Supporting Information 1 – Additional methods & results

Evolutionary and demographic consequences of temperature-induced masculinization under climate warming: the effects of mate choice

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Formulas for calculating effective population size, sex ratio selection, linkage and generation time

Generation time (T; mean age of reproduction) was calculated following Case (1999):

$$T = \frac{1}{R_0} \sum_{x=1}^{max} l_x b_x x \, ,$$

where R_0 is the average number of female offspring produced by a female over her lifetime, l_x is the annual survival rate and b_x is the average number of daughters produced when she is x years old. In all our simulations, this yielded a generation time of 3 years.

Effective population size (N_e) is an important measure for conservation biology and it is strongly affected by ASR. Therefore, we estimated N_e for each year in each run using the formula by Hartl and Clark (2007: page 124) as

$$N_e = \frac{4 N_m N_f}{N_m + N_f} \, ,$$

where N_m is the number of adult males and N_f is the number of adult females. In each run, we recorded the year when the ultimate population decline started, i.e. when N_e permanently decreased below the early population equilibrium N_e, calculated as the average N_e during 10 years before the start of climate warming when the population was in a stable state (i.e. last 10 years of the burn-in period).

In some simulations that we ran as sensitivity tests for our parameter settings, we explored the effects of reduced WW viability. Because in our model density-dependent selection occurred before genotype-dependent mortality, extra mortality of WW individuals caused unrealistically rapid decline in the adult population size. To compensate for this, we calculated N_e based on a corrected adult population size that would be expected if WW mortality occurred during the zygote stage (i.e. before the density-dependent larval mortality). In these specific scenarios N_e was calculated the same way as above, but N_m and N_f respectively were calculated as the number adult males and females saved from the simulations multiplied by the correction factor Cf:

$$Cf = \frac{phi \times \left(N - O_{WW} \right) \times \frac{O_{ZZ}}{O_{ZZ} + O_{ZW}} + phi \times (N - O_{WW}) \times \frac{O_{ZW}}{O_{ZZ} + O_{ZW}} + phi \times O_{WW}}{phi \times O_{ZZ} + phi \times O_{ZW} + phi \times \frac{phi\_aa}{phi} \times O_{WW}} \, ,$$

where O_{ZZ}, O_{ZW}, and O_{WW} are the number of offspring by each genotype calculated by the model for 3 years (i.e. the average generation time) before the current year, N is their total number, phi is the first-year survival of ZZ and ZW offspring, and phi_aa is the first-year survival of WW offspring.

To better understand forces behind the changes of C_R frequency, we calculated s, the selection coefficient resulting from sex-ratio selection. In each year in each run, we recorded progeny sex ratio of females expressing preference towards sex-reversed males and normal males, denoted by x_R and x_N respectively. In scenario 10% C_R every female carrying allele C_R preferred sex-reversed males (dominant C_R), while in scenario 90% C_R only $C_R C_R$ homozygotes expressed such preference (recessive C_R). Selection coefficient s against $C_N C_N$ was calculated following the usual definition (e.g.Hartl and Clark 2007: page 226), i.e. as the difference of the relative fitnesses of the two homozygotes. $C_R C_R$ is taken as the reference genotype and the relative fitness of $C_N C_N$ compared to it is calculated as the number

of descendants of an average $C_N C_N$ individual two generations later divided by that of an average $C_R C_R$ individual. The genotype in the generation in focus (referred to as generation P) that produces more advantageous progeny sex ratio relative to the population sex ratio (i.e. ASR) of the next generation (referred to as generation $F1$) will have more descendants two generations later, i.e. in generation $F2$. In our model the preference locus C affects progeny sex ratio directly only in females, and we neglected the smaller indirect effect in males originating from linkage disequilibrium with the threshold locus and supposed that $C_R C_R$ and $C_N C_N$ males have equal progeny sex ratios.

First the relative fitness of $C_N C_N$ *females* was calculated compared to $C_R C_R$ *females* originating from their different progeny sex ratios. We used the male per female ratio (i.e. the odds of being a male) in generation $F1$ referred to as z, and calculated from ASR as ASR/(1-ASR). z gives the relative value of a daughter compared to a son as an average female of generation $F1$ will leave z times as many offspring as an average male of the same generation. Let α be the average number of offspring of a male in the generation $F1$, so the average number of offspring of a female in $F1$ is $z\alpha$. Furthermore, in the calculation of the number of $F2$ descendants we need the number of offspring of an average female in generation P, referred to as β, and supposed to be the same for $C_R C_R$ and $C_N C_N$ females (as the C locus affects the sex ratio of the offspring, but has no effect on their number). An average $C_N C_N$ female of generation P has $x_N \beta$ sons and $(1 - x_N)\beta$ daughters in $F1$, and in turn the number of her $F2$ descendants is as follows:

$$x_N \beta \cdot \alpha + (1 - x_N)\beta \cdot z\alpha,$$

while the number of $F2$ descendants of an average $C_R C_R$ female is:

$$x_R \beta \cdot \alpha + (1 - x_R)\beta \cdot z\alpha.$$

The relative fitness of a $C_N C_N$ female in generation P (taking a $C_R C_R$ female as the reference) is:

$$\frac{x_N + (1 - x_N)z}{x_R + (1 - x_R)z}.$$

The selection coefficient against $C_N C_N$ among females will be denoted by s' to distinguish it from s, the selection coefficient measuring the strength of sex-ratio selection in the whole population, among both males and females. One can express s' in terms of the relative fitness of $C_N C_N$ females using the definition of the selection coefficient:

$$\frac{x_N + (1 - x_N)z}{x_R + (1 - x_R)z} = 1 - s'$$

As half of the alleles on the C locus in generation $F1$ comes from generation P females and their distribution between the sexes is affected by the mothers' genotype on the C locus, while the other half comes from generation P males with negligible effect of the fathers' genotype on the C locus on offspring sex ratio, we calculate s as

$$s \approx \frac{s'}{2} = \frac{\dfrac{x_N + (1 - x_N)z}{x_R + (1 - x_R)z}}{2}.$$

The above selection coefficient s can predict allele frequency changes between generation $F1$ and $F2$ using the progeny sex ratios of the females in generation P. As we had overlapping generations, when calculating s for year t, we used the progeny sex ratios recorded in year t-T, where T is the generation time, but we used year t ASR to calculate z, the male per female ratio.

We calculated the coefficient (D) of linkage disequilibrium (LD; see Slatkin 2008) to explore if and when linkage disequilibria occurred between allele C_R and 1) chromosome *A* and 2) the *thr_{low}* allele.

$$D = p_{C_R B} p_{C_N b} - p_{C_R b} p_{C_N B} \text{ ,}$$

where C_R and C_N are the alleles occurring on the preference locus, B and b are the alleles occurring on another locus and p is the probability of co-occurrence of two specified alleles in a single gamete. Deviation of D from zero means linkage disequilibrium between the two loci. If D is positive, the two alleles occur together more frequently than expected in case of independent inheritance, while negative D means that co-occurrence is less frequent than expected. Note that the value of D can range between -0.25 and 0.25, but is typically closer to 0 if the allele frequencies are far from 0.5 (similarly to frequency of C_R in our simulations).

Table S1. Examples for species exhibiting sex-chromosome linked body colour, other morphological traits and behaviour that can influence mating success.

| Class	Species	Chromosome (system)[1]	Description	Publication
Insecta	*Danaus chrysippus*	neo-W (ZW)	In a hybrid zone of two subspecies *(D. c. chrysippus and dorippus)* in East Africa, fusion occurred in *D. c. chrysippus* between chromosome W and an autosome which previously coded a distinguishing colour of the two subspecies.	Smith et al. 2016
	Drosophila sp.	X (XY)	Several traits are X-linked, such as wing vibration index, mating speed, mating frequency, pheromones, song characters and locomotory activity.	Reinhold 1998; Long and Rice 2007
	Choristoneura fumiferana / C. pinus	Z (ZW)	Female fecundity and body size, pheromone composition and female calling time are Z-linked.	Sperling 1994
	Colias philodice / C. eurytheme	Z (ZW)	Male ultraviolet wing colour, black wing border and wing pigmentation, pheromone composition of males and adult size were found to be Z-linked.	Sperling 1994
	Cyrtodiopsis dalmanni	X (XY)	The X chromosome accounts for 25% of change in the eyespan: body size ratio across selected lines. This ratio is important in female mate choice.	Wolfenbarger and Wilkinson 2001
	Papilio glaucus	W (ZW)	*P. g. glaucus* females inherit a W-linked allele that causes melanic colour. Surprisingly, in *P. g. glaucus x canadensis* hybrids this melanism is suppressed.	Hagen and Scriber 1989
Actinopterygii[2]	*Cynotilapia afra* and *Pseudotropheus elongatus*	W (ZW and XY)	Experimental hybridization of these species suggested that in a complex system of ZW/ZZ and XX/XY, the presence of chromosome W causes a female-like body colour.	Parnell and Streelman 2013
	Neochromis omnicaeruleus	X (XY)	Blotched pattern is determined by colour genes in linkage with X-linked female-determining genes (dominant over male-determining function of Y). There is a large variation in mating preferences for body colour across males collected from a single population.	Pierotti et al. 2009
	Oryzias latipes	Y (XY)	In d-rR strain medaka, white pigmentation is X-linked recessive trait, while orange pigmentation is Y-linked and dominant. Sex-reversed XY d-rR strain females show male-type (orange/red) pigmentation.	Aida 1921; Edmunds et al. 2000

	Poecilia reticulata	Y (XY)	There are several Y-linked body colour genes in this species, and female preference might have facilitated the reduction of X/Y recombination at these loci. Females show significant variance in their mating preferences for male ornaments.	Brooks and Endler 2001; Wright et al. 2017
		Y (XY)	Fin shape and size, courtship and attractiveness are also Y-linked.	Lindholm and Breden 2002
	Xiphophorus pygmaeus	Y (XY)	Alleles at a Y-linked gene cause either blue or gold body colour in males. Female preference for colour differs among populations.	Kingston et al. 2003
		Y (XY)	Size is also Y-linked.	Lindholm and Breden 2002
	Gambusia holbrooki	Y (XY)	Breeding tests suggest that the rare melanic body colour variant (mottled-black) is Y-linked and its expression is influenced by temperature.	Horth 2006
Amphibia	*Glandirana rugosa*	X (XY)	The allele encoding a wild-type colour is dominant (can be present on both Y and X). A recessive allele coding whitish-yellow body colour was found on X.	Miura et al. 2011
	Pleurodeles waltl	W (ZW)	Recessive mutant allele linked to W changes the coloration of the ventral skin after metamorphosis: black spots on a grey background, instead of yellowish tint.	Collenot et al. 1989
Reptilia	*Python regius*	X and Y (XY)	Inheritance pattern of "coral glow" colour suggests sex-linkage of the responsible (incomplete dominant) allele with some level of recombination between X and Y.	Mallery Jr. and Carrillo 2016
	Pogona vitticeps	Z or W (ZW/ZZ)	Tail length, boldness, and activity level depend more on genotype compared to phenotype based on measures of ZZ males and ZW or ZZ females.	Li et al. 2016
Aves	*Erythrura gouldiae*	Z (ZW)	A Z-linked locus with two alleles determines head colour where red is dominant over black (two coexisting morphs). Mating preference for morph also seems to be Z-linked.	Pryke 2009
	Taeniopygia guttata	Z (ZW)	Genes with likely contribution in song control appear to be Z-linked.	Tomaszycki et al. 2009

	Gallus gallus domesticus	Z (ZW)	A Z-linked gene is responsible for the small body size of the Sebright Bantams breed.	Custodio and Jaap 1973
Mammalia	*Mus musculus domesticus*	Y (XY)	Both the pseudoautosomal and non-recombining parts of Y contribute to the variation in aggression.	Sluyter et al. 1994
	Mus minutoides	Y (XY)	Agression seems to be Y-linked in the African pigmy mouse. Due to an X-linked mutation, male-to-female sex reversal occurs in this mammal and XY females are more fertile and more aggressive than XX females.	Saunders et al. 2016

[1] Chromosome: the sex chromosome harbouring a gene encoding a distinguishing body colour or pattern. System: sex determination system (ZW is short for ZW/ZZ and XY is short for XX/XY).

