For a species with XY chromosomal sex determination the probability that a chromosomal fusion will join a sex chromosome and an autosome can be calculated with equation 1.

(1)

where is the diploid autosome count and is the diploid number. However, calculation of this probability becomes more complex if we would like a more general representation that would apply to species with XO or multi-XY sex determination systems (e.g. XXY, XYYY). In particular we must account for the rare possibility that two non-homologous Y or X chromosomes could fuse. This probability can be calculated with the equation 2.

(2)

where is again the diploid autosome count, is the diploid chromosome count in damns, is the diploid chromosome count in sires, is the number of X chromosomes carried by males, and is the number of Y chromosomes carried by males. The first ratio in equation 2 provides the probability that a fusion in a female will involve only autosomes or only sex chromosomes . Likewise, the second ratio provides the probability that a fusion in males will involve only autosomes or only sex chromosomes . In both cases the term two in the denominator controls for the fact that we assume an equal contribution of fusions from both males and females. We recognize that the and terms could be represented in terms of , , and however, this leads to a less intuitive form of the equation. Note that formula 2 is equally applicable to female heterogametic systems by reversing the sire and damn terms, and replacing X terms with Z and Y terms with W. Evaluating this equation across a range of chromosome number we see that the number of autosomes present in the genome has a striking impact of the probability of sex chromosome autosome fusions, and that for species with few chromosomes a large proportions of fusions should be expected to join sex chromosomes and autosomes even if these have equal fitness effects as fusions between autosomes and sex chromosomes.



Figure XXX Probability of sex chromosomes autosome fusions. Using equation 2 we can calculate the proportion of fusions that joing autosomes and sex chromosomes under the three most common male heterogametic chromosomal sex determination systems. For species a diploid autosome count of 6 or fewer regardless of the sex chromosome system greater than 40% of all fusions should join sex chromosomes and autosomes.

CODE:

Pfsa <- function(Da, scs){

if(scs=="XO"){

Xs <- 1

Y <- 0

Ds <- Da + 1

Dd <- Da + 2

}

if(scs=="XY"){

Xs <- 1

Y <- 1

Ds <- Da + 2

Dd <- Da + 2

}

if(scs=="XYY"){

Xs <- 1

Y <- 2

Ds <- Da + 3

Dd <- Da + 2

}

if(scs=="XXY"){

Xs <- 2

Y <- 1

Ds <- Da + 3

Dd <- Da + 4

}

res <- 1 - ((Da\*(Da-2)+2\*Xs\*(2\*Xs-2))/(2\*Dd\*(Dd-2))) -

((Da\*(Da-2)+max(c(Xs,Y))\*(max(c(Xs,Y))-1))/(2\*Ds\*(Ds-2)))

return(res)

}

maxnum <- 60

XO <- Pfsa(Da=seq(from=2, to=maxnum, by=2), scs="XO")

XY <- Pfsa(Da=seq(from=2, to=maxnum, by=2), scs="XY")

XYY <- Pfsa(Da=seq(from=2, to=maxnum, by=2), scs="XYY")

XXY <- Pfsa(Da=seq(from=2, to=maxnum, by=2), scs="XXY")

rates <- c(XO,XY,XYY,XXY)

types <- rep(c("XO", "XY", "XYY","XXY"), each=length(XO))

autosomes <- rep(seq(from=2, to=maxnum, by=2), times=4)

res <- data.frame(rates, types, autosomes)

ggplot(res, aes(y=rates, x=autosomes)) + geom\_point(aes(colour=types), stat="identity", position="identity", alpha=0.5, size=3) + geom\_line(aes(colour=types), stat="identity", position="identity", alpha=0.5) + theme\_bw() + theme(text=element\_text(family="sans", face="plain", color="#000000", size=15, hjust=0.5, vjust=0.5)) + scale\_size(range=c(1, 3)) + xlab("Diploid autosome count") + ylab("Proportion of fusions joining autosome and gonosome")