	2.73	0.6309	752.5	584
DxA	4	1	D	1	968	970	950	936	900	842	756	584	508	488	452	386	380	344	312	318	10.11	0.4336	655.9	416
DxA	4	2	D	1	980	974	970	954	918	876	796	662	566	550	498	434	400	370	336	330	10.36	0.3928	641.3	338

					Day																			
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	9	11	12	13	16	18	20	24	27	i	r	K	P10
DxA	5	1	D	1	998	996	992	992	988	999	990	994	999	994	994	994	999	990	984	999	.	.	28	6
DxA	5	2	D	1	980	976	978	978	978	982	974	984	986	976	970	950	936	844	668	552	4.679	0.3002	743.3	16
DxA	6	1	D	1	988	984	988	988	984	988	992	992	990	990	986	992	992	988	984	988	.	.	18	8
DxA	6	2	D	1	984	990	990	992	988	994	986	990	988	994	990	994	999	994	974	999	.	.	18	10
DxA	7	1	D	1	978	982	982	978	976	982	986	980	986	978	976	986	984	982	964	986	.	.	40	20
DxA	7	2	D	1	976	980	984	986	978	986	984	982	984	992	984	990	986	986	966	986	.	.	40	18
DxA	8	1	D	1	968	966	962	944	910	866	802	520	290	290	272	242	238	242	.	.	1.056	0.6696	764.9	480
DxA	8	2	D	1	974	964	950	922	868	794	702	424	360	336	298	264	248	222	.	.	4.217	0.5744	745.1	576
DxA	9	1	D	1	968	970	956	938	900	840	754	596	542	528	484	422	404	354	316	.	12.64	0.4111	634.3	404
DxA	9	2	D	1	980	966	954	920	852	758	684	550	494	476	436	362	258	.	.	.	16.78	0.4284	683.8	450
DxA	10	1	D	1	978	982	984	984	980	990	986	986	988	990	982	990	988	958	828	688	2.317	0.4337	654.8	14
DxA	10	2	D	1	996	990	992	994	986	996	996	992	996	996	988	988	984	930	758	576	23.55	0.1759	8	8
DxA	11	1	D	1	986	976	970	964	904	836	772	730	694	704	670	596	570	598	546	546	15.9	0.3678	433.3	270
DxA	11	2	D	1	992	982	982	970	948	942	918	852	770	720	644	482	450	430	368	340	5.737	0.3276	645	148
DxA	12	1	D	1	994	980	970	964	886	808	766	722	696	690	670	616	598	590	542	.	13.53	0.4032	408	278
DxA	12	2	D	1	976	972	962	946	904	848	772	718	670	650	646	570	532	520	540	514	15.54	0.3738	471	282
DxA	13	1	D	1	988	982	976	964	932	890	818	710	680	670	626	570	534	500	482	494	11.34	0.3632	498.1	290
DxA	13	2	D	1	980	976	972	964	938	916	868	760	710	672	664	602	546	532	528	502	9.521	0.3517	476.9	240
DxA	14	1	D	1	982	980	970	954	914	868	792	688	648	628	618	598	574	578	552	556	4.771	0.5018	424	312
DxA	14	2	D	1	982	978	970	952	916	866	782	656	594	562	566	536	516	.	.	.	2.822	0.5704	466.2	344
DxA	15	1	D	1	976	974	966	952	920	864	776	666	618	610	608	584	560	596	588	560	2.258	0.6122	417.6	334
DxA	15	2	D	1	972	964	948	922	866	766	656	602	586	608	554	504	462	466	488	464	11.15	0.4918	504.4	398
DxA	16	1	D	1	982	976	970	958	940	928	920	898	882	878	848	802	764	660	546	508	21.88	0.3511	910.7	102
DxA	16	2	D	1	996	988	988	984	978	984	980	980	984	986	972	986	988	980	972	992	.	.	20	20
DxA	17	1	D	1	999	988	984	990	986	990	982	988	994	999	986	994	982	992	974	996	.	.	12	12
DxA	17	2	D	1	984	980	976	980	972	980	974	974	980	986	966	984	988	980	952	.	3.144	.	23.83	26
