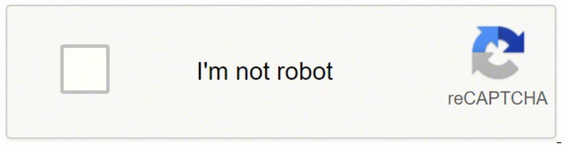

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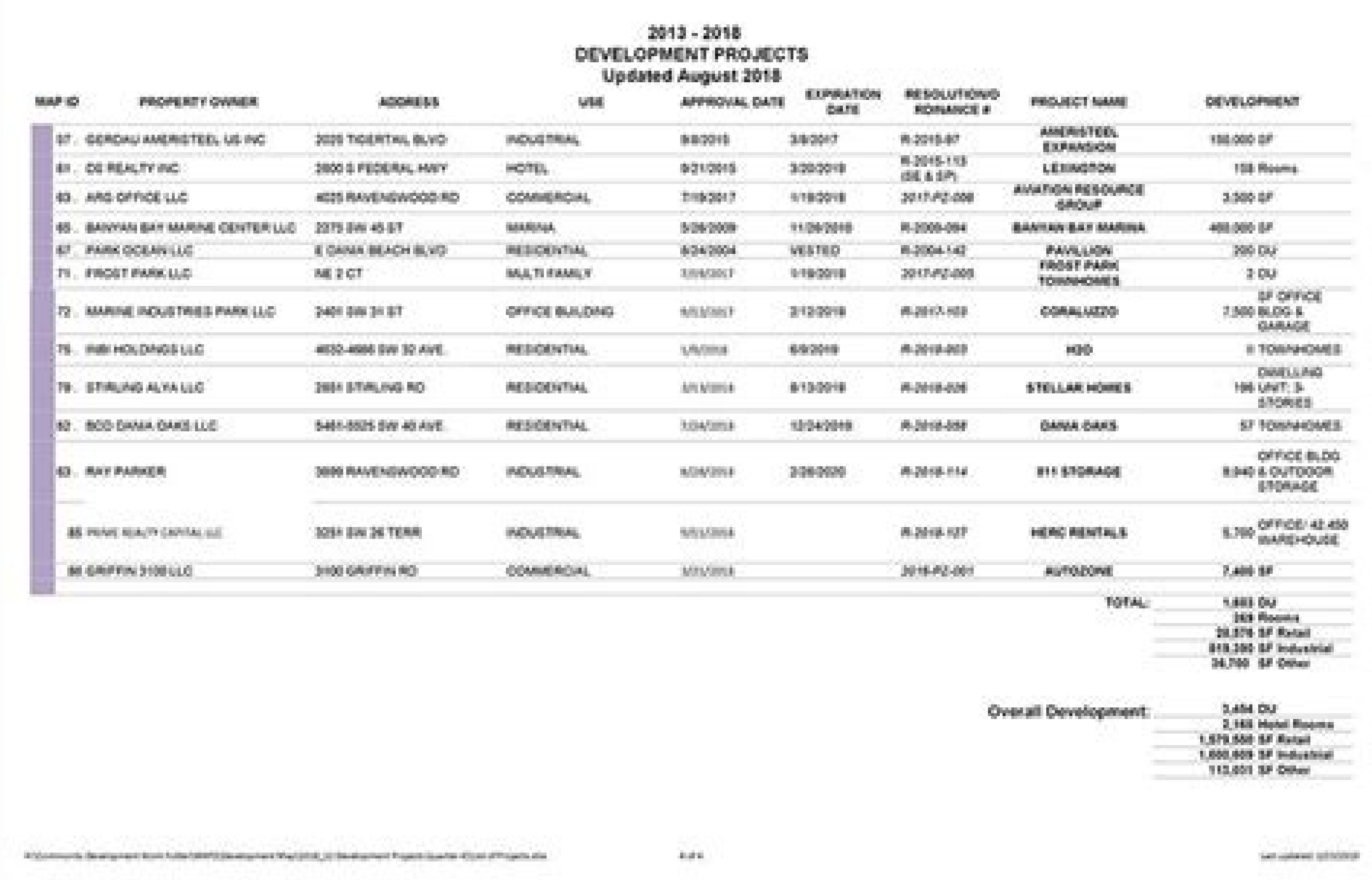

2013 - 2018
DEVELOPMENT PROJECTS
Updated August 2018

MAP ID	PROPERTY OWNER	ADDRESS	USE	APPROVAL DATE	EXPIRATION DATE	RESOLUTION/ORDINANCE #	PROJECT NAME	DEVELOPMENT
57	GERDAU AMERISTEEL US INC	2020 TIGERTAIL BLVD	INDUSTRIAL	9/8/2015	3/8/2017	R-2015-87	AMERISTEEL EXPANSION	150,000 SF
61	DE REALTY INC	2800 S FEDERAL HWY	HOTEL	9/21/2015	3/20/2019	R-2015-113 (SE & SP)	LEXINGTON	158 Rooms
63	ARG OFFICE LLC	4025 RAVENSWOOD RD	COMMERCIAL	7/19/2017	1/19/2018	2017-PZ-008	AVIATION RESOURCE GROUP	3,500 SF
65	BANYAN BAY MARINE CENTER LLC	2275 SW 45 ST	MARINA	5/26/2009	11/26/2018	R-2009-094	BANYAN BAY MARINA	400,000 SF
67	PARK OCEAN LLC	E DANIA BEACH BLVD	RESIDENTIAL	6/24/2004	VESTED	R-2004-142	PAVILLION	200 DU
71	FROST PARK LLC	NE 2 CT	MULTI FAMILY	[illegible]	1/19/2018	2017-PZ-005	FROST PARK TOWNHOMES	2 DU
72	MARINE INDUSTRIES PARK LLC	2401 SW 31 ST	OFFICE BUILDING	[illegible]	2/12/2019	R-2017-103	CORALUZZO	7,500 SF OFFICE BLDG & GARAGE