[2] Among fish, occurrence of sex-linked colour is especially well documented across Poeciliidae (e.g. *Poecilia* and *Xiphophorus*) species (Lindholm and Breden 2002, McKinnon and Pierotti 2010). Further examples for sex-linked colour in Lepidoptera are listed in Sperling (1994).

Note that genetic background of body colour (and related mating preference) is mostly unknown among amphibians, but several species show sexual dichromatism (Bell and Zamudio 2012). Colouration has been shown to play a role in mate choice in some amphibians and reptiles (see examples in Fig. 1 in the main text), and in many fish species (Madsen and Shine 1992, Lindholm and Breden 2002, Kingston et al. 2003, Pierotti et al. 2009, Richards-Zawacki et al. 2012, Maan and Sefc 2013).
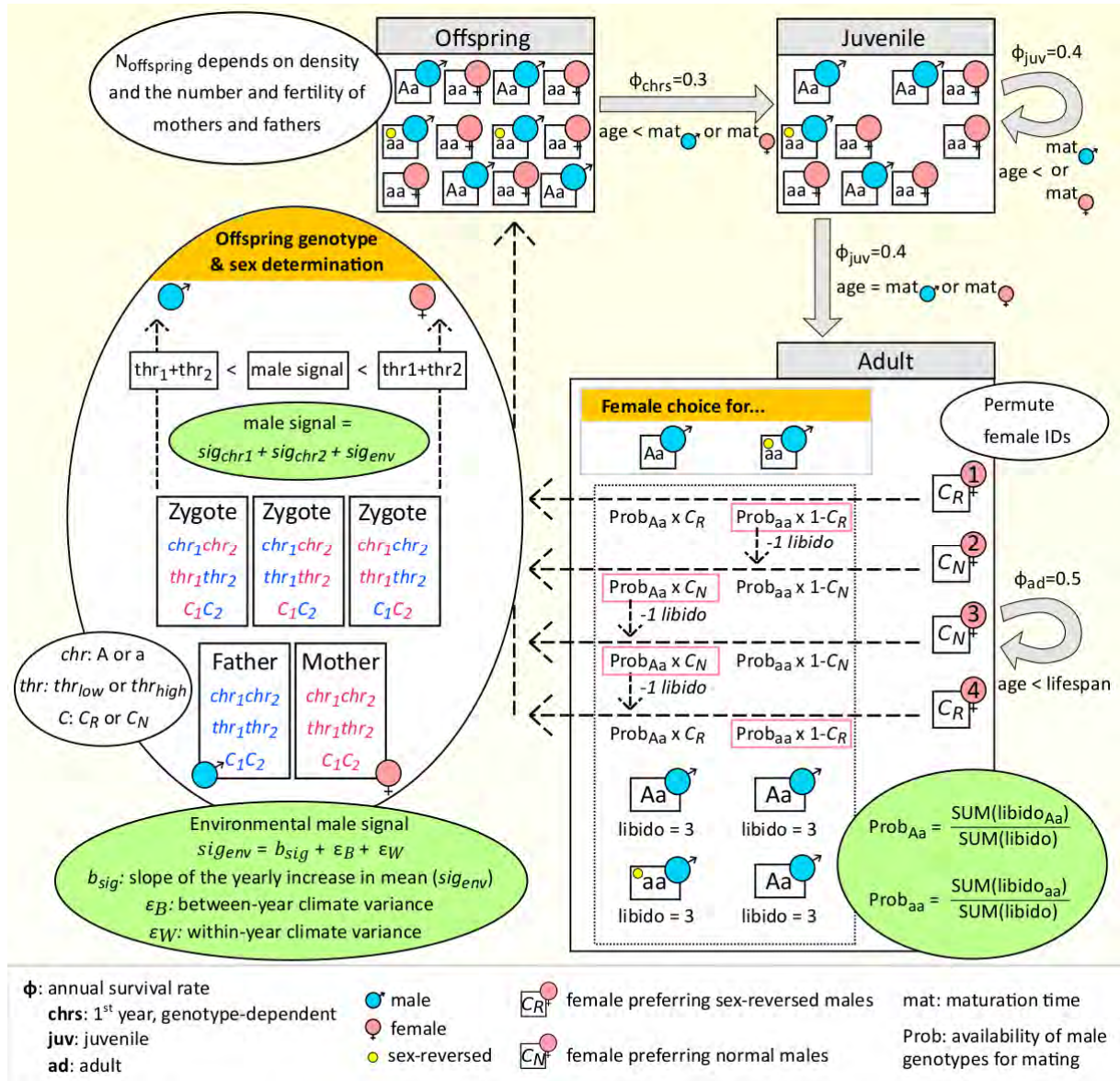
Figure S1. Life history, breeding and inheritance in our model. In our simulations maturation time was 2 years for both sexes and maximum lifespan was 12 years. Grey arrows indicate a new year and, in case of survival, aging 1 year. Amount of environmental male signal (sig_{env}) increases with time due to climate warming. The population goes extinct when there is only one sex (male) left across all age groups.

Table S2. Model parameters and settings used in the simulations.

Parameter	Notation	Value	Further information
Sex ratio of offspring and juveniles in the initial population: proportion of ZW or XY individuals.	$Aa0$	0.5	Corresponding to Bókony et al. (2017: XY0, ZW0.
Number of adult females in the initial population. The number of adult males is set to the same value.	$NF0$	100	Corresponding to Bókony et al. (2017: NF0.
Levels of genetic male signal produced by a single "a" or "A" allele on the sex-determining locus.	sig_a	1	Lacking empirical data and given that there is no consensus across similar models (Quinn et al. 2011, Schwanz et al. 2013), values of sig_a and sig_A were chosen arbitrarily.
	sig_A	1.5	
The initial sex determination system is defined by parameter thr0. If thr0×2 ≥ sig_a+sig_A, then the initial system is ZW/ZZ; otherwise, it is XX/XY. Furthermore, if set_thr is FALSE, thr0 defines the mean value of the normal distribution of which thr0 alleles will be chosen.	$thr0$	1.375	With the above settings of sig_a and sig_A this value defines a ZW/ZZ system.
		1.125	With the above settings of sig_a and sig_A this value defines an XX/XY system.
Number of different threshold alleles present in the initial population. If set_thr is TRUE, the value of this paramater is ignored.	n_thr0	2	We followed Schwanz et al. (2013) when we assumed that a single locus would define individual threshold for male signal. Number of alleles was set following empirical data by Chandler et al. (2009), Wessels et al. (2014) and Schroeder et al. (2016). Notably in reality this threshold may be influenced by multiple loci (Roff 1998, Holleley et al. 2016).
Vector defining the relative frequency of each threshold allele in the initial population, if set_thr_prob is TRUE. Relative frequency vaules must be given in the same order as allele values.	thr_prob0	c(0.5, 0.5)	Relative frequency vaules must be given in the same order as allele values.
Values of threshold alleles are defined by the vector def_thr0, if set_thr is TRUE.	def_thr0	c(1.31, 1.375)	Individual threshold for the level of male signal that is required for male development is the sum of the two threshold alleles carried. We set the lower threshold allele value so individual threshold of homozygotes would be just above the male signal value of genetically female individuals (following Schwanz et al. 2013). The higher allele value was arbitrarily set to the mean of male signal values of genetic males and genetic females. With the above settings of *'sig_a'* and *'sig_A'*,
		c(1.06, 1.125)	

			def_thr0=c(1.31, 1.375) refers to a ZW/ZZ system, while *def_thr0*=c(1.06, 1.125) refers to an XX/XY system.
Boolean defining if values of the threshold alleles are chosen manually (TRUE) or picked randomly from a normal distribution around *thr0* (FALSE). If TRUE, parameter *'def_thr0'* defines the threshold alleles.	*set_thr*	TRUE	In preliminary studies, we also explored simulations with randomly chosen thr allele values, but for simplicity, we finally decided to set them manually.
Boolean defining if relative frequencies of thr allele values are set manually in the initial population (i.e. as defined by thr_prob0). If FALSE, a frequency value will be chosen for each threshold allele from a normal distribution around 0.5, with values being forced to be between 0.25 and 0.75. (Note: this works only with exactly two thr alleles).	*set_thr_prob*	TRUE	In preliminary studies, we also explored simulations with randomly chosen initial thr allele frequencies, but for simplicity, we finally decided to set them manually.
Mean level of environmental male signal in the initial population.	*sig_env0*	0	Corresponding to Bókony et al. (2017): m_masc0.
Extent of annual increase in environmental male signal, referring to climate warming.	*b_sig*	0.003	Similar, but not the same as Bókony et al. (2017): b_masc. After 30 years of warming, probability of sex reversal is about 9% among genetically female individuals with the *'def_thr0'* values used here. We used this setting based on the findings of Alho et al. (2010).
Standard deviation of the annual mean of environmental male signal, referring to annual stochasticity in climate warming.	*sd_sig*	0.01	Defines the error term ε_B in the regression equation for calculating sig_{env} (see Methods). Corresponding to Bókony et al. (2017): sd_masc.
Standard deviation of the individual levels of environmental male signal, referring to individual differences in temperature experienced during the sensitive period of sexual development.	*sd_indivsig*	0.05	Defines the error term ε_W in the regression equation for calculating sig_{env} (see Methods). Individuals developing in different microhabitats in the same breeding site and/or at different times during the same breeding season may experience somewhat different temperatures.
Boolean defining whether aa individuals can become males or not. If TRUE, then all aa individuals will always become	*aa_no_masc*	FALSE	FALSE: corresponding to p_rel_WW_masc=1 in (Bókony et al. 2017), TRUE: corresponding to p_rel_WW_masc=0 in Bókony et al. (2017).