DxA	18	1	D	1	994	988	982	972	948	916	862	660	442	366	326	312	304	300	.	.	37.3	0.4722	.	340
DxA	18	2	D	1	992	986	984	976	960	952	932	874	736	632	530	434	400	372	922	344	0.118	0.5468	509.7	126
DxA	19	1	D	1	998	990	984	972	938	890	808	638	522	518	468	406	390	342	298	.	4.974	0.3895	644.9	362
DxA	19	2	D	1	990	978	968	940	884	788	698	520	462	456	418	358	358	322	314	.	6.251	0.4689	648.3	480
DxA	20	1	D	1	996	988	984	980	968	968	952	926	898	890	862	704	590	486	406	388	2.445	0.1848	656.3	74
DxA	20	2	D	1	994	994	994	992	990	986	976	970	938	922	904	762	626	510	446	420	0.427	0.2368	598	30
DxA	21	1	D	1	988	984	990	990	984	990	984	982	984	984	984	970	952	910	772	682	0.412	0.095	.	18
DxA	21	2	D	1	972	972	968	972	960	970	966	964	970	970	954	960	956	942	892	864	.	.	.	36

					Day																				
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	9	11	12	13	16	18	20	24	27	i	r	K	P10
DxA	22	1	D	1	990	986	988	976	970	962	960	938	904	872	830	624	550	498	460	456	0.928	0.2487	555.2	62
DxA	22	2	D	1	988	990	990	998	986	986	984	986	990	986	986	990	990	986	990	994	8.133	0.3491	11.61	14
DxA	23	1	D	1	998	984	978	966	954	944	924	836	722	652	574	482	444	404	372	318	4.745	0.2917	637.1	164
DxA	23	2	D	1	982	978	978	972	962	962	954	940	910	892	870	728	634	558	462	410	4.192	0.1711	646.6	60
DxA	24	1	D	1	988	984	984	972	962	958	948	908	850	816	758	472	362	344	272	272	1.184	0.2652	738.7	92
DxA	24	2	D	1	984	978	974	976	958	950	948	928	894	880	848	682	578	460	380	314	4.066	0.1818	738	72
DxA	25	1	D	1	982	978	972	968	956	956	946	924	882	852	816	626	536	450	348	304	4.645	0.1965	738.2	76
DxA	25	2	D	1	998	988	992	992	978	980	974	964	968	964	942	888	776	668	602	616	0.119	0.2633	414.9	36
DxA	L1+	1	D	1	986	982	984	980	972	986	978	982	988	988	982	978	986	982	968	984	.	.	18	18
DxA	L2+	1	D	1	960	966	970	958	954	972	964	960	966	974	958	966	976	964	956	962	40.2	0.7957	35.29	40
DxA	D1+	1	D	1	970	980	966	962	954	912	858	644	408	354	304	276	270	268	278	.	.	.	.	356
DxA	D2+	1	D	1	988	980	970	952	912	870	786	622	532	506	462	412	388	350	296	316	8.472	0.4027	656.4	378
DxA	U+	1	D	1	986	978	978	984	978	982	976	972	972	968	944	816	672	504	364	362	0.065	0.3096	666.5	28
DxA	L1-	1	D	1	980	974	974	966	948	932	890	708	408	328	268	206	.	.	.	.	.	.	.	292
DxA	L2-	1	D	1	984	978	970	974	938	914	860	622	384	304	256	212	214	.	.	.	0.821	0.5091	796.5	378
DxA	D1-	1	D	1	986	982	972	940	904	828	714	380	320	326	276	224	.	.	.	.	0.654	0.6632	734.1	620
DxA	D2-	1	D	1	968	950	930	890	794	662	540	330	274	274	250	258	.	.	.	.	3.128	0.6179	747.7	670
DxA	U-	1	D	1	988	994	999	990	990	998	990	980	980	970	966	926	864	800	648	510	1.459	0.0909	.	20

					Day																			
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	9	10	12	13	16	18	20	24	27	i	r	K	P10