75	INBI HOLDINGS LLC	4630-4686 SW 32 AVE	RESIDENTIAL	[illegible]	6/9/2019	R-2018-003	H2O	8 TOWNHOMES
79	STIRLING ALYA LLC	2851 STIRLING RD	RESIDENTIAL	[illegible]	8/13/2019	R-2018-026	STELLAR HOMES	196 DWELLING UNIT; 3-STORIES
82	BCD DANIA OAKS LLC	5461-5525 SW 40 AVE	RESIDENTIAL	[illegible]	12/24/2019	R-2018-058	DANIA OAKS	57 TOWNHOMES
83	RAY PARKER	3699 RAVENSWOOD RD	INDUSTRIAL	[illegible]	2/26/2020	R-2018-114	911 STORAGE	8,940 OFFICE BLDG & OUTDOOR STORAGE
85	[illegible]	3251 SW 26 TERR	INDUSTRIAL	[illegible]		R-2018-127	HERC RENTALS	5,700 OFFICE/ 42,450 WAREHOUSE
86	GRIFFIN 3100 LLC	3100 GRIFFIN RD	COMMERCIAL	[illegible]		2018-PZ-001	AUTOZONE	7,400 SF

TOTAL:
1,683 DU
269 Rooms
28,576 SF Retail
819,390 SF Industrial
36,700 SF Other

Overall Development:
3,454 DU
2,168 Hotel Rooms
1,579,550 SF Retail
1,600,609 SF Industrial
113,031 SF Other

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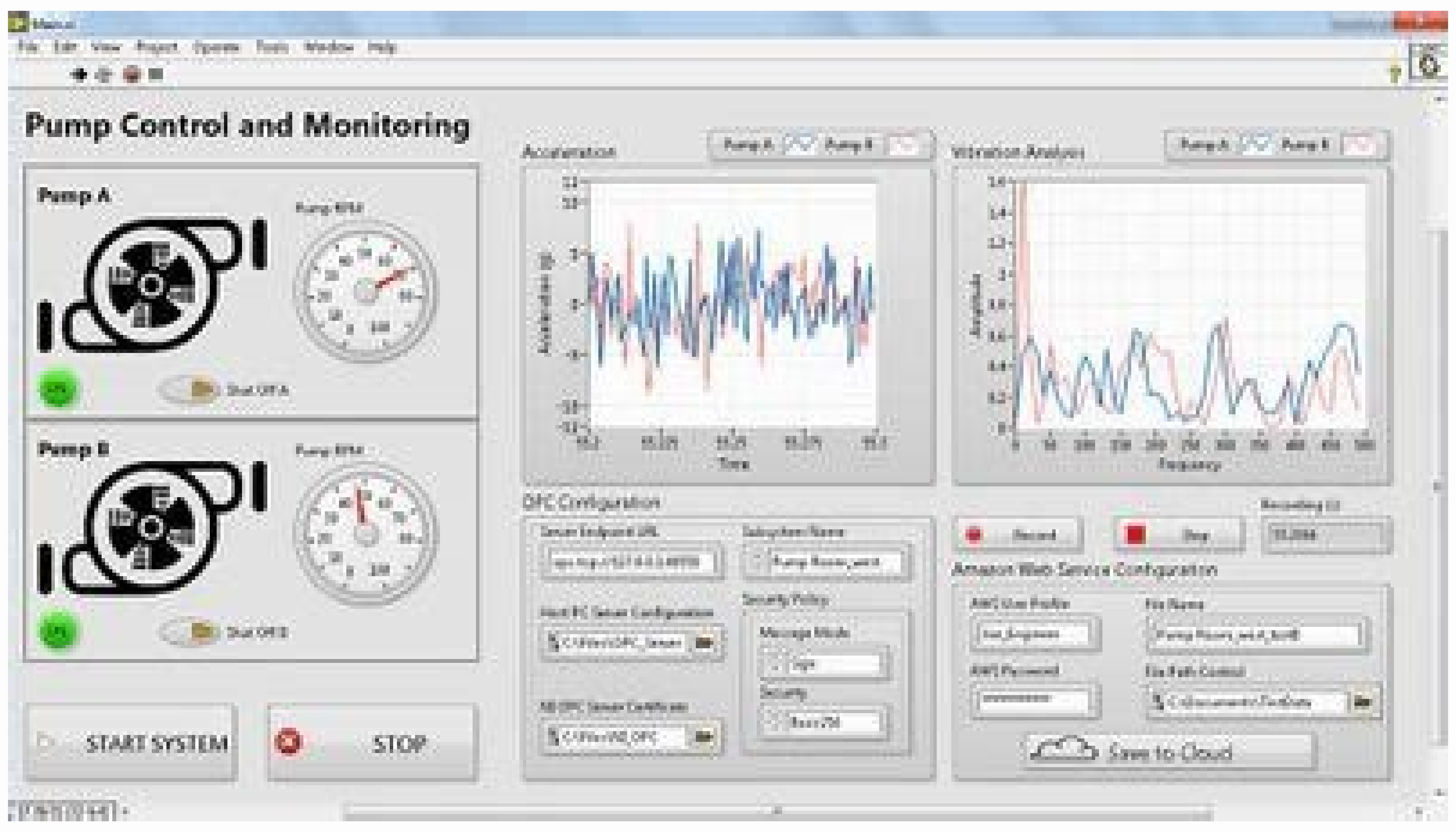
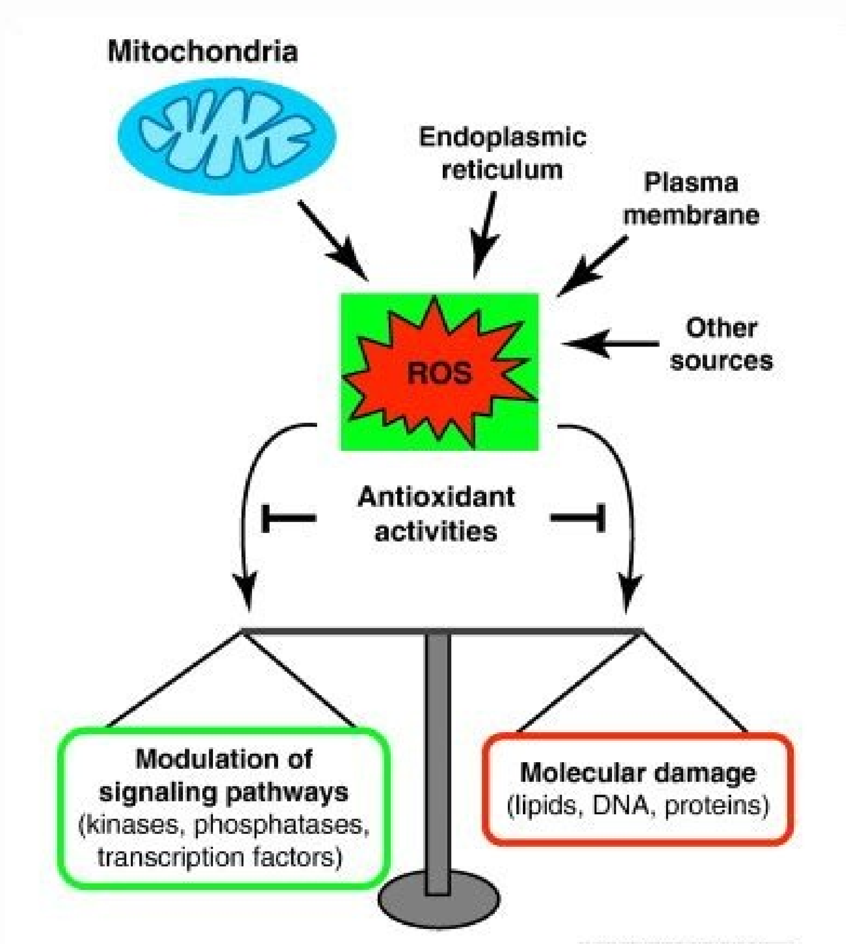
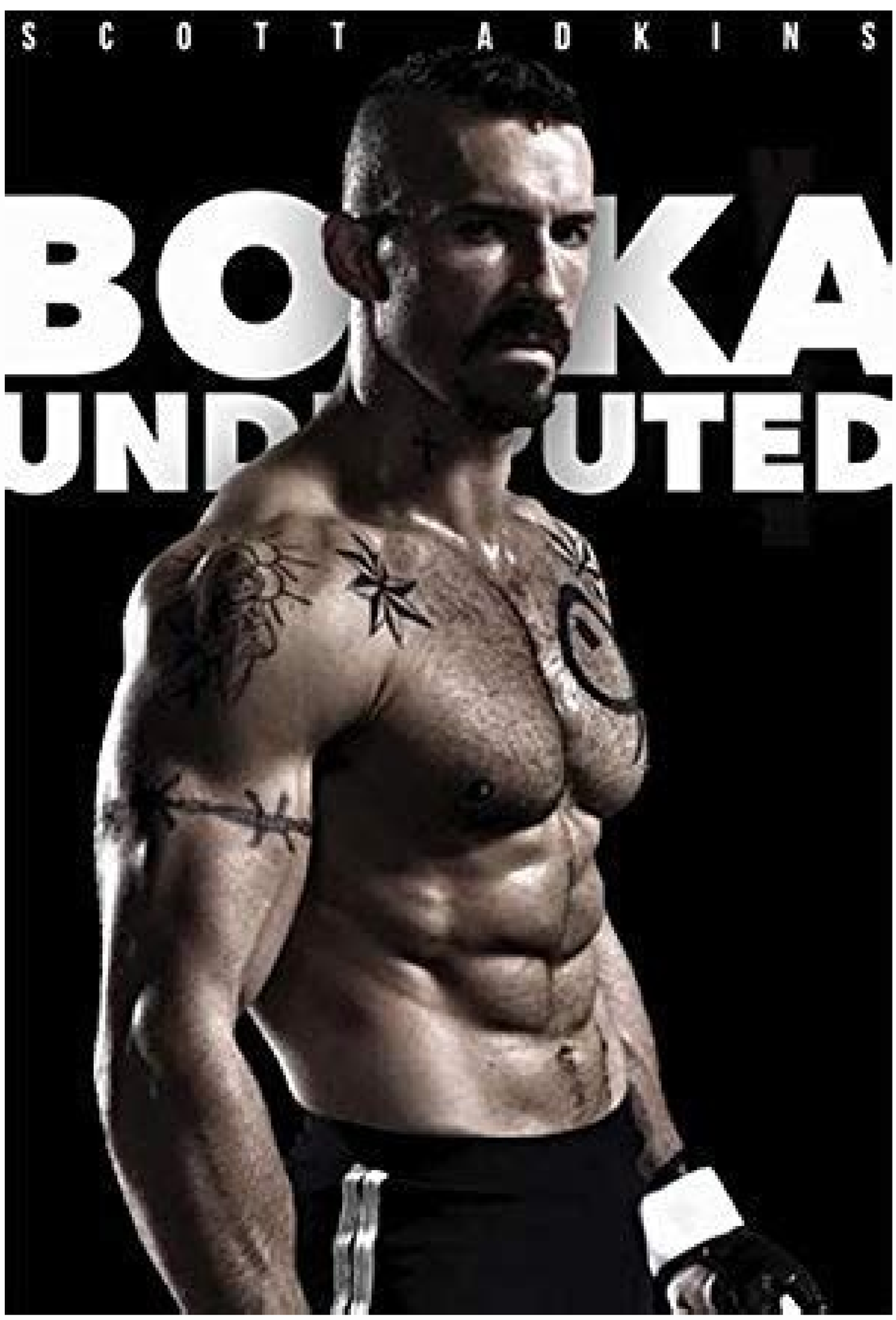




TRENDS in Cell Biology



Karyotype là gì.