females, regardless of environmental conditions.			In our simulations we assumed that aa (WW) individuals can sex-reverse.
Vector containing the preference alleles present in the initial population (values between 0 and 1 should be chosen, meaning the probability that the female would choose the normal male from a pool of one normal male and one sex-reversed male). Individual female preference is calculated as the average value of the two alleles carried by the female if *dom_pref* =FALSE, or as the value of the dominant allele if *dom_pref* =TRUE.	*def_pref0*	0.9	As a baseline scenario, we ran simulations where all the females preferred normal males. The allele value of 0.9 encodes 90% chance of choosing a normal male over a sex-reversed male. We did not set preference to 100% because females should mate even when only males of less desired quality are present (i.e. refusing reproduction is not beneficial). In the sensitivity analyses, we also ran scenarios assuming that females mate indiscriminately (allele value = 0.5).
		c(0.1, 0.9)	In scenarios 10% C_R and 90% C_R, we allowed two alleles on the C locus: one encoding 90% preference for normal males (or no preference, in sensitivity analyses) and the other 10% preference for normal males (i.e. 90% preference for sex-reversed males).
Vector containing the relative frequency of each preference allele in the initial population (given in the same order as allele values in *'def_pref0'*).	*pref_prob0*	1	This value was set when *'def_pref0'* was set to 0.9, resulting in uniform preference for normal males across all females.
		c(0.1, 0.9)	In this scenario, the allele encoding preference for masculinized individuals is rare (10%). Recent studies suggest that sex reversal may occur naturally in some species (Alho et al. 2010, Perrin 2016, Lambert et al. 2019). Among such conditions, a certain level of variance could be maintained in female mating preferences prior to considerable climate warming.
		c(0.9, 0.1)	In this scenario, the allele encoding preference for masculinized individuals is common (90%). A pre-existing sensory bias can be present in the population, e.g. due to some valuable food of similar colour to that appearing on the body of sex-reversed individuals (Ryan 1998, Rodd et al. 2002). This preference allele plays little if any role in mating as long as sex reversal is very rare, thus it is (nearly) neutral in the initial population.
Dominance of a specific preference allele (defined under parameter 'dominant'). If FALSE: type of inheritance of female preference is intermediate, if TRUE: one allele is fully dominant over the other(s).	*dom_pref*	TRUE	Due to the lack of empirical data, we assumed that the inheritance of preference alleles is either intermediate or dominant-recessive; in this paper we only show the results of the latter in detail.

Value of the dominant preference allele. This is used only if dom_pref is TRUE.	*dominant*	0.1	We assumed that the allele encoding 90% preference for sex-reversed males was dominant when rare but recessive when common. We did not study the other two combinations because a rare recessive allele is unlikely to have enough time to spread under rapid climate change while a common dominant allele has a very high chance of fixation.
		0.9	
Boolean defining if proportion of female offspring should be calculated for mothers with respect for their relative preference for sex-reversed or normal males. *(Note: this function works only if def_pref0 contains exactly two values!)*	calc_success	TRUE	This option enables the user to track the progeny sex ratio of females that prefer normal or sex-reversed males. This helps the interpretation of results but increases run time considerably.
Boolean defining if coefficient (D) of linkage disequilibrium should be calculated between the allele encoding relative preference for sex-reversed males and 1) the threshold allele of lower value, 2) chromosome A. Furthermore, proportion of this preference allele will be calculated among alleles inherited from 1) fathers and 2) mothers. *(Note: this function works only if exactly two preference alleles and two threshold alleles are set in the initial population!)*	calc_linkage	TRUE	Linkage disequilibrium (LD) may occur between loci linked to different chromosomes (that is, D values deviating from zero; Slatkin 2008). This option enables the user to track D values over time, which helps the interpretation of results but increases run time.
Maximum number of offspring that can survive density-dependent selection during the early developmental (larval) stage.	*N_max*	2000	Corresponding to Bókony et al. (2017): N_max.
Survival rate following the larval stage until the end of the first winter; may depend on genotypic sex (AA, Aa or aa).	*phi_AA*	0.3	Corresponding to Bókony et al. (2017): phi_ZZ.
	phi_Aa	0.3	Corresponding to Bókony et al. (2017): phi_WZ and phi_XY.
	phi_aa	0.3	Corresponding to Bókony et al. (2017): phi_WW and phi_XX. In most of our simulations, survival was independent of genotype. However, in sensitivity analyses, we ran scenarios with reduced WW survival (*phi_aa* = 0.225, 0.15, 0.075, or zero).

Annual survival rate of juveniles (i.e. from the end of the first winter until sexual maturity). Independent from genotype and phenotype.	*phi_juv*	0.4	Corresponding to Bókony et al. (2017): phi_juv.
Annual survival of mature individuals; depends on phenotypic sex.	*phi_m*	0.5	Annual survival rate of phenotypic males. Corresponding to Bókony et al. (2017): phi_m. The same adult survival rate was assumed in simulated fish populations by Wang and Höök (2009), and average survival rate is similar in lizard species as well (Bókony et al. 2019).
	phi_f	0.5	Annual survival rate of phenotypic females. Corresponding to Bókony et al. (2017): phi_f.
Mean number of offspring annually produced by a female which can successfully develop into viable juveniles if there is no density-dependent selection.	*f_fert*	200	Corresponding to Bókony et al. (2017): fert.
Fertility of aa or Aa males relative to AA males. If any of these numbers is <1, then the number of offspring produced each year is min(*N_max*; *Nmother* × *f_fert* × mean(*m_fert*), where *N_max* is the carrying capacity, *Nmother* is the number of females that found a mating partner, *f_fert* is the average number of offspring each female can recruit in the absence of density-dependence, and *m_fert* is the relative fertility of each male that engaged in mating compared to the fertility of normal males.	*m_fert_aa*	1	Corresponding to Bókony et al. (2017): alpha_WW, alpha_XX.
	m_fert_Aa	1	Corresponding to Bókony et al. (2017): alpha_WZ. In our simulations we assumed that sex-reversed males are as fertile as normal males. Additionally, we ran simulations where sex-reversed males' fertility was 75% of normal males' (based on the meta-analysis of (Senior et al. 2012); these results are not shown in this paper.
Maximum number of clutches that a male can fertilize during each breeding season.	*libido*	3	A male can successfully mate with multiple females within the same breeding season. However, sperm quality and quantity is limited, and males can get exhausted after a few fertilizations (Hettyey et al. 2009).
Age of sexual maturity, measured in years. If set to 1, the selection specified in phi_juv will not affect these individuals.	*mat_m*	2	Age of sexual maturity in phenotypic males. Corresponding to Bókony et al. (2017): mat_m. Empirical data suggest that the age of maturation is around 2 years in several amphibian, fish, and lizard species (Goodwin et al. 2006, Bókony et al. 2017, 2019).
	mat_f	2	Age of sexual maturity in phenotypic females. Corresponding to Bókony et al. (2017): mat_f.

Maximum age (measured in years) that an individual can reach.	*lifespan*	12	Corresponding to Bókony et al. (2017): lifespan. 12-years lifespan is realistic among amphibians and fish as well (Goodwin et al. 2006, Bókony et al. 2017).
Number of simulation runs with the same settings.	*n_runs*	100	Populations were affected by several stochastic factors and repeated simulations were therefore needed, but simulations ran for considerable time.
Maximum number of years to simulate after the burn-in period. Running will stop earlier if the population goes extinct.	*t_Max*	400	The simulation stops when one of the phenotypic sexes disappears from the population, but maximum 400 years after burn-in (our simulated populations never persisted that long).
Number of years which allows the initial population to reach a stable state without climate change (burn-in period).	*t_burn_in*	50	The burn-in period allows the population to reach a stable structure (age groups, sex chromosome genotypes, etc.) before climate warming starts.
Boolean determining if plots of the burn-in period are to be shown from the first run. Useful for specifying the optimal value of t_burn_in.	*show_burn_in*	TRUE	When testing new settings, it can be useful to inspect graphs of sex ratios, allele frequencies etc. in the initial population.

Table S3. Linear contrasts comparing the three scenarios in either XX/XY or ZW/ZZ initial sex-determination system. All p-values in the table were adjusted by simultaneous Bonferroni correction.

Starting system	Variable	Scenarios[1]	p	Mean1	Mean2	Difference	SE	Difference in generations
XX/XY	Year of extinction	0% - 10%	1	122.77	122.81	0.04	0.44	0.01
		0% - 90%	<0.0001	122.77	126.72	3.95	0.44	1.32
		10% - 90%	<0.0001	122.81	126.72	3.91	0.44	1.3
	Length of XX/XY (years)	**0% - 10%**	<0.0001	36.88	30.87	-6.01	0.84	-2
		0% - 90%	<0.0001	36.88	28.49	-8.39	0.84	-2.8
		10% - 90%	0.164	30.87	28.49	-2.38	0.84	-0.79
	Length of final period (years)	**0% - 10%**	<0.0001	85.89	91.94	6.05	0.98	2.02
		0% - 90%	<0.0001	85.89	98.23	12.34	0.98	4.11
		10% - 90%	<0.0001	91.94	98.23	6.29	0.98	2.1
	Year when 5-yr average ASR first exceeded 0.6	0% - 10%	1	53.90	54.70	0.80	1.08	0.27
		0% - 90%	0.003	53.90	58.20	4.30	1.08	1.43
		10% - 90%	0.042	54.70	58.20	3.50	1.08	1.17
ZW/ZZ	Year of extinction	0% - 10%	1	294.26	293.35	-0.91	0.72	-0.3
		0% - 90%	0.090	294.26	292.07	-2.19	0.72	-0.73
		10% - 90%	1	293.35	292.07	-1.28	0.72	-0.43
	Length of ZW/ZZ (years)	**0% - 10%**	0.003	35.73	32.57	-3.16	0.79	-1.05
		0% - 90%	<0.0001	35.73	29.96	-5.77	0.79	-1.92
		10% - 90%	0.038	32.57	29.96	-2.61	0.79	-0.87
	Length of transition (years)	**0% - 10%**	<0.001	91.42	86.42	-5.00	1.08	-1.67
		0% - 90%	<0.0001	91.42	59.68	-31.74	1.08	-10.58
		10% - 90%	<0.0001	86.42	59.68	-26.74	1.08	-8.91
	Length of XX/XY (years)	0% - 10%	1	101.22	99.63	-1.59	0.98	-0.53
		0% - 90%	1	101.22	99.27	-1.95	0.98	-0.65
		10% - 90%	1	99.63	99.27	-0.36	0.98	-0.12
	Length of final period (years)	**0% - 10%**	<0.0001	65.89	74.73	8.84	1.25	2.95
		0% - 90%	<0.0001	65.89	103.16	37.27	1.25	12.42
		10% - 90%	<0.0001	74.73	103.16	28.43	1.25	9.48
	Mean ASR during transition	**0% - 10%**	<0.0001	0.72	0.63	-0.09	0.00	-
		0% - 90%	<0.0001	0.72	0.49	-0.23	0.00	-
		10% - 90%	<0.0001	0.63	0.49	-0.14	0.00	-
	Year when 5-yr average ASR first exceeded 0.6	**0% - 10%**	<0.001	53.22	61.20	7.98	1.76	2.66
		0% - 90%	<0.0001	53.22	212.38	159.16	1.76	53.05
		10% - 90%	<0.0001	61.20	212.38	151.18	1.76	50.39

[1] Scenarios: 0% C_R, 10% C_R and 90% C_R (referring to the proportion of allele C_R in the initial population that encoded strong female preference for sex-reversed males).