AxD	1	1	D	2	988	982	980	978	976	960	944	854	786	498	422	252	232	.	.	.	0.2	0.49	779	146
AxD	1	2	D	2	984	980	990	968	974	978	962	912	878	738	676	346	242	224	.	.	0.6	0.33	829	88
AxD	2	1	D	2	988	982	980	974	966	956	936	862	816	610	506	340	308	256	234	.	1.1	0.35	750	138
AxD	2	2	D	2	988	980	978	968	958	926	884	670	562	354	294	218	.	.	.	.	1	0.46	799	330
AxD	3	1	D	2	990	980	984	980	972	962	950	912	894	868	842	798	766	756	716	670	9.7	0.23	325	88
AxD	3	2	D	2	980	978	974	972	974	970	962	902	854	700	626	418	330	274	232	.	1.8	0.28	767	98
AxD	4	1	D	2	974	972	972	966	968	960	960	906	870	700	574	330	290	256	232	.	0.5	0.37	763	94
AxD	4	2	D	2	996	988	980	978	970	966	960	864	804	534	422	300	270	250	236	.	0.1	0.52	747	136
AxD	5	1	D	2	984	979	974	958	940	906	870	646	554	340	292	228	232	.	.	.	1.3	0.45	784	354
AxD	5	2	D	2	982	978	982	982	960	950	938	866	836	684	596	406	352	296	248	.	2.8	0.28	747	134
AxD	6	1	D	2	984	974	980	964	956	940	908	744	650	460	310	228	222	.	.	.	38	0.48	.	256
AxD	6	2	D	2	986	980	976	970	964	966	952	802	724	476	390	272	240	206	.	.	38	0.49	.	198
AxD	7	1	D	2	968	964	962	956	940	898	860	694	600	434	354	260	256	228	.	.	3.4	0.38	772	306
AxD	7	2	D	2	978	976	960	962	940	932	898	726	638	444	346	268	232	212	.	.	.	.	.	274
AxD	8	1	D	2	990	984	980	976	968	954	948	774	678	450	358	242	220	198	.	.	14	0.07	.	226
AxD	8	2	D	2	999	996	994	990	962	922	880	604	520	364	246	202	.	.	.	.	0.8	0.5	801	396
AxD	9	1	D	2	980	976	972	966	964	854	828	782	684	428	344	236	232	.	.	.	3.1	0.36	813	218
AxD	9	2	D	2	990	984	984	972	968	966	960	900	846	694	590	390	302	256	236	.	1.2	0.31	766	100
AxD	10	1	D	2	988	988	976	976	970	966	940	834	782	552	454	288	258	238	220	.	38	0.49	.	166
AxD	10	2	D	2	988	988	994	984	990	988	984	988	992	992	986	988	980	982	996	998	.	.	1	1
AxD	11	1	D	2	984	980	962	944	890	804	718	370	308	256	252	214	218	.	.	.	0.9	0.63	777	630
AxD	11	2	D	2	970	966	952	938	908	842	762	422	370	308	272	226	.	.	.	.	7	.	.	578
AxD	12	1	D	2	992	988	978	964	944	898	842	612	468	324	270	234	.	.	.	.	1	0.5	777	388
AxD	12	2	D	2	986	980	972	950	922	870	798	516	404	324	304	234	.	.	.	.	1.2	0.53	746	484
AxD	13	1	D	2	990	984	972	962	918	852	786	504	366	308	298	228	.	.	.	.	1	0.56	751	496
AxD	13	2	D	2	984	974	964	938	868	764	674	424	390	318	318	230	226	.	.	.	3.8	0.51	746	576
AxD	14	1	D	2	999	992	990	974	954	902	848	588	422	338	330	250	224	.	.	.	0.6	0.56	745	412
AxD	14	2	D	2	988	982	970	970	940	882	802	426	404	338	300	220	.	.	.	.	.	.	.	574
AxD	15	1	D	2	994	990	988	984	980	980	972	946	944	882	824	610	510	462	374	366	0.8	0.25	639	54
AxD	15	2	D	2	976	980	982	980	972	968	966	934	918	826	736	534	504	474	410	.	0.7	0.29	576	66

					Day																			
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	9	10	12	13	16	18	20	24	27	i	r	K	P10