As a result of chromosomal rearrangements accompanying the formation of MLI1 in M. Coregulation of tandem duplicate genes slows evolution of subfunctionalization in mammals. 8 chromosomes, namely on chromosome 4 (Fig. 2b), and confirmed the previously reported localization of a cluster of 28S rDNA in one of the small chromosomes14. The CyDASControl Here, the functions of ISCN Analysis (see above), drawing ideograms of aberrant chromosomes (see above), and drawing of complete karyograms (see above) are combined in an Internet Explorer hosted .NET control running on your computer. The next stages of M. In our studies we probably mainly karyotyped somatic cells, since the regeneration blastema that are induced by the amputation are likely driven by somatic stem cells35, but in previously performed crossing experiments, controlled crosses between euploid and aneuploid worms the resulting offspring clearly suggested aneuploid gamete formation14.It should be noted that in many types of organisms whole-chromosome aneuploidy often leads to severe detrimental effects, such as serious malformations, diseases, and lethality19, 36. lignano (and also Macrostomum sp. Higher values will be ignored, but may be very useful for statistical reasons. A direct WGD then occurs in the hybrid genome, which results in allotetraploidy (Fig. 3c). Biol. lignano, nonfunctional ancestral telomeres and centromeres were apparently lost. & Meyer, A. For example, C. We propose three possible scenarios for M. Evol. & Ishida, S. 8 is a hidden hexapoid—similar to M. Q. FISH with labeled rDNA detected only one cluster of 28S rDNA on Macrostomum sp. Phylogenet. lignano and Macrostomum sp. T. 14), which might thus allow us to distinguish this chromosome from MLI4.Fluorescence in situ hybridization in Macrostomum sp. lignano, with suggested tetrasomy for its largest chromosome (2n = 10) being the most common karyotype, but with aneuploidy of chromosome 1 (2n = 9 and 2n = 11) also occurring with appreciable frequency14. EvoDevo (2020) BMC Genomics (2020) Scientific Reports (2020) By submitting a comment you agree to abide by our Terms and Community Guidelines. The remaining steps were performed according to the standard procedure48. 8 chromosome 5 (Fig. 1a,b).Generation of microdissected DNA probes followed by modified CISS-hybridization provides compelling evidence in support of a hidden tetraploidy in the usual 2n = 8 karyotype of M. Shaking up the tree of life. Genomics. The rearrangements shown are the most frequent rearrangements, with the most frequent displayed on top, and the other rearrangements following in clockwise direction with decreasing frequency. 8 chromosomes 1 and 2; MLI2, to Macrostomum sp. MLI1 appeared to be homologous to Macrostomum sp. No additional regions with increased FISH signals were revealed in the regions painted with Mli3_4. lignano chromosomes with probe Mli2 revealed in the q-arm of MLI1 (MLI1q) a region homologous to a very substantial part of MLI2 (Fig. 2a,c,e). lignano is 2n = 8, with two large and six small metacentrics, while the karyotype of several other Macrostomum species (namely, M. 8. laevis tetraploid karyotype by Zoo-FISH. 6, 31658, doi:10.1038/srep31658 (2016).ADS CAS Article PubMed PubMed Central Google Scholar Soltis, P. Microtus. Like FISH with Mli2, FISH with Mli3_4 produced some signal in all pericentromeric regions (Fig. 2e, orange). 8, respectively) are indicated by arrowheads. WGDs have occurred in many lineages, including amphibians, fishes, yeasts, flowering plants, and vertebrates, all of which are being studied by modern genomics1, 2. & Dujon, B. In the description field, the textual description of a rearrangement giving raise to one or more derivative chromosome(s) is entered, either using the ISCN detailed notation (e.g. "der(22)(22pter->22q112::9q34->9qter)" (the detailed notation showing symbols for aberration type, e.g. "t(9;22)(9pter->q34::22q112->22qter;22pter->22q112::9q34->9qter)" is not supported because it does not work with more complicated rearrangements) or the ISCN short notation (e.g. "t(9;22)(q34;q112)"). The modified technique used here allowed us to obtain high-quality chromosome spreads and to also reliably identify chromosome 2 (MLI2). Syst. V., Mordvinov, V. Fluorescence in situ hybridization (FISH) in Macrostomum lignano Following CISS-hybridization, the DNA probes Mli1, Mli2, and Mli3_4 all painted intensively the pericentromeric regions, suggesting that all these regions contain clusters of homologous repeats (Fig. 2a). 65, 1088–1098 (2011).Article PubMed Google Scholar Rieger, R. The analysis comprises lots of information which can be extracted from the ISCN formula: composite karyotype: denotes whether the karyotype was marked "composite" ("[cp]") clone size: size of the clone, if it was noted, otherwise 0. 108, 1490–1495 (2011).ADS Article PubMed PubMed Central Google Scholar Janssen, T. carpio has undergone a fourth WGD only about 8 MYA ago, and most of the duplicated ancestral genes remain present in the C. Cell Dev. Primarily, many cases of tri- and tetrasomy on chromosome 1 were revealed (and also some pentasomy in Macrostomum sp. C., Reeders, S. 104, 17004–17009 (2007).ADS CAS Article PubMed PubMed Central Google Scholar Kaessmann, H. Sex reduces genetic variation: a multidisciplinary review. The .NET Framework 2.0 must be installed (it is freely available from Microsoft). The caudal regeneration blastema is an accumulation of rapidly proliferating stem cells in the flatworm Macrostomum lignano. Sex allocation adjustment to local sperm competition in a simultaneous hermaphrodite. lignano line DV1/10 genome was derived from the more ‘normal’ 2n = 8 M. If an error was encountered in the description of the rearrangement, a message is displayed to show the problem. 119, 171–184 (2007).CAS Article PubMed Google Scholar Torres, E. 8 using chromosome-specific microdissected DNA probes. In contrast to the aneuploidy described in M. 8, respectively. Nature Rev. The usual karyotype of M. Inverted DAPI images are to the right of the FISH images. F. lignano Given the above-mentioned karyotype variability observed within the DV1 inbred line14, we here aimed at establishing a line with a pure-breeding and thus more predictable karyotype. The only striking karyotypic difference between Macrostomum sp. Chromosome slides and DNA probes were denatured separately. Origin of human chromosome 2: an ancestral telomere-telomere fusion. This would suggest that the ‘normal’ 2n = 10 karyotype of Macrostomum sp. & Canestro, C. Specifically, a 10× excess of unlabelled PCR product generated from genomic DNA of M. B. Ecol. Drawing a Karyogram draws the ideograms of all derivative and non-derivative chromosomes of the karyotype (more...). lignano.The most striking finding of our recent studies, however, was that M. It appears possible that that hidden tetraploidy in the M. & Neuhauss, S. If you want to circumvent these limitations of the online version, you may use the desktop version of CyDAS which is available from the Download section. The chromosomes are designated by Arabic numerals. 354, 817–821 (2016).ADS CAS Article PubMed Google Scholar Wang, J. 8 specimens was supported by the Swiss National Science Foundation (SNSF, project 31003A-143732 to LS). S., Soltis, D. In a selection of 100 newly karyotyped worms, 96 had the expected 2n = 10 karyotype. If so, the observed 2n = 8 karyotype would represent a tetraploid, and the observed 2n = 9 and 2n = 10 aneuploids could therefore be considered as hidden penta- and hexaploids, showing no genetic imbalance. 14). & Soltis, D. Whole genome duplication events in plant evolution reconstructed and predicted using myosin motor proteins. lignano may represent a form of hidden polyploidy14.In the current study, we test the proposition that the M. A., Meyers, B. Evolution Tree shows putative pathways of karyotype development during tumour progression. 