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Supporting Information 4 - Graphs showing 100 runs per scenario

Evolutionary and demographic consequences of temperature-induced masculinization under climate warming: the effects of mate choice.

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Fig S2. Relative frequency of the _thr_low allele. X axis: years of climate warming. Y axis: relative frequency. On the left: scenarios 0% C_R (a), 10% C_R (b) and 90% C_R (c) starting with XX/XY system. On the right: scenarios 0% C_R (d), 10% C_R (e) and 90% C_R (f) starting with ZW/ZZ system. Curves indicate separate runs (100 repeated runs per scenario).
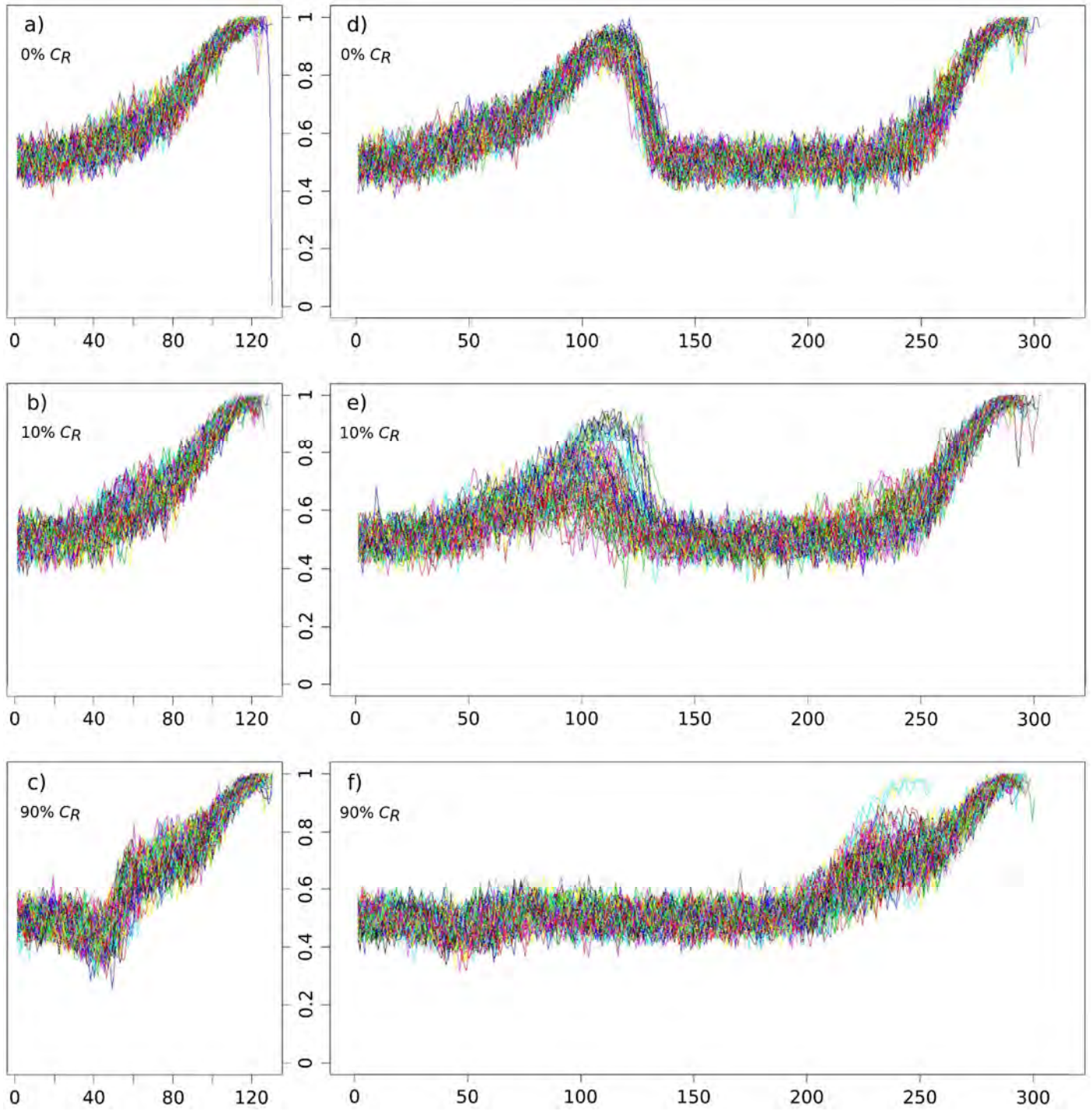
Fig S3. Effective population size. X axis: years of climate warming. Y axis: effective population size (calculated from the number of adult males and adult females present in the population). On the left: scenarios 0% C_R (a), 10% C_R (b) and 90% C_R (c) starting with XX/XY system. On the right: scenarios 0% C_R (d), 10% C_R (e) and 90% C_R (f) starting with ZZ/ZW system. Curves indicate separate runs (100 repeated runs per scenario).
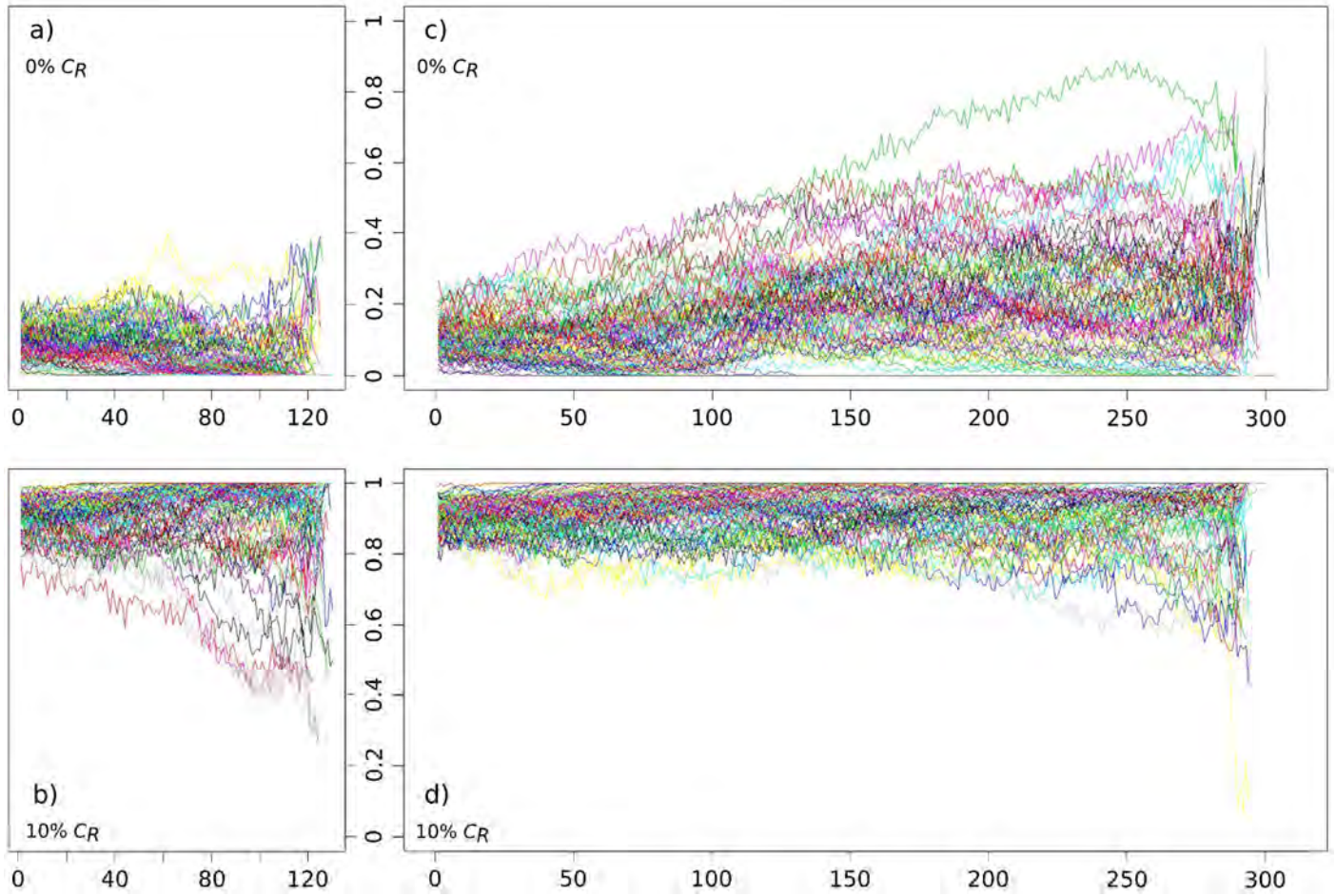
Fig S4. Relative frequency of preference allele C_R. X axis: years of climate warming. Y axis: relative frequency. On the left: scenarios 10% C_R (a) and 90% C_R (b) starting with XX/XY system. On the right: scenarios 10% C_R (c) and 90% C_R (d) starting with ZW/ZZ system. Curves indicate separate runs (100 repeated runs per scenario).