AxD	16	1	D	2	978	968	948	918	854	756	668	442	310	246	228	.	.	.	.	.	4.4	0.51	807	558
AxD	16	2	D	2	978	976	956	938	888	812	712	402	302	240	226	210	.	.	.	.	1.3	0.58	794	598
AxD	17	1	D	2	988	984	982	962	944	918	866	690	542	328	232	218	.	.	.	.	0.8	0.48	822	310
AxD	17	2	D	2	988	982	968	950	920	862	796	568	448	272	220	216	.	.	.	.	2.1	0.47	818	432
AxD	18	1	D	2	980	984	960	960	928	892	856	694	552	346	290	250	282	292	.	.	.	.	.	306
AxD	18	2	D	2	980	966	940	902	832	732	608	334	320	294	266	.	.	.	.	.	2.2	0.61	739	666
AxD	19	1	D	2	994	992	990	982	964	914	864	608	464	278	234	228	234	.	.	.	0.3	0.6	782	392
AxD	19	2	D	2	992	986	982	978	980	976	980	934	878	696	550	224	212	200	.	.	0.1	0.53	815	66
AxD	20	1	D	2	982	964	940	898	836	742	660	448	312	250	222	.	.	.	.	.	6.4	0.5	817	552
AxD	20	2	D	2	994	988	982	954	922	868	804	562	412	296	272	238	260	.	.	.	37	0.46	614	438
AxD	21	1	D	2	998	990	994	988	992	994	988	984	982	974	970	944	890	830	700	542	.	.	.	16
AxD	21	2	D	2	988	992	996	990	992	996	990	986	982	978	974	940	886	802	604	462	.	.	.	14
AxD	22	1	D	2	992	992	996	980	986	990	986	980	976	984	974	970	958	918	708	454	.	.	.	20
AxD	22	2	D	2	984	976	988	982	978	978	982	986	980	982	976	962	964	918	878	776	.	.	.	14
AxD	23	1	D	2	986	988	984	976	980	982	984	984	976	982	980	974	970	940	906	804	.	.	.	16
AxD	23	2	D	2	984	982	982	988	976	984	986	982	980	976	972	960	956	928	896	804	.	.	.	18
AxD	24	1	D	2	980	982	984	976	978	974	980	982	978	982	984	978	974	964	972	.	.	.	.	1
AxD	24	2	D	2	990	984	984	970	968	970	966	958	970	950	946	926	866	778	600	422	.	.	.	42
AxD	25	1	D	2	984	984	988	976	980	984	980	986	992	980	986	986	982	984	986	988	.	.	1	1
AxD	25	2	D	2	990	992	986	988	988	990	984	986	984	986	988	974	984	978	982	990	.	.	1	1
AxD	L1+	1	D	2	980	972	980	962	976	968	960	936	906	830	794	682	618	556	518	476	4.6	0.2	530	40
AxD	L2+	1	D	2	980	972	974	974	980	970	980	964	960	960	944	920	892	886	838	804	13	0.16	790	20
AxD	D1+	1	D	2	988	984	978	966	962	936	886	690	614	432	326	248	240	.	.	.	.	.	.	114
AxD	D2+	1	D	2	994	982	986	976	976	976	964	938	926	834	778	668	642	618	532	496	3.8	0.21	492	36
AxD	U+	1	D	2	982	982	980	974	982	974	972	960	956	914	862	658	590	532	464	418	6.4	0.22	715	28
AxD	L1-	1	D	2	988	988	986	980	982	988	988	988	992	992	994	976	970	986	996	994	.	.	.	12
AxD	L2-	1	D	2	988	986	988	986	986	986	988	986	986	984	988	986	988	988	972	920	.	.	.	6
AxD	D1-	1	D	2	988	988	976	956	928	878	812	710	678	600	602	554	506	482	498	456	8.2	0.38	507	188
AxD	D2-	1	D	2	982	964	950	910	844	718	660	580	584	562	532	516	456	448	.	.	5.8	0.55	497	340
AxD	U-	1	D	2	986	980	974	962	960	950	938	906	888	822	772	610	508	462	352	320	0.7	0.24	571	62

					Day																			
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	9	10	12	13	16	18	20	24	27	i	r	K	P10