17, 37, doi:10.1186/s13059-016-0908-1 (2016).Article PubMed PubMed Central Google Scholar Van de Peer, Y., Maere, S. Trends Genet. With respect to the chromosome arms, FISH with probe Mli2 painted intensively chromosome MLI2 and a contiguous region on the long arms of all four MLI1 copies (Fig. 2a,c,e), while probe Mli1 painted all chromosomes (as previously observed in ref. lignano (T. The genomes of many extant species show evidence of past whole genome duplications (WGDs). & Pritchard, J. lignano line DV1/10 (a,c,e) and Macrostomum sp. 8Identical FISH experiments with the same combinations of chromosome-specific DNA probes and labeled 28S rDNA probe from M. Nature Genet. Drawing aberrant chromosomes With this program, ideograms for derivative chromosome(s) can be drawn. Microdissected DNA probes Mli1 and Mli2 were generated, respectively, from 15 copies of chromosome MLI1 (the largest chromosome) and MLI2 (the largest among the small chromosomes) of M. Interestingly, all MLI1 copies were painted identically (see below for details on the 28S rDNA probe). (a) Autotetraploid (2n = AAAA) formation from a diploid species (2n = AA); (b) Hybrids (2n = AABB) formed from crosses between two closely related diploid species 1 (2n = AA) and 2 (2n = BB) with polyploidy through unreduced gamete formation, (c) Hybrids (2n = AB) formed from hybridization between species 1 (2n = AA) and 2 (2n = BB) without polyploidy, but followed by one WGD. BMC Biology. 15, 241–247 (1999).CAS Article PubMed Google Scholar Birchler, J. F., Jackson, S. Under Scenario C (Fig. 3c), the first stage includes interspecies hybridization (or allopolyploidization) between two closely related ancestral species. For the Web Service's documentation see here. (a) A metaphase spread of the M. Yeast. The evolutionary fate and consequences of duplicate genes. If errors are encountered during analysis, they are shown in the text field instead of the result. 25, R538–R542 (2015).CAS Article PubMed PubMed Central Google Scholar Gorelick, R. Genome Res. Curr. 179, 737–746 (2008).CAS Article PubMed PubMed Central Google Scholar Siegel, J. The authors declare that they have no competing interests. Deutsche Version Some example programs are available for online analysis of cytogenetic data: ISCN Analysis allows the user to analyse simple or polyclonal karyotypes (more...). & Compton, D. It was created via full-sib and half-sib inbreeding for 24 generations, and has since been kept at small population sizes to maintain a high level of homozygosity44. H. Trends in Genetics. 8, whole-chromosome aneuploidy in many taxa (including plants, invertebrates, mammals) often results in severe developmental disorders, diseases, and lethality18,19,20. The measurements were performed on 10 metaphase spreads and the reported values represent means ± 1 SD. Scenario A (Fig. 3a) includes a direct WGD of the ancestral genome at the first stage. lignano genome in a way similar to how the M. Minor errors (e.g. slightly wrong chromosome count, sloppily denoted sex chromosomes, upper case instead of lower case characters, ...) are automatically corrected and the corrected version is shown in the description field. & Boore, J. Effects of mating status on copulatory and postcopulatory behaviour in a simultaneous hermaphrodite. & Chris Pires, J. (b) A metaphase spread of Macrostomum sp. lignano line DV1/10 with 2n = 10 (4 m + 2 m + 2 m + 2 m). These chromosomal rearrangements may have solved, at least in part, the meiotic problems that one could expect to occur in tetraploids. Positional RNA-Seq identifies candidate genes for phenotypic engineering of sexual traits in Macrostomum lignano. As far as the M. With FISH, we did not reveal remnants of ancestral pericentromeric or telomeric DNA repeats at the ancestral chromosome fusion sites. It is important to mention that we uncovered a high frequency of aneuploids, and in a few cases also other numerical and structural chromosome abnormalities, within this inbred DV1 line14. 8.After 3 months of culture maintenance (4 generations), 100 DV1/10 worms were randomly selected and karyotyped. In Polyploidy and Genome Evolution. Clarification of the mechanisms underlying genome evolution in Macrostomum species now requires further studies, including comparative genomics of species closely related to M. 20, 1313–1326 (2010).CAS Article PubMed PubMed Central Google Scholar Zadesenets, K. 8 in (b,d,f) is indicated by arrows. 8 chromosome 3; MLI3, to Macrostomum sp. Nat. 8 — a sibling species of M. S., Karamysheva, T. The evolutionary significance of ancient genome duplications. Morphometry showed that MLI2 was somewhat longer than the Mli2 painted region in MLI1q (Table 1). Int. We speculate that some level of tolerance to aneuploidy for small chromosomes could derive from the presence of the hidden tetraploidy in the M. lignano — revealed that it usually has one additional pair of large chromosomes (2n = 10) showing a high homology to MLI1, thus suggesting hidden hexaploidy in its genome. Evidence exists that interspecific hybrids themselves very commonly produce higher frequencies of unreduced gametes than their progenitor species23. 8), while we also observed some rare cases of gain or loss of small chromosomes in both species (unpublished data). After a denaturation step at 75 °C in 70% formamide/2× SSC for 3 min, the slides were dehydrated through a pre-cooled ethanol series (70%, 80% and 96%) and then left for air drying. incomplete: shows whether the karyotyoe was marked "incomplete" ("inc") double minutes: the double minutes of the karyotype markers: the marker chromosomes in the karyotype rings: ring chromosomes whose origin could not be described more closely chromosome count field: the data given in the chromosome count field chromosome count: lower and upper limit of the chromosome count ploidy level: ploidy calculated from chromosome count or taken from ploidy information in the chromosome count field sex chromosomes: non-aberrant sex chromosomes count of aberration elements aberration : a description of each aberration element, the number of metaphases the aberration was found in, its quantitative changes in SCCN, qualitative changes in SCCN, and break points; in case of derivative chromosomes ("der" or "ider" aberrations), the ISCN detailed description is shown; in some cases, fusion products may be given (the feature "fusions" is still in early development) in the summary section, break points, structural and quantitative aberrations are shown summed up for all aberrations of the karyotype, as well as a Complex Karyotype Aberration Score. 21, 2495–2508 (2007).CAS Article Google Scholar Mason, A. With respect to the latter, for many species there exist data on mosaic individuals that are characterized by abnormal karyotypes of some of their somatic cells40, including, for example, cancer cells that often contain numerous chromosome rearrangements. For drawing, the scaling and a cutoff-level can be selected. Evidence for karyotype polymorphism in the free-living flatworm, Macrostomum lignano, a model organism for evolutionary and developmental biology. Distribution of repetitive DNA sequences in chromosomes of five opisthorchid species (Trematoda, Opisthorchiidae). lignano was added to the DNA probe mix to decrease the fluorescent signal coming from labeled DNA repeats. lignano genome. The drawing sequence indicates the sequence in which chromosomes are to be drawn; "BR" indicates a line break. 14), leading to double-labeled regions (Fig. 2c,e). lignano chromosome, MLI1, would not lead to gene dosage imbalance, gene dosage might of course still be disturbed by aneuploidy of one of the small chromosomes. V., Katokhin, A. Aneuploidy. Origins, evolution, and phenotypic impact of new genes. For karyotyping and FISH experiments, the suspension was dropped onto cold wet microscope slides (76 mm × 26 mm, 1 mm thick), and for metaphase microdissection, the suspension was dropped onto clean cold wet cover slips (60 mm × 24 mm, 0.17 mm thick).Generation of chromosome-specific microdissected DNA probesChromosome microdissection was carried out as previously described49. Dependence on Karyotype Complexity shows how often a selected rearrangement was encountered in relation to the total number of rearrangements encountered in the karyotypes. Microscopy was performed at the Interinstitutional Shared Center for Microscopic Analysis of Biological Objects (ICG SB RAS, Novosibirsk). Recently, an unusual karyotypic diversity was revealed in this species. tropicalis (2n = 20) revealed an allotetraploid — i.e. cross-species hybridization — origin of the X. Genes & Dev. To test this we explore the genome structure in both M. CyDASControl is an Internet Explorer embedded control for ISCN analysis, drawing ideograms of aberrant chromosomes, and developing karyograms (more...). 