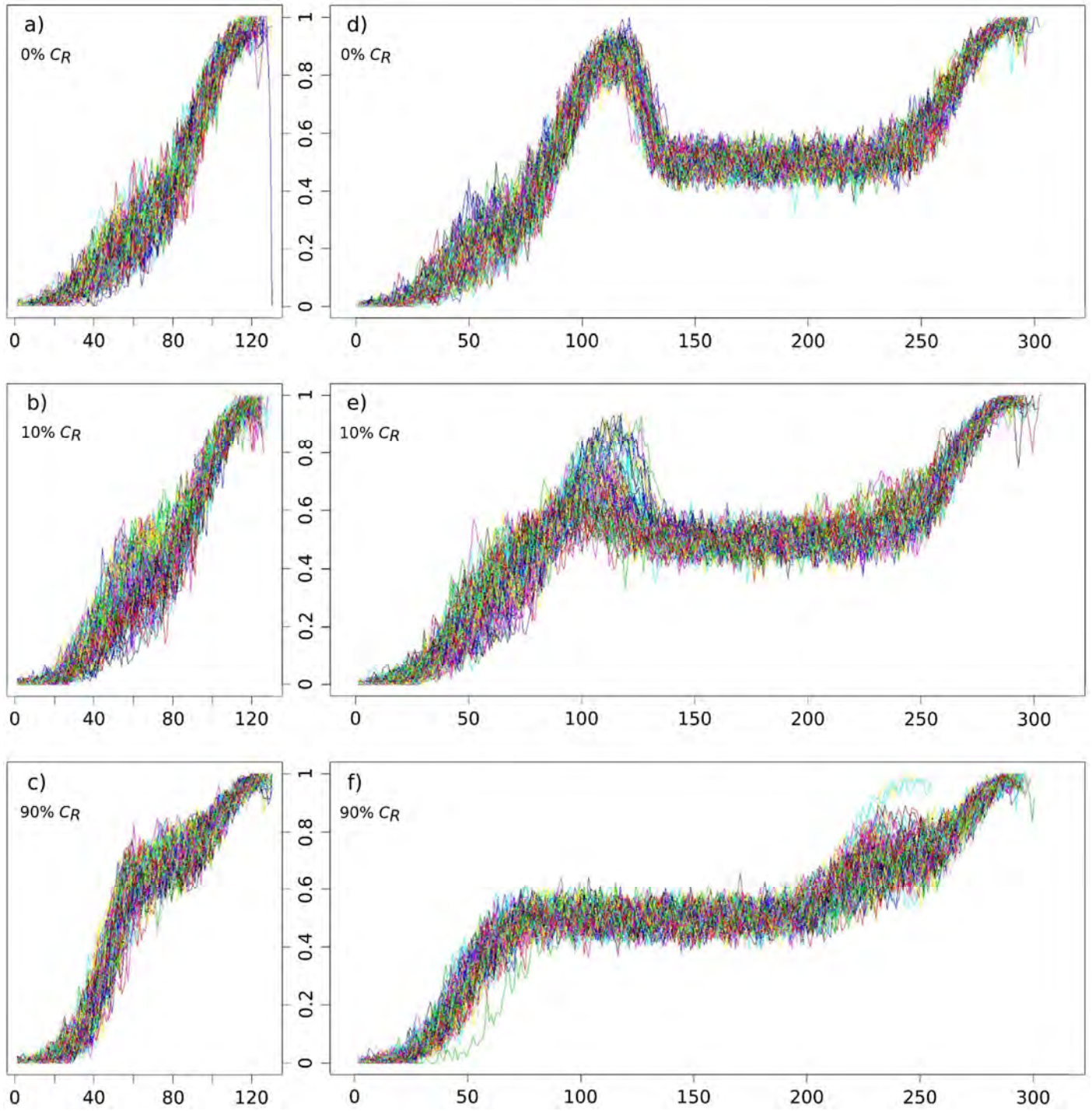
Fig S5. Masculinization rate. X axis: years of climate warming. Y axis: relative frequency of phenotypic males among genetically female individuals. On the left: scenarios 0% C_R (a), 10% C_R (b) and 90% C_R (c) starting with XX/XY system (female genotypes: *Aa, aa*). On the right: scenarios 0% C_R (d), 10% C_R (e) and 90% C_R (f) starting with ZW/ZZ system (female genotype: *aa*). Curves indicate separate runns (100 repeated runs per scenario).
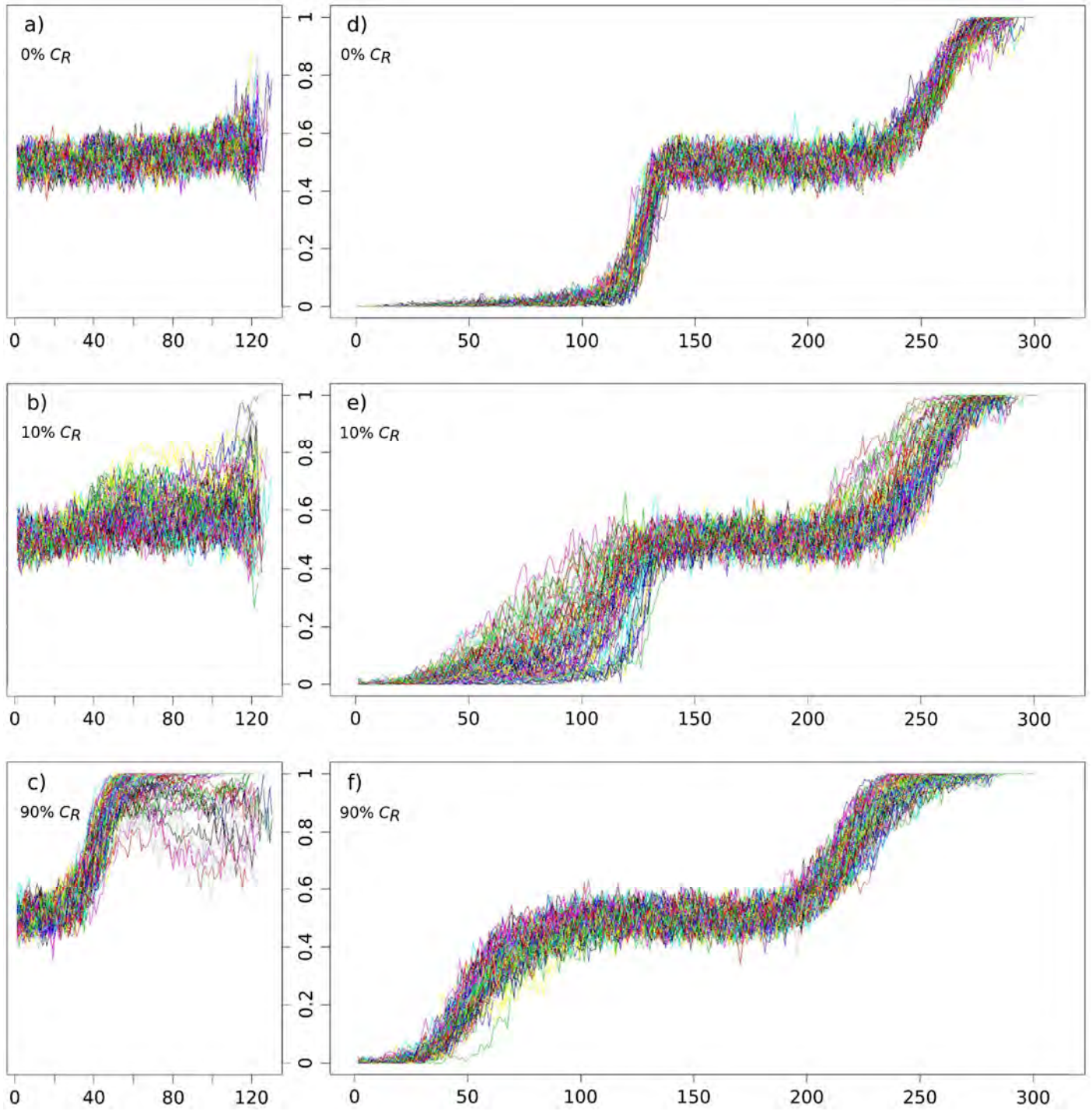
Fig S6. Relative frequency of genotype *aa* among adults. X axis: years of climate warming. Y axis: relative frequency. On the left: scenarios 0% C_R (a), 10% C_R (b) and 90% C_R (c) starting with XX/XY system. On the right: scenarios 0% C_R (d), 10% C_R (e) and 90% C_R (f) starting with ZW/ZZ system. Curves indicate separate runs (100 repeated runs per scenario).
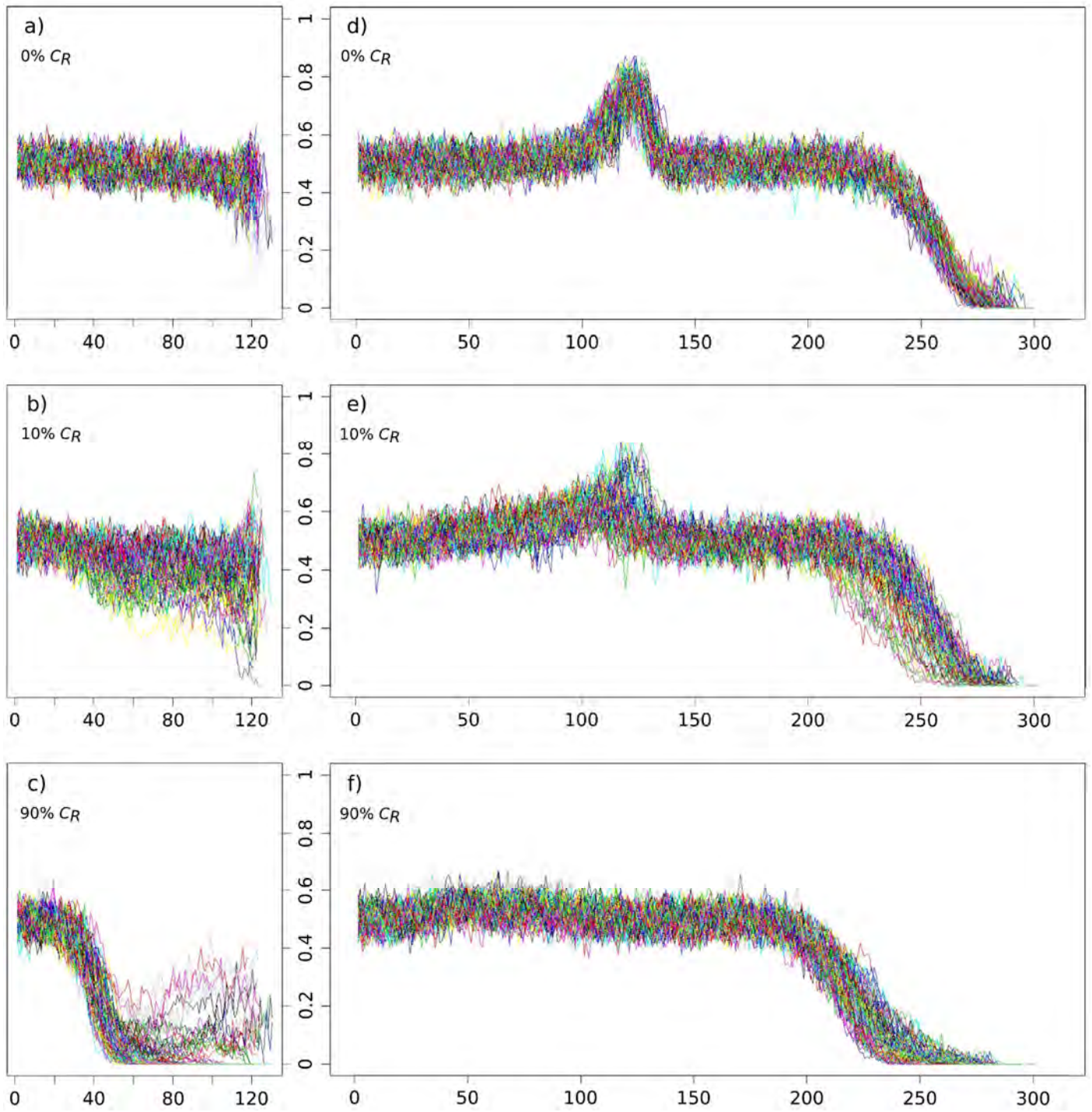
Fig S7. Relative frequency of genotype *Aa* among adults. X axis: years of climate warming. Y axis: relative frequency. On the left: scenarios 0% C_R (a), 10% C_R (b) and 90% C_R (c) starting with XX/XY system. On the right: scenarios 0% C_R (d), 10% C_R (e) and 90% C_R (f) starting with ZW/ZZ system. Curves indicate separate runs (100 repeated runs per scenario).