DxA	1	1	D	2	990	990	994	988	988	988	992	988	990	988	992	990	990	986	976	918	.	.	.	8
DxA	1	2	D	2	994	992	994	994	992	986	992	998	996	994	990	990	992	992	998	999	.	.	8	8
DxA	2	1	D	2	988	992	990	984	988	984	986	984	984	990	990	988	982	982	988	988	5.7	0.46	14	14
DxA	2	2	D	2	982	980	980	980	980	980	978	980	980	980	980	980	984	978	988	988	.	.	22	22
DxA	3	1	D	2	966	960	946	940	924	870	822	572	484	414	322	288	272	268	.	.	3.4	0.43	728	178
DxA	3	2	D	2	976	968	954	930	896	828	758	494	406	316	280	238	242	250	.	.	2.9	0.48	758	242
DxA	4	1	D	2	970	962	960	954	924	880	808	618	564	480	442	386	372	348	260	.	6.4	0.4	666	192
DxA	4	2	D	2	978	972	964	946	930	870	800	588	494	382	322	312	292	282	.	.	2.5	0.46	711	200
DxA	5	1	D	2	980	986	982	970	974	980	980	982	980	978	978	978	970	960	942	846	2.7	0.02	.	20
DxA	5	2	D	2	976	982	982	972	970	972	974	970	970	972	968	964	952	908	766	592	0.4	0.1	.	26
DxA	6	1	D	2	994	996	994	996	994	992	988	992	986	998	996	990	996	990	994	999	2.4	0.45	7	12
DxA	6	2	D	2	988	994	996	996	986	988	990	986	990	996	984	998	990	996	990	988	7.1	0.3	9.2	10
DxA	7	1	D	2	982	982	982	980	984	980	980	982	988	984	982	980	978	978	990	986	.	.	20	20
DxA	7	2	D	2	988	986	988	988	986	992	992	988	994	992	990	990	992	986	998	996	.	.	8	8
DxA	8	1	D	2	972	980	970	954	934	902	854	620	496	380	344	284	268	.	.	.	1.5	0.47	725	146
DxA	8	2	D	2	970	966	960	942	906	852	796	524	422	336	304	260	246	242	.	.	2.4	0.48	750	204
DxA	9	1	D	2	980	972	964	930	894	828	746	610	576	516	486	414	388	344	286	.	14	0.46	654	254
DxA	9	2	D	2	972	972	962	932	894	826	730	574	550	488	454	392	364	328	340	306	11	0.45	655	270
DxA	10	1	D	2	984	990	994	990	992	990	992	988	994	990	986	990	988	988	982	938	7.3	.	746	8
DxA	10	2	D	2	970	972	976	970	978	980	970	972	974	978	976	976	974	956	862	628	.	.	.	30
DxA	11	1	D	2	999	998	984	958	926	860	794	746	722	680	676	604	598	566	568	564	9.6	0.39	420	206
DxA	11	2	D	2	994	988	984	978	966	946	914	808	764	630	558	468	438	424	386	338	3.4	0.31	615	86
DxA	12	1	D	2	986	978	970	948	908	832	744	678	656	636	628	550	526	530	510	.	9.5	0.44	461	256
DxA	12	2	D	2	986	982	976	956	932	876	808	698	662	616	610	558	542	516	510	482	6.7	0.39	478	192
DxA	13	1	D	2	990	988	980	978	964	932	884	768	732	688	672	586	562	588	536	524	5	0.33	448	116
DxA	13	2	D	2	984	978	978	964	952	924	880	772	742	692	676	606	574	574	536	510	8.2	0.33	456	120
DxA	14	1	D	2	982	980	976	962	930	890	820	674	652	610	590	530	502	510	.	.	4.2	0.41	478	180
DxA	14	2	D	2	982	978	966	948	916	866	786	668	648	604	590	532	484	480	498	464	9	0.41	508	214
DxA	15	1	D	2	982	982	970	950	924	864	794	730	716	698	714	688	654	616	552	506	20	0.48	418	206
DxA	15	2	D	2	980	974	958	938	898	814	696	664	652	620	616	562	500	498	490	488	15	0.48	487	304

					Day																			