35, 119–125 (2015).CAS Article PubMed Google Scholar Wendel, J. Such a dependence is visualized with the Dependence Network. The karyogram functionality is far enhanced in comparison to the Online Example: You start from a simple karyotype which need not be aberrant, and introduce aberrations step by step. 8.The previously documented karyotype diversity in M. Polyploidy and genome evolution in plants. 290, 1151–1155 (2015).ADS Article Google Scholar Lan, X. So while relatively little is currently known about the early stages of post-WGD genome evolution in vertebrates, even less is known in invertebrates.In general, WGD, as is true for other kinds of gene duplication events, leads to changes in the make-up of the whole genome and karyotype and thereby opens up possibilities for the evolution of new molecular functions, e.g. by facilitating neo- or subfunctionalization of genes and gene networks11,12,13. 28, 189–214 (2012).CAS Article PubMed PubMed Central Google Scholar Ijdo, J. The field-work for collection of Macrostomum sp. 76, 721–739 (2012).CAS Article PubMed PubMed Central Google Scholar Pennisi, E. 8 with 2n = 10 (4 m + 2 m + 2 m + 2 m). A. PLoS One. To date, only few studies have proposed that many WGDs in both plants and animals may have resulted from unreduced gamete formation23, 27.It has been proposed that WGDs are usually followed by massive and rapid gene loss and structural rearrangements30,31,32. M. Two rounds of whole genome duplication in the ancestral vertebrate. Forts Zool. Earlier results suggested that it would likely be difficult to establish a pure-breeding 2n = 8 line, as 2n = 8 individuals were consistently underrepresented in that line, possibly as a result of a maintained polymorphism (i.e. selection against certain homozygous combinations of the MLI1 chromosomes14). Janssen and L. Dependence Network Many distinct rearrangements occur during cancer progression and karyotype evolution. Higher values will be ignored. 92, 82–107 (2015).CAS Article PubMed Google Scholar Altug-Teber, O. The fate of recent duplicated genes following a fourth-round whole genome duplication in a tetraploid fish, common carp (Cyprinus carpio). Web Service Some functionality is already available as a Web Service. Evolution of plant genome architecture. Genome sequence and genetic diversity of the common carp. However, the question about the origin of worms having abnormal karyotypes has to remain open for now and will require more detailed investigations of meiosis and karyotype inheritance patterns.The instability of the M. 8 chromosome 4 (i.e. the chromosomes with the 28S rDNA cluster); and MLI4, to Macrostomum sp. & Wing, R. Therefore, what we formerly considered to be cases of aneuploidy of MLI1, namely the 2n = 9 and 2n = 10 karyotypes, now instead appear to be cases of hidden polyploidy. 99, 323–329 (2002).CAS Article PubMed Google Scholar Download referencesWe are thankful to Dita B. lignano, MLI1, while two clusters each of pericentromeric and telomeric repeats have apparently been lost from MLI1 due to chromosomal rearrangements, since our FISH experiments revealed no remnants of telomeres or centromeres in either MLI1p or MLI1q14. For analysing data, the maximum number of cases read, and a pre-processing of data can be selected. Moreover, microdissected DNA probe Mli3_4 was generated from 15 copies of chromosomes MLI3 and MLI4 (note that these two chromosomes are too similar in size to be reliably distinguished on chromosome spreads; see also Results). An experimental page for step by step development of a karyogram is also available. Dependence on Karyotype Complexity The Aberration Count Distribution shows how often a selected rearrangement was encountered in relation to the total number of rearrangements encountered in the karyotypes. lignano and its sibling species Macrostomum sp. S. Scripting must be enabled. This suggests that both clusters of pericentromeric and telomeric repeats were probably lost from the painted region of MLI1q.Table 1 Morphometry of the MLI1 arms with respect to the regions painted with Mli2. The first multi-gene phylogeny of the Macrostomorpha sheds light on the evolution of sexual and asexual reproduction in basal Platyhelminthes. F., Belling, J. 85, 453–461 (2013).Article Google Scholar Arbore, R. However, on the high-quality prometaphase and early-metaphase plates we obtained in the current study, MLI2 could also be reliably identified, while MLI3 and MLI4 could not be reliably distinguished (Fig. 1a). 8 and M. The 28S rDNA probe was generated and hybridized on metaphase chromosomes as previously described14. Drawing a Karyogram The ideograms of all chromosomes - both derivative and non-derivative - inferred from an ISCN formula are shown. & Conery, J. In contrast to other teleost species, which have undergone three rounds of WGD, C. 31, 5–10 (2015).CAS Article PubMed Google Scholar Dowling, T. laevis genome7. Mol. 109, 14746–14753 (2012).ADS CAS Article PubMed PubMed Central Google Scholar Orr, B., Godek, K. Genome and transcriptome of the regeneration-competent flatworm, Macrostomum lignano. Moreover, about 25% of the recently duplicated genes that were analyzed showed some level of functional divergence, and among these cases neo- and sub-functionalization appear to be the main outcomes8. To date we have karyotyped several hundreds of individual worms but have never found clear cases of mosaic individuals. lignano karyotype has arisen due to a WGD and subsequent fusion of one full haploid chromosome set into this large metacentric chromosome, leading to the usual 2n = 8 karyotype of this species. 43, 127–132 (2005).Article Google Scholar Schärer, L., Littlewood, D. Animal Behaviour. The search for smaller lost regions will require additional techniques, such as high-throughput sequencing and FISH with unique DNA fragments, but this goes beyond the scope of the current study.When considering the difference in length between MLI2 and the Mli2-painted region of MLI1q, we should take into account the fact that we have previously identified a higher level of condensation of MLI1 compared to the condensation observed in the other M. Possible evolutionary scenarios for the emergence of the M. For this reason, we only used prometaphase and early metaphase chromosomes for morphometry in the present study. 23, 937–950 (2006).CAS Article PubMed Google Scholar Blakeslee, A. 8 in ref. 28, 593–619 (1997).Article Google Scholar Morales, L. Growth arrest and chromosome instability in aneuploid yeast. 46, 1212–1219 (2014).CAS Article PubMed Google Scholar Egger, B. Zool. Among hundreds of karyotyped worms we found only a few specimens with aneuploidy for one of the small chromosomes, and interestingly, also these worms did not show any significant abnormalities (although they were too rare to be included in crossing experiments to test their siring ability). New insights into the troubles of aneuploidy. The study of Macrostomum sp. ISCN Analysis This simple program allows the user to analyse both simple (monoclonal) karyotypes as well as polyclonal karyotype. Rep. Dependence Network shows statistical dependence between pairs of rearrangements (more...). lignano chromosomes in metaphase14. Drawing ideograms of aberrant chromosomes draws ideograms of derivative chromosomes (more...). Whole-genome duplication in teleost fishes and its evolutionary consequences. BMC Evol. & Andersson, D. lignano (counterstained with DAPI). 8, were maintained under standard laboratory conditions42, 43. For technical reasons, the maximum number of cases to be analysed cannot exceed 500. For example, studies of aneuploidy in model species from different taxa (plants, invertebrates, mammals) have revealed that aneuploidy has severe effects on development and growth18, 37,38,39, and in humans, aneuploidy is associated with abnormalities in cell function (including cancer) and organismal development40.In the current study, we provide evidence that the large chromosome, MLI1, in the M. lignano genome arose through a single WGD, followed by chromosomal rearrangements, which fused one full haploid set of chromosomes in the ancestral karyotype into one large chromosome. A WGD is usually followed by rediploidization as a result of gene divergence3. & Rubtsov, N. Laboratory cultures of marine Macrostomida (Turbellaria). & Heng, H. Genetics. 