Fig S8. Adult sex ratio. X axis: years of climate warming. Y axis: proportion of males among adults. On the left: scenarios 0% C_R (a), 10% C_R (b) and 90% C_R (c) starting with XX/XY system. On the right: scenarios 0% C_R (d), 10% C_R (e) and 90% C_R (f) starting with ZW/ZZ system. Curves indicate separate runs (100 repeated runs per scenario).
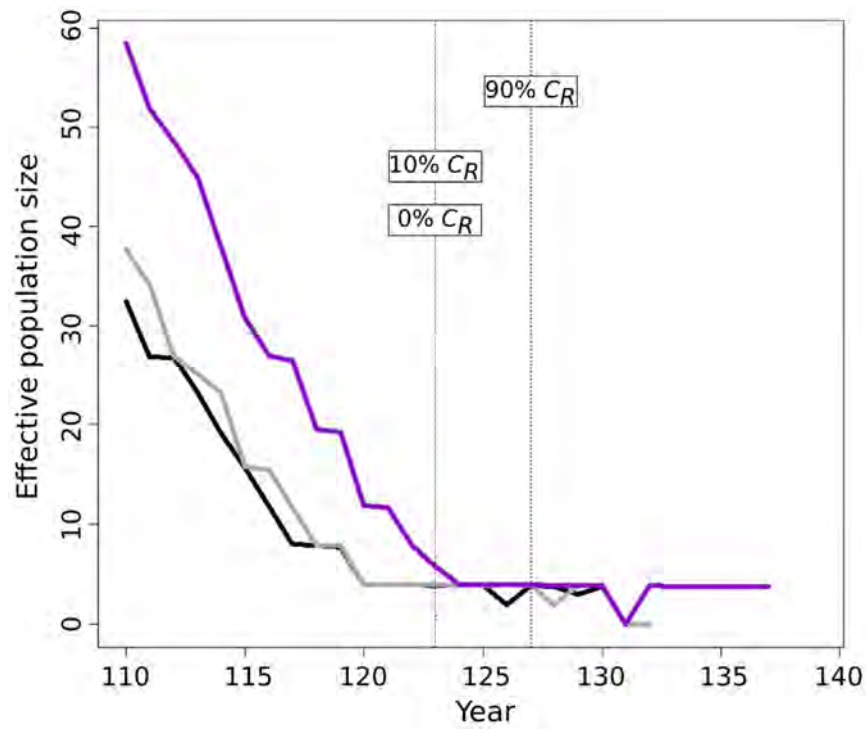
Fig S9. Median effective population size during the last decades before extinction in originally XX/XY populations. Years denote the number of years since the start of climate warming. Median effective population size calculated from the persisting populations out of a total of 100 in each year are shown for each scenario: 0% C_R (black), 10% C_R (grey) and 90% C_R (prurple). Vertical dotted lines indicate the median extinction time for each scenario (note: this is the same in scenarios 0% C_R and 10% C_R).

Supporting Information 5 – Sensitivity analysis

Evolutionary and demographic consequences of temperature-induced masculinization under climate warming: the effects of mate choice

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General information:

Figures in this document show the results of simulations that we ran to assess sensitivity of our results described in the main text for certain parameter settings. All figures show median values calculated from 100 runs. Vertical dotted lines indicate the end of each sex-determination period:
- in simulations starting with XX/XY system: XX/XY, and final period
- in simulations starting with ZW/ZZ system: ZW/ZZ, transition, XX/XY, and final period

Dashed lines indicate the start of ultimate population decline.
For comparison with the main results, see Figure 1 (ASR, relative frequencies of genotypes and threshold alleles) and Figure 5 (relative frequency of C_R allele) in the main text.
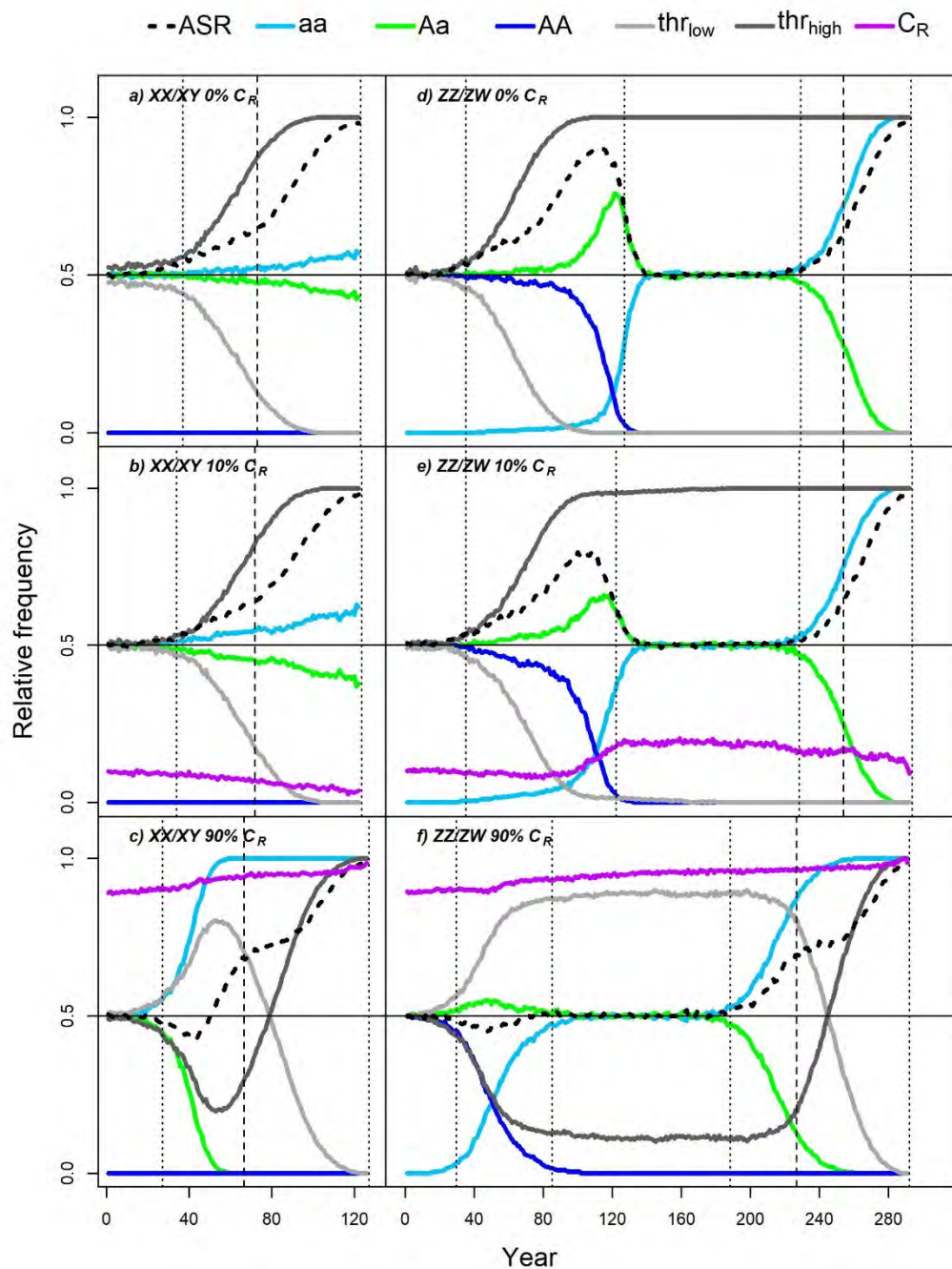
Figure S10. Intermediate inheritance with two strong preference alleles (C_R=0.1, C_N=0.9)

In this situation, the expression of female preference is distributed in the starting populations as follows:

- 10% C_R scenario: 1% prefer sex-reversed males, 18% show no preference, 81% prefer normal males
- 90% C_R scenario: 81% prefer sex-reversed males, 18% show no preference, 1% prefer normal males

The results (ASR, relative frequencies of sex-chromosome genotypes and threshold alleles, timing of transitions and extinction) are very similar to the results shown in the main text (dominant/recessive inheritance), except for one difference: starting with a rare C_R in an XX/XY system, C_R does not disappear (although its frequency decreases steadily).
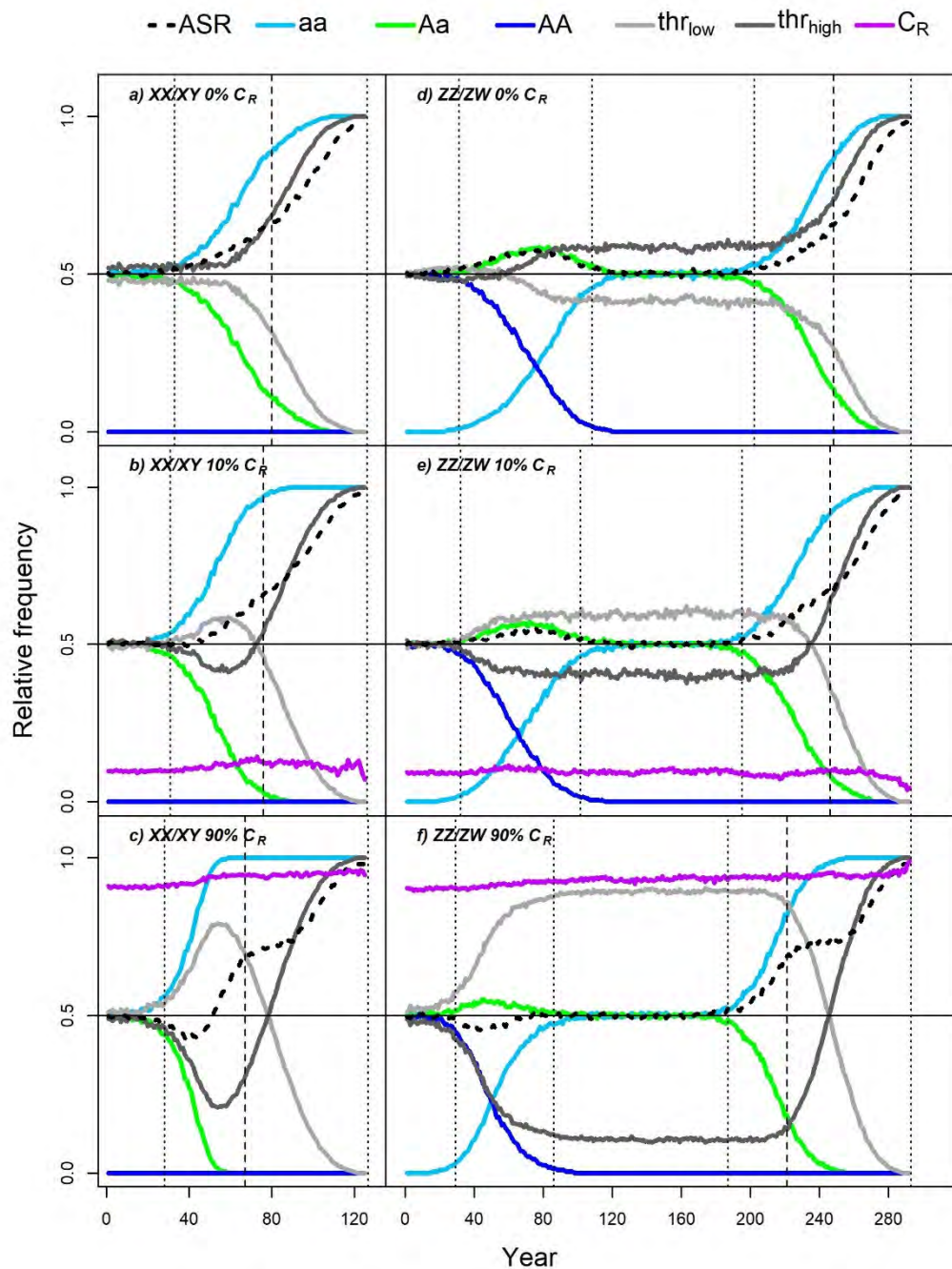
Figure S11. C_R versus no preference (C_R=0.1, C_N=0.5; dominant/recessive)