Mating	Cross	Spore	Ass. Env.	Rep.	1	2	3	4	5	6	7	9	10	12	13	16	18	20	24	27	l	r	K	P10
DxA	16	1	D	2	998	990	982	968	956	952	946	940	944	944	940	932	902	838	656	570	.	.	.	54
DxA	16	2	D	2	986	986	988	986	992	986	984	990	998	996	986	994	992	990	996	998	.	.	16	16
DxA	17	1	D	2	986	992	988	988	986	990	984	988	992	992	990	990	990	984	994	992	.	.	16	16
DxA	17	2	D	2	988	990	986	986	982	984	990	988	994	990	986	996	990	980	972	942	9.9	0.02	427	10
DxA	18	1	D	2	988	986	978	968	952	932	896	694	608	426	338	274	276	268	.	.	1	0.45	737	104
DxA	18	2	D	2	988	988	988	972	966	954	928	842	800	636	536	436	420	378	352	354	1.6	0.33	634	72
DxA	19	1	D	2	990	980	974	972	936	886	806	638	608	518	474	410	378	356	310	.	6.1	0.39	643	194
DxA	19	2	D	2	986	980	972	956	912	838	726	586	542	478	438	380	358	322	312	.	7.2	0.43	654	274
DxA	20	1	D	2	988	990	986	980	974	968	958	950	936	926	902	826	760	670	496	416	6	0.14	900	42
DxA	20	2	D	2	994	994	994	984	982	984	982	970	966	932	908	792	668	540	430	406	0.5	0.21	628	18
DxA	21	1	D	2	994	986	990	988	990	982	984	982	982	978	970	966	952	918	798	678	.	.	.	16
DxA	21	2	D	2	998	994	982	988	992	988	990	988	984	990	986	978	978	974	952	904	.	.	. .	10
DxA	22	1	D	2	988	990	982	964	966	954	946	928	916	888	870	812	774	734	676	552	16	0.26	698	54
DxA	22	2	D	2	999	999	990	999	994	996	996	996	999	992	990	992	994	990	980	998	1.9	0.01	11	4
DxA	23	1	D	2	990	976	970	968	954	926	900	782	734	594	476	414	396	370	366	324	3	0.34	645	100
DxA	23	2	D	2	988	994	984	978	978	974	966	944	938	902	878	730	618	544	414	402	2	0.18	646	34
DxA	24	1	D	2	990	988	986	982	974	968	948	888	834	724	650	362	336	338	312	316	0.7	0.34	696	52
DxA	24	2	D	2	996	994	990	988	974	966	942	890	872	810	766	604	520	444	352	308	6	0.22	715	58
DxA	25	1	D	2	984	982	976	974	970	966	958	926	904	820	772	466	386	372	298	284	0.7	0.29	710	42
DxA	25	2	D	2	998	990	988	986	982	980	970	946	932	844	800	570	490	448	402	382	0.6	0.28	612	30
DxA	L1+	1	D	2	976	982	980	990	978	980	980	980	984	980	982	978	972	970	984	972	.	.	20	20
DxA	L2+	1	D	2	994	992	994	988	992	994	988	990	996	992	992	992	994	988	988	998	.	.	12	12
DxA	D1+	1	D	2	994	999	992	984	978	962	944	802	706	488	386	310	286	272	272	.	0.3	0.49	723	56
DxA	D2+	1	D	2	982	976	972	952	934	898	860	694	630	526	476	428	398	352	288	.	6.2	0.36	653	140
DxA	U+	1	D	2	996	998	996	986	988	990	992	990	988	974	970	898	774	588	428	418	.	.	.	8
DxA	L1-	1	D	2	994	986	988	978	970	960	940	836	750	586	456	304	258	238	234	286	38	0.49	.	60
DxA	L2-	1	D	2	984	982	980	972	962	942	912	754	692	492	344	242	250	250	246	.	0.9	0.42	765	88
DxA	D1-	1	D	2	982	972	958	948	906	828	746	460	364	314	286	226	.	.	.	.	1.6	0.54	752	254
DxA	D2-	1	D	2	978	968	948	918	860	780	688	410	306	232	212	182	.	.	.	.	3.3	0.52	821	312
DxA	U-	1	D	2	986	984	982	982	982	984	978	978	978	972	962	958	938	890	722	530	0	0.41	598	22