8, which is mainly represented by aneuploidies of the largest chromosome, prompted us to explore the organization of this chromosome in both M. The age of these WGDs therefore makes them unsuitable for the study of the first steps of genome evolution towards rediploidization6, and there are relatively few animal species that are known to have gone through WGDs recently. & Vizoso, D. Thus, the FISH painting of M. Nevertheless, it is still possible that the respective lengths of MLI2 and its homologous region in MLI1q, as inferred by morphometry, were affected by the level of condensation in chromosomes MLI1 and MLI2. Proc Natl Acad Sci USA. Our results suggest that post-WGD chromosome evolution has fused almost one full haploid set of chromosomes into the largest chromosome of M. The advantages and disadvantages of being polyploid. Chromosome Res. In some previously performed crossing experiments, we indeed observed a small fraction of offspring with karyotypes that were unexpected when considering their parental karyotypes (unpublished data), suggesting that meiotic errors could potentially be a reason for the appearance of worms with abnormal karyotypes. Simultaneous FISH with Mli2 and Mli3_4 painted chromosome MLI1 completely (Fig. 2e), with some colocalization in the pericentromeric regions (Fig. 2e, orange).FISH with the 28S rDNA (green) and the Mli2 (red) probes revealed a 28S rDNA cluster at the ends of the p-arm of MLI1 (Fig. 2a). Under Scenario B, individuals of two ancestral species both produce unreduced (diploid) gametes due to meiotic failure, and the fusion of two diploid gametes results in allotetraploidy (Fig. 3b). Aneuploidy: cells losing their balance. lignano line DV1/10 is the absence of the 28S rDNA repeats in the largest chromosome of Macrostomum sp. lignano or a closely related ancestor due to tetrasomy of the largest chromosome. Analysis of Data Sets for Gains, Losses and Breakpoints analyses large data sets, e.g. downloaded from the Mitelman DB, for gains and losses, and breakpoints (more...). Sci. We also note that no cluster of telomeric repeats was previously observed at the proximal end of the painted region (i.e. there were no interstitial telomeric sequences in MLI1, see ref. Here, we try to describe these evolutionary pathes by analysing the karyotype data from many patients at many stages of tumour progression. 61, 84–86 (2012).CAS Article PubMed Google Scholar Rubtsov, N. 352, 1009–1013 (2016).ADS CAS Article PubMed PubMed Central Google Scholar Hellsten, U. Conversely, FISH of the Macrostomum metaphase chromosomes with the Mli1 probe revealed no region in the small metacentrics left unpainted. FISH with Mli3_4 revealed specific signals in two pairs of small chromosomes (identified as MLI3 and MLI4; Fig. 2e, red) and in the region of MLI1 that remained unpainted with Mli2 (Fig. 2e, green). W., Baldini, A., Ward, D. The M. The site " must be added to the trusted zone. It is not necessary to include all chromosomes in the field, also duplicates are possible. 12, 14, doi:10.1186/s12983-015-0106-0 (2015).Article PubMed PubMed Central Google Scholar Wasik, K. Preparation of Xenopus tropicalis whole chromosome painting probes using laser microdissection and reconstruction of X. lignano inbred line DV1 has been widely used in a range of studies14, 44,45,46,47. Parasitol. 10, 725–732 (2009).Article PubMed Google Scholar Inoue, J., Sato, Y., Sinclair, R., Tsukamoto, K. Analysis of Data Sets for Gains, Losses and Breakpoints This program shows how large data sets can be analysed with CyDAS for recurrent gains and losses as well as recurrent break points. Evolution by gene loss. A new model organism among the lower Bilateria and the use of digital microscopy in taxonomy of meiobenthic Platyhelminthes: Macrostomum lignano, n.sp (Rhabditophora, Macrostomorpha). lignano were performed on chromosomes of Macrostomum sp. Explore content BMC Dev. Res. Evolution. lignano with 2n = 10—and that we can therefore expect exciting results from comparative genomics of M. Moreover, this mechanism is even more important for the generation of genomic diversity in plants24, 28, 29. 3, e314, doi:10.1371/journal.pbio.0030314 (2005).Article PubMed PubMed Central Google Scholar Hufton, A. Mouse autosomal trisomy, two’s company, three’s a crowd. (more...). 8 genome through aneuploidy in M. Our previous results led us to suggest that the karyotype in M. One of them is the African clawed frog Xenopus laevis (2n = 36), in which the last WGD dates back about 40 MYA6. This prompted the questions about how to interpret these considerable levels of aneuploidy in these two Macrostomum species. Microbiol. & Wells, R. & Kurabayashi, A. Accelerated gene evolution and subfunctionalization in the pseudotetraploid frog Xenopus laevis. Ohno’s dilemma: evolution of new genes under continuous selection. Google Scholar Ladurner, P., Schärer, L., Salvenmoser, W. & Kollmar, M. 13, 202, doi:10.1186/1471-2148-13-202 (2013).Article PubMed PubMed Central Google Scholar Xu, P. After selecting the desired resolution of the ideogram and the coloring (black and white only or default colors; the desk top version allows for changing the colors), a map viewer to be linked with the chromosomal bands, and the scale, the button "Draw" is clicked and the chromosome is drawn. Dev. Chromosomal duplication and Mendelian phenomena in Datura mutants. a table shows then the amounts of gains, losses and structural aberrations per chromosomal band. Konopatskaia for providing algae and f/2 medium in Novosibirsk. Of the other three, one had 2n = 9 (3 large metacentrics and 6 small metacentrics), one had 2n = 11 (5 large metacentrics and 6 small metacentrics), and one had 2n = 15 (6 large metacentrics and 9 small metacentrics). The loss of telomeric regions may have occurred immediately during the chromosome fusion event at stage two or later, while the centromeres with pericentromeric repeats were probably lost in the following stages of evolution21, 22.Figure 3Possible scenarios for autoploid (a) and allopolyploid (b,c) formation of the M. According to an earlier morphometric analysis of metaphase chromosomes, the average lengths of chromosomes MLI2, MLI3, and MLI4 were 2.74 ± 0.27 µm, 2.49 ± 0.025 µm, and 2.24 ± 0.29 µm, respectively14. Genome Biology. Chromosome fission or duplication in Macrostomum lignano (Macrostomorpha, Plathelminthes) - remarks on chromosome numbers in ‘archoophoran turbellarians’. 8 worms were cultivated as an outbred culture (i.e. starting every generation with 100 hatchlings to maintain genetic diversity) initiated from about 90 field-collected individuals (see also Table 1 in ref. 8 (b). Cell fusion as the formation mechanism of unreduced gametes in the gynogenetic diploid hybrid fish. 8 genome was derived from the M. lignano (Fig. 1a). & Secor, C. 52, 388–390 (1920).ADS CAS Article PubMed Google Scholar Hernandez, D. If you find something abusive or that does not comply with our terms or guidelines please flag it as inappropriate. Rapid genome reshaping by multiple-gene loss after whole-genome duplication in teleost fish suggested by mathematical modeling. tuba, and M. Reorganization of the X chromoso me in voles of the genus. In the description field, a textual description of the karyotype(s) is entered. 18, 431–439 (2010).CAS Article PubMed Google Scholar Li, J.-T. J. K. I. carpio genome34. The scaling factor for the images is set to a maximum of 1. L. Another WGD was recently discovered in the genus Cyprinus, which dates back to about 8 MYA and which resulted in the genome of the common carp Cyprinus carpio 8. lignano genome evolution (Fig. 3). 14).So while trisomy and tetrasomy for the largest M. Front Zool. Moreover, the global changes in genome and karyotype reorganization, including subsequent chromosome rearrangements after WGD, may also lead to reproductive isolation from the ancestral form.We have recently proposed that the clade containing the free-living flatworm Macrostomum lignano may have experienced a recent genome duplication14 as compared to other species in the genus Macrostomum 14,15,16,17. With respect to the former, karyotypic abnormalities could of course also arise as result of mistakes occurring during meiosis20, although it has been argued that in species with sexual reproduction, meiosis and syngamy may actually