In this situation, the expression of female preference is distributed in the starting populations as follows:

- 10% C_R scenario: 19% prefer sex-reversed males, 81% show no preference
- 90% C_R scenario: 81% prefer sex-reversed males, 19% show no preference

In these scenarios, the lack of preference for normal males results in faster extinction of the original male genotype, later spread of thr_{high}, and less marked ASR bias towards males during the ZZ/ZW-XX/XY transition compared to the scenarios in the main text. Also, the frequency of C_R shows little change over time in the 10% C_R scenarios (it is not selected against when rare because the majority of the females are indiscriminate). However, the effects of C_R on ASR and transition times are very similar to the scenarios in the main text.

Figure S12. C_R versus no preference (C_R=0.1, C_N=0.5), intermediate inheritance

In this situation, the expression of female preference is distributed in the starting populations as follows:

- 10% C_R scenario: 1% prefer sex-reversed males with 0.9 probability, 18% prefer sex-reversed males with 0.7 probability, 81% show no preference
- 90% C_R scenario: 81% prefer sex-reversed males with 0.9 probability, 18% prefer sex-reversed males with 0.7 probability, 1% show no preference

These results are very similar to the previous case (C_R versus no preference; dominant/recessive). Thus, the frequency of C_R changes very slightly or not at all when it is "competing" with a no-preference allele; this result does not depend on the type of inheritance. However, the effects of C_R on ASR and transition times are very similar to the scenarios in the main text.
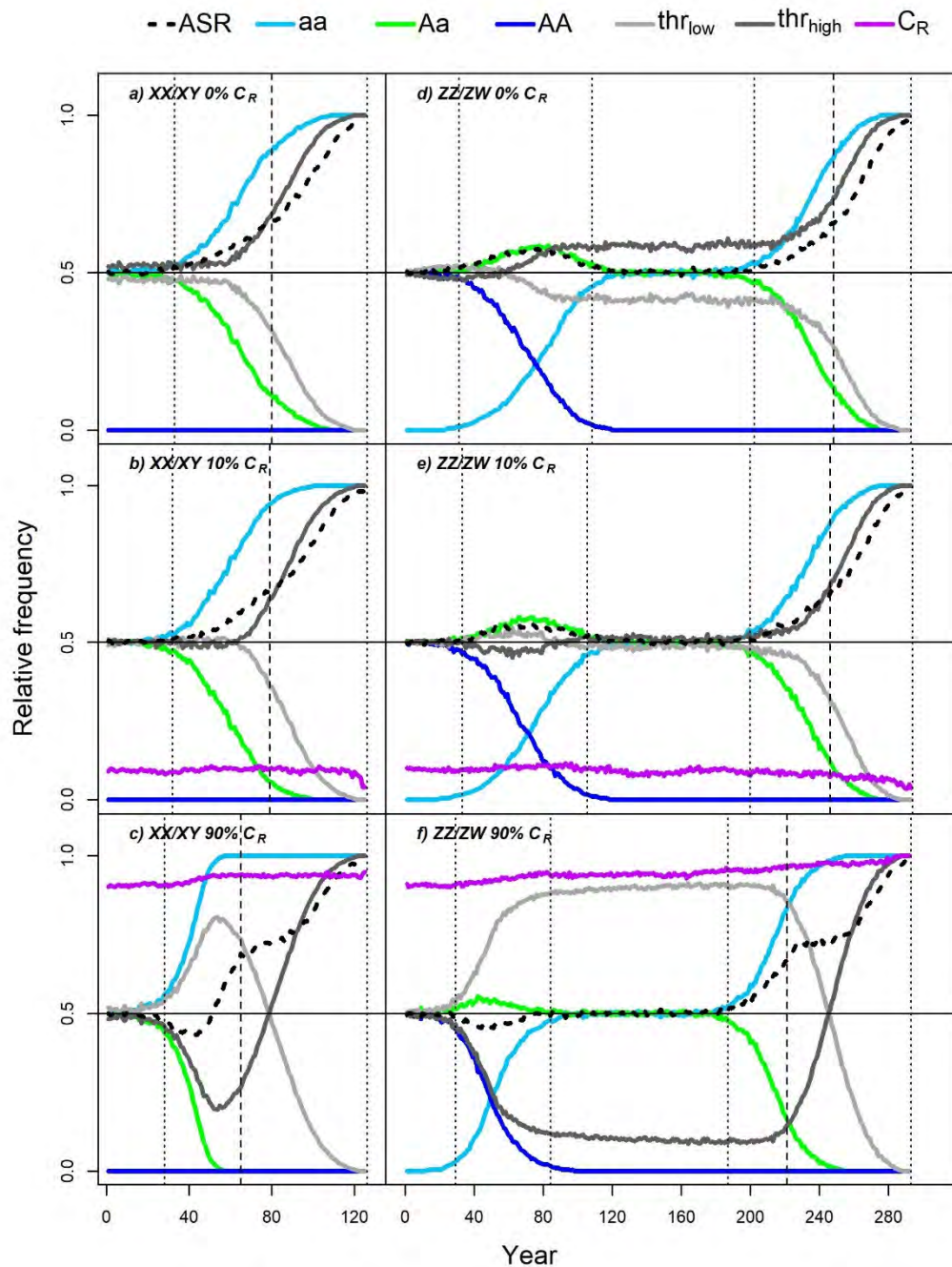
Figure S13. Multiallelic threshold

The number of *thr* alleles was set to 10, such that each allele started with a frequency of 0.1, and their values were evenly distributed between the lowest and highest value used in the main-text simulations.

The results are similar to those in the main text. Note: in the graphs below, solid grey curves show the frequency of the lowest and highest *thr* allele (from the original 10 alleles).
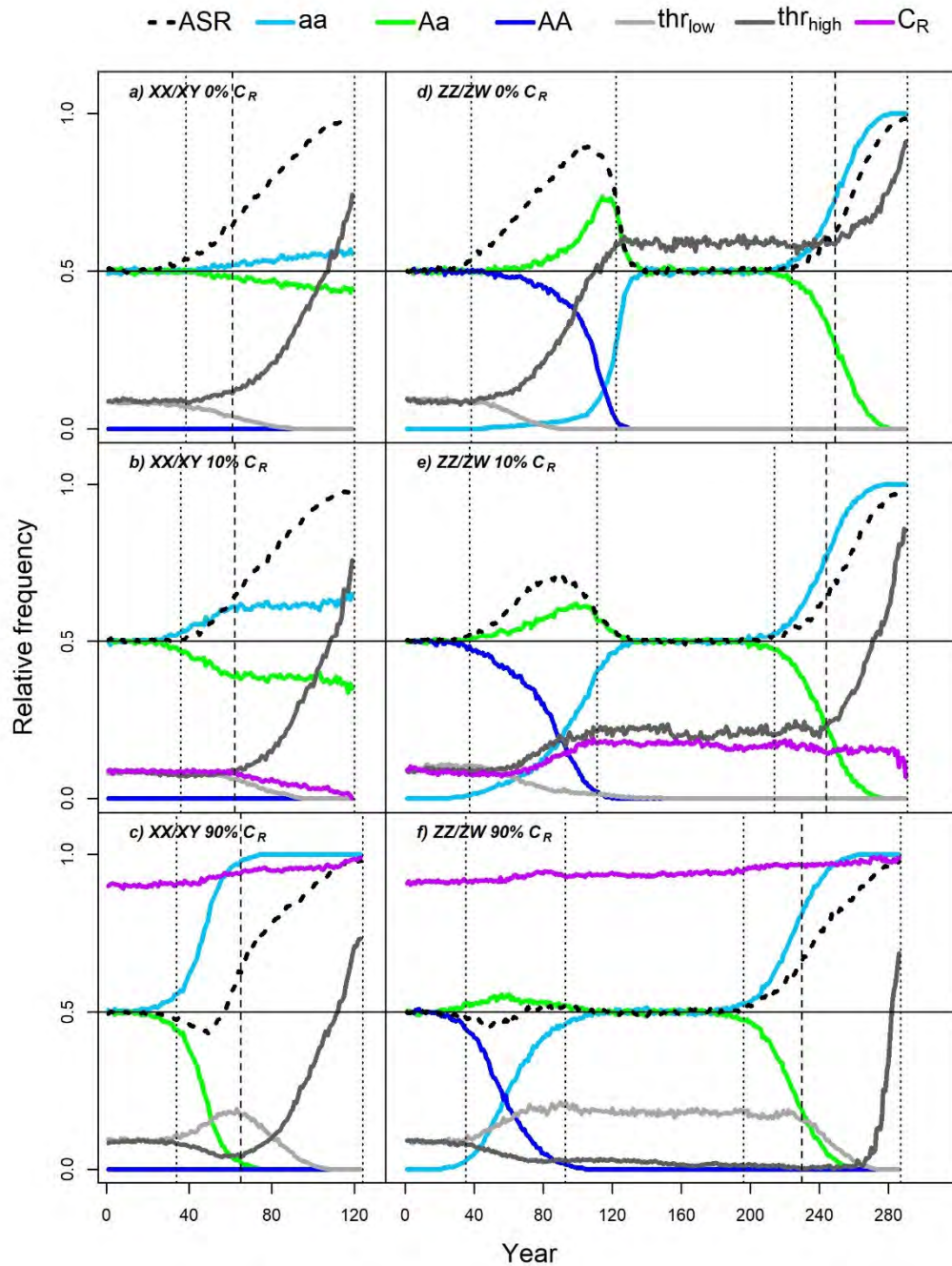
## Scenarios with reduced WW viability