represent a barrier to the spread of abnormal karyotype formation41. 8, 9051–9055 (1991).ADS Article Google Scholar Capper, R. Rev. The background FISH signal in the other chromosomal regions presumably comes from labeled interspersed DNA repeats and suggests insufficient suppression of repetitive DNA hybridization.Figure 2Two-color fluorescence in situ hybridization (FISH) of the M. New insights into the karyotype evolution of the free-living flatworm Macrostomum lignano (Platyhelminthes, Turbellaria) The free-living flatworm Macrostomum lignano is a model organism for evolutionary and developmental biology studies. Evolutionary role of interspecies hybridization and genetic exchanges in yeasts. Then select from the menu the type of aberration you want to introduce and then click on the desired breakpoints. & Postlethwait, J. Polyploidy in fish and the teleost genome duplication. 8 show unexpectedly high levels of intraspecific karyotype diversity. J., Waeschenbach, A., Yoshida, W. In the description field, the ISCN formula is entered following the ISCN standards. Therefore, one presumably full haploid genome was packed into MLI1, leading to hidden tetraploidy in the M. Specifically, worms are either ‘normal’ 2n = 8, or they are aneuploid with one or two additional large chromosome(s) (i.e. 2n = 9 or 2n = 10, respectively). The region of chromosome MLI1 painted with the Mli2 probe appeared to be somewhat shorter than chromosome MLI2, and we think that the loss of the repeat clusters alone likely cannot fully explain this shortening. These results allow us to conclude that no large chromosomal regions were lost during the chromosomal rearrangements that led to MLI1 formation (given the observed chromosome condensation levels and FISH conditions used here, we expect that we could have detected such regions if they were larger than about 3 Mb). 14).Establishing the DV1/10 subline of M. Science. 8 with salmon sperm DNA as a DNA carrier, as previously described14, with a minor modification to include -chromosome in situ suppression (CISS) - hybridization. Soltis, P. Cyprinus carpio. & Farnham, M. A cutoff of 0 means that gains and losses or structural aberration, resp., will be scaled relative to their maximum value. lignano 14. Initial DNA amplification of the collected chromosomes was performed using a GenomePlex Single Cell Whole Genome Amplification Kit (WGA4) (Sigma-Aldrich) according to the manufacturer’s protocol. 112, 14918–14923 (2015).ADS CAS Article PubMed PubMed Central Google Scholar Albalat, R. We therefore instead aimed at establishing a pure-breeding 2n = 10 line (further called DV1/10) initiated from two worms that were selected from among a range of karyotyped specimens14 and which had a 2n = 10 karyotype and tetrasomy of chromosome MLI1.Metaphase chromosome preparationChromosome spreads were prepared using the cell suspension method in Carnoy’s fixative (methanol: glacial acetic acid, 3:1) as described previously, with some modifications14, 48. & Rieger, R. lignano and high-throughput sequencing of microdissected DNA libraries derived from individual chromosomes.Members of two closely related species of the free-living flatworm genus Macrostomum, M. The painting patterns obtained (Fig. 2b,d,f) were almost identical to those observed in M. E. lignano. B., Van de Peer, Y. Therefore, the question about putatively lost chromosomal regions, other than the above-mentioned clusters of pericentromeric and telomeric repeats, must remain open at this stage.The data obtained here are in a good agreement with the idea that the M. 67, 3233–3242 (2013).CAS Article PubMed Google Scholar Marie-Orleach, L., Janicke, T. FISH with microdissected DNA probes was performed on metaphase chromosomes of M. lignano genome arose due to a WGD and/or an interspecific hybridization event between closely related Macrostomum species. The desk top version also allows you to order the rearrangements interactively. Genet. PLoS Biol. Yesterday’s polyploids and the mystery of diploidization. 5, 8199, doi:10.1038/srep08199 (2015).CAS Article PubMed PubMed Central Google Scholar Braasch, I. (a,b) 28S rDNA (green) and Mli2 (red); (c,d) Mli1 (green), Mli2 (red), co-localized FISH signal (orange); (e,f) Mli2 (green) and Mli3_4 (red), co-localized FISH signal (orange). C. 8 karyotypes among worms from our laboratory cultures and natural populations also renders plausible the formation of the Macrostomum sp. 18, 1582–1591 (2008).CAS Article PubMed PubMed Central Google Scholar Wolfe, K. Of the other four, one was 2n = 10 (with 4 large and 5 small of the usual metacentrics, plus one small submetacentric chromosome), two were 2n = 11 (5 large metacentrics and 6 small metacentrics), and one was 2n = 14 (6 large metacentrics and 8 small metacentrics).Generation of chromosome-specific microdissected DNA probesAfter metaphase chromosome preparation and Giemsa staining, chromosome MLI1 could always be clearly distinguished from the other chromosomes based on its size (Fig. 1), whereas the three pairs of smaller chromosomes often appeared similar in morphology and size. Specifically, a straight ploidy series, with the 2n = 8, 2n = 9, and 2n = 10 karyotypes representing, respectively, tetra-, penta-, and hexaploids, could explain why the individuals of M. A simple karyotype is analysed as such, while for a polyclonal karyotype a composite karyotype is calculated first, and then that composite karyotype is analysed. 112, 12462–12467 (2015).ADS CAS Article PubMed PubMed Central Google Scholar Zadesenets, K. et al. 36, 525 (1988). Mating behavior and the evolution of sperm design. The Macrostomum sp. Early vertebrate whole genome duplications were predated by a period of intense genome rearrangement. Our results provide evidence for hidden tetra- and hexaploidy in the genomes of the ‘normal’ 2n = 8 and 2n = 10 karyotypes of M. Vizoso for assistance in establishing the study species in Novosibirsk, and Tim Janicke and Georgina Rivera Ingraham for assistance in collecting specimens of Macrostomum sp. Morphometric analysis of chromosome MLI1 showed that in all the chromosome spreads analyzed, the MLI1 arm containing the painted region was longer than the other arm of this chromosome (Table 1). However, traces of duplication events may remain for long time periods and can be detected by complex comparative genomic analysis (e.g. identification of inter- and intra-genomic collinearity; phylogenetic reconstruction of gene family evolution; analysis of K S age distribution33). 43, 114–126 (2005).Article Google Scholar Janicke, T. 11, e0164915, doi:10.1371/journal.pone.0164915 (2016).Article PubMed PubMed Central Google Scholar Egger, B. lignano genome has evolved from an ancestral genome following a WGD event and that a subsequent fusion of one full set of chromosomes has then led to the formation of the large metacentric MLI1 chromosome. For analysing data, the maximum number of cases read, and banding resolution can be selected. This research (establishment of the DV1/10, chromosome slide preparation, generation of microdissected DNA probes, FISH experiments, morphometric analysis) was supported by the Russian Foundation for Basic Research (RFBR research project No. 16-34-60027 mol_a_dk). M., Williams, B. S., Marchant, D. Unreduced gametes: meiotic mishap or evolutionary mechanism? Cytogenet. Moreover, on prometaphase chromosomes we could identify a cluster of 28S rDNA at the end of the q-arm of MLI3 (see also ref. 6, 836–846 (2005).CAS Article PubMed Google Scholar Bergthorsson, U. 9, 41, doi:10.1186/1471-213X-9-41 (2009).Article PubMed PubMed Central Google Scholar Niwa, O., Tange, Y. & Amon, A. The PCR products were labeled with Flu- or TAMRA-dUTP (Genetyx, Novosibirsk) in additional 20 PCR cycles using WGA3 kit (Sigma-Aldrich).Fluorescence in situ hybridization (FISH)FISH with 28S rDNA probe was used as a quality control of in situ hybridization. Mli2-painted regions of MLI1 (chromosome 1 and 2 of Macrostomum sp. & Nishida, M. & Veitia, A. The optimized technique for chromosome preparation allowed identification and collection of chromosomal material belonging to definite chromosomes (at least, MLI1 and MLI2).Figure 1Metaphase spreads of M. Annu. 2, 333–341 (2001).CAS Article PubMed Google Scholar Lynch, M. The ISCN formula is automatically update, even for terribly complex aberrations! Please note that this control has some requirements: The CyDASControl requires Microsoft Internet Explorer version 6 or later. 17, 179–391 (2016).Article Google Scholar Mühlhausen, S. However, phylogenetic lineages exist in which no massive gene loss has occurred since the WGD. Opin. Evolution Tree The rearrangements occuring during tumour progression seem to follow some common evolution pathes. lignano line DV1/10 chromosomes. The nature of telomere fusion and a definition of the critical telomere length in human cells. Chromosome MLI2 in (a,c,e) (chromosome 3 of Macrostomum sp. While the typical lifetime of duplicated genes has been estimated to be in the order of several millions of years4, 5, the WGDs in the vertebrate and teleost lineages took place mostly about 500 and 350 MYA (million years ago), respectively. hystrix, M. R. Some of the rearrangements occur preferrable together with specific other rearrangements, and other rearrangements seem to almost exclude each other. Instead, the karyotypes of nearly all analyzed cells belonging to the one specimen were always identical, indicating a reliable and precise mechanism of mitosis in these species. The hypotonic treatment was considerably prolonged and was performed in hypotonic 0.56% KCl solution for 2 hours at RT. Most of them (97 specimens) had the expected chromosome number 2n = 10. spirale) is 2n = 6, with three pairs of small (sub)metacentric chromosomes, which are of similar size to the small metacentrics of M. Schärer, unpublished data), has a karyotype that is similar to that of M. Furthermore, no intensive signal that was similar to the FISH signal in the pericentromeric region of MLI2 was observed within the painted region of MLI1q. lignano genome evolution under Scenarios B and C then follow as under Scenario A. The second stage includes global chromosomal rearrangements, such as bringing one full haploid set of chromosomes in the ancestral genome into one large chromosome. Our thanks extend to Irina D. The number of rearrangements analysed and a threashold value for a dependence to be shown can be adjusted. Cross-species fluorescence in situ hybridization (FISH) using DNA probes generated from chromosomes of the only known diploid clawed frog species, X. After FISH, chromosomes were counterstained with DAPI dissolved in Vectashield antifade solution (Vector Laboratories, USA).Microscopic analysisMicroscopic images of chromosomes were captured and analyzed using a CCD-camera installed on an Axioplan 2 imaging microscope equipped with filtercubes #49, #10, and #15 (ZEISS, Germany) and using the ISIS4 software package (MetaSystems GmbH, Germany) at the Inter-institutional Shared Center for Microscopic Analysis of Biological Objects (Institute of Cytology and Genetics SB RAS, Novosibirsk, Russian Federation). & Schärer, L. 5, 31, doi:10.1186/1741-7007-5-31 (2007).Article PubMed PubMed Central Google Scholar Krylov, V. After one additional year of culture maintenance (20 generations), the DV1/10 line was karyotyped again. 8) having additional copies of the large chromosome do not show severe abnormalities and even produce viable offspring (yet to be shown for Macrostomum sp. lignano (a) and Macrostomum sp. The results obtained in the current studies may thus suggest that the Macrostomum sp. 8 (b,d,e) chromosomes using microdissected DNA probes and a 28S rDNA probe from M. E.) 341-383 (Springer, 2012).Glasauer, S. Moreover, Macrostomum sp. While this scenario does not appear very likely (since it requires the likely rare combination of unreduced gametes in both species plus hybridization), we here nevertheless include it as a theoretical possibility. The DNA probe mix was denatured at 96 °C for 3 min and incubated at 37 °C for 1 h (for pre-annealing of repetitive DNA). Gene balance hypothesis: connecting issues of dosage sensitivity across biological disciplines. Furthermore, some laboratory lines of M. 8 may have recently arisen from M. Specific transcriptional changes in human fetuses with autosomal trisomies. lignano genome is concerned, further studies require high-quality genome assemblies and comparative analyses of the genomes of species that are closely related to M. At the current point of our study, it is impossible to determine whether allopolyploidy occurred through a WGD, followed by long-term evolution or whether it was part of a speciation process through interspecific hybridization.Studies on genome evolution have over the last decades shown that interspecific hybridization is a much more important mechanism of speciation than was previously thought23,24,25,26,27. Data from many sources can be analysed, if they were exported into a text file in the Mitelman format (or directly downloaded from the Mitelman database; see HowTo Download data from the Mitelman database) or special other formats for karyotype banding analysis or comparative genome hybridisation (CGH) (see HowTo on Data Formats). Click into the yellow bar on top the window and enter the first karyotype. The location of the data file is entered into the "File" field (you may select it using the "Browse" button on the right to it. Dehal, P. (ed. Aneuploid worms did not show visible behavioral or morphological abnormalities and were successful in reproduction. carpio has undergone one additional round of species-specific WGD, which has resulted in a duplicated chromosome set (2n = 100)9, 10. lignano genome, since any gene dosage imbalance resulting from small chromosome aneuploidy might be less harmful in the tetraploid background compared to normal diploids.Aneuploidy can potentially result from errors in both meiosis and mitosis. The desired banding resolution of the ideograms and the coloring (black and white only or default colors; the desk top version allows for changing the colors), a map viewer to be linked with the chromosomal bands, and the scale, can be adjusted. 8 genomes are discussed. In this study, we generated microdissected DNA probes from chromosome 1 (further called MLI1), chromosome 2 (MLI2), and a pair of similar-sized smaller chromosomes (MLI3, MLI4). & Fisher, E. 8, a sibling species of M. The role of hybridization and introgression in the diversification of animals. The extended homologous regions in the small and large chromosomes could lead to problems during meiotic chromosome conjugation. FISH using these probes revealed that MLI1 consists of contiguous regions homologous to MLI2-MLI4, suggesting that MLI1 arose due to the whole genome duplication and subsequent fusion of one full chromosome set into one large metacentric chromosome. 289, 1045–1060 (2014).CAS Article PubMed Google Scholar Comai, L. lignano showed a high frequency of aneuploidy of the largest chromosome (further called MLI1), and aneuploid worms showed no visible morphological or reproductive abnormalities14.Interestingly, Macrostomum sp.

Introduction Global developmental delay (GDD) affects 1%–3% of the population of children under 5 years of age, making it one of the most common conditions presenting in paediatric clinics; causes are exogenous, genetic (non-metabolic) or genetic (metabolic). Recent advances in biotechnology and genetic testing mean that the investigations available to perform for … Fritillaria (fritillaries) is a genus of spring flowering herbaceous bulbous perennial plants in the lily family ().The type species, Fritillaria meleagris, was first described in Europe in 1571, while other species from the Middle East and Asia were also introduced to Europe at that time. The genus has about 130–140 species divided among eight subgenera. Assisting students with assignments online. Assisting students with assignments online. avis stake spinomenal casino de la baule casino gratuit sans depot variante du poker avec 5 des. ... We will provide you with a FREE Turnitin report with every essay upon request, so you'll know your paper is really plagiarism-free! QA Department. The family Ursidae is one of nine families in the suborder Caniformia, or "doglike" carnivorans, within the order Carnivora.Bears' closest living relatives are the pinnipeds, canids, and musteloids. Modern bears comprise eight species in three subfamilies: Ailuropodinae (monotypic with the giant panda), Tremarctinae (monotypic with the spectacled bear), and Ursinae (containing six …