Figure S14. 75% WW survival

When the survival of WW offspring is 75% of the survival of other genotypes, the spread of C_R and its effects are similar to the scenarios with 100% WW viability: C_R reduces the ASR bias and speeds up the transition. Because of the higher mortality of WW individuals (which are more likely to develop into phenotypic females), the newly evolved XX/XY system maintains a somewhat male-biased ASR until system destabilization.
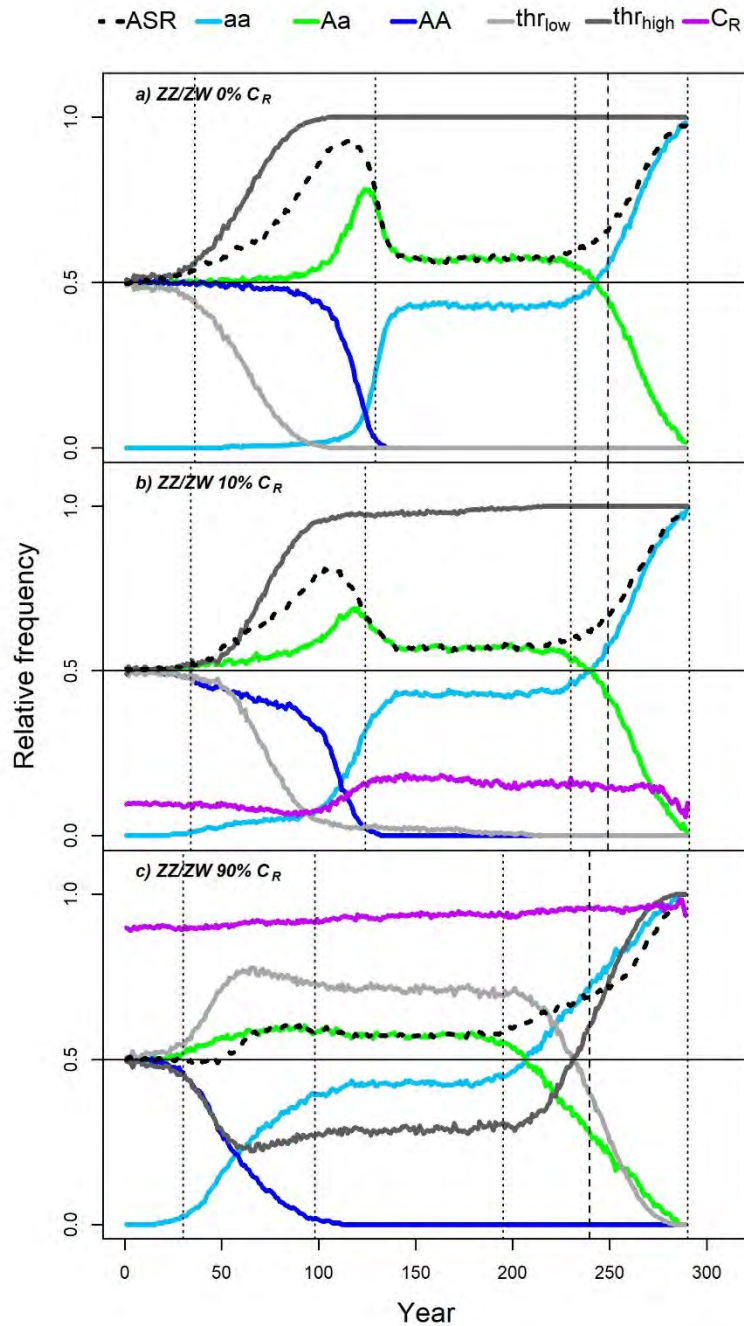
Figure S15. 50% WW survival

Again, the effects of C_R are similar to the 100% WW viability scenarios. Relative frequency of the widespread C_R allele increases only slightly, whereas the rare C_R allele disappears, although it increases for a short time when ASR becomes highly male-biased before transition. After transition, ASR remains relatively male-biased.
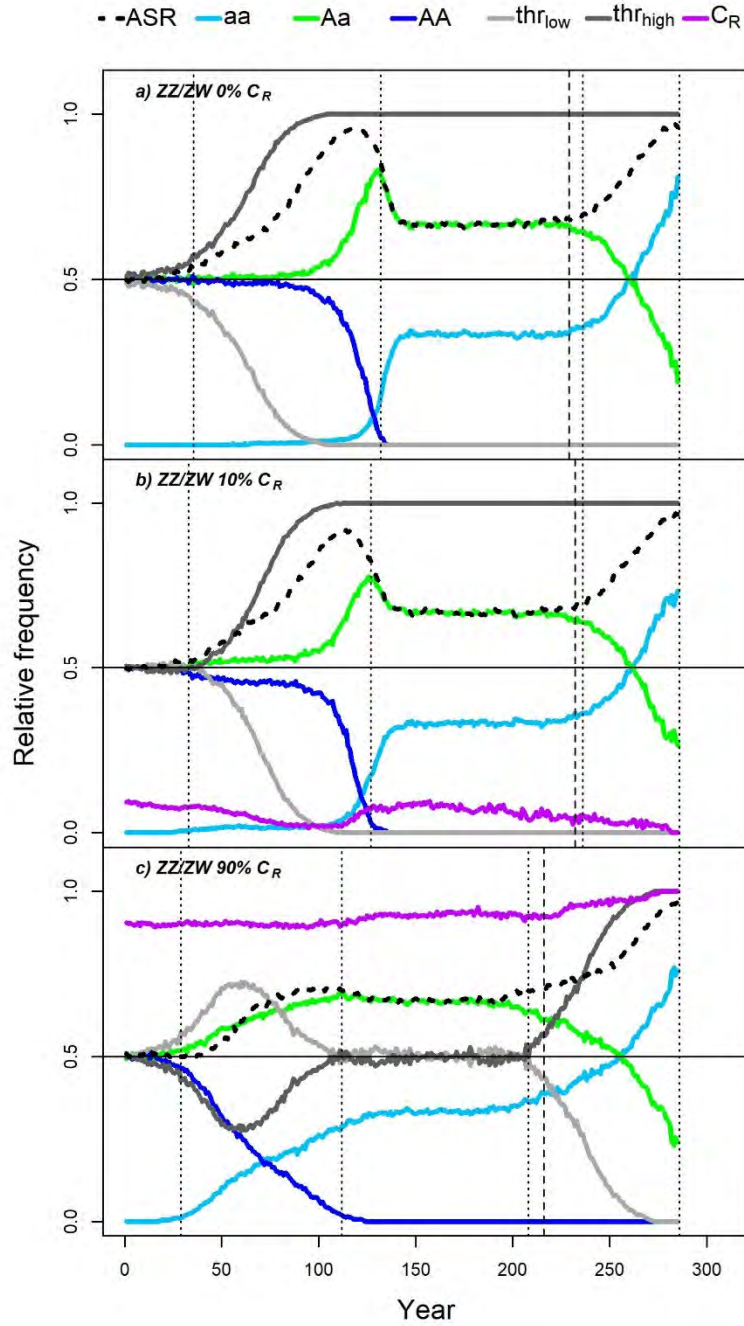
Figure S16. 25% WW survival

When the survival of WW offspring is only 25% of the survival of other genotypes, most of the populations cannot transition to an XX/XY system and die out after ca. 120 years when no C_R allele is present. However, the presence of C_R saves the population from this early extinction by enabling the switch to XX/XY system (in slightly more than half of the runs when C_R is rare; always when C_R is widespread; see Fig. 5 in the main text). This switch happens rapidly when ASR has become highly male-biased; during this short time the relative frequency of C_R increases. After transition, the population maintains a strongly male-biased ASR.
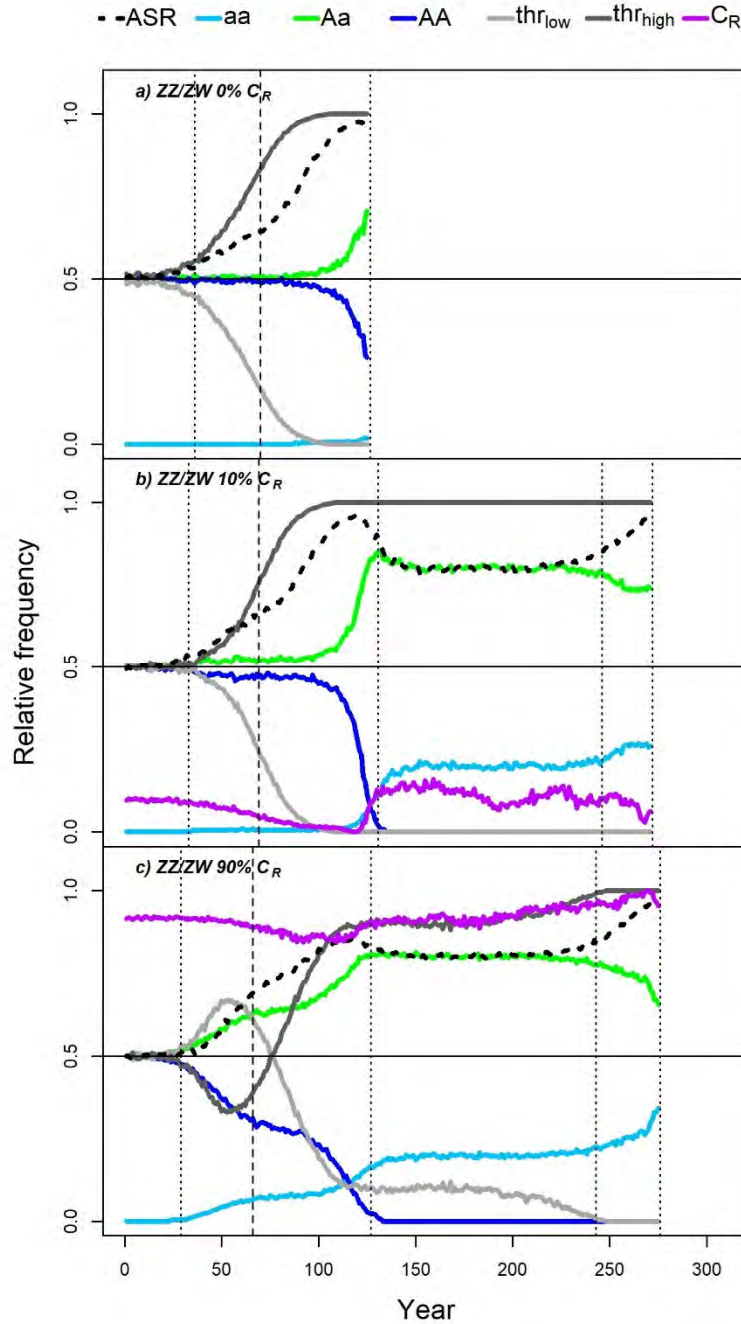
Figure S17. WW lethality

WW lethality makes the ZZ/ZW system behave similarly to the XX/XY system: no transition from ZZ/ZW to XX/XY, and the population dies out after ca. 120 years. The effects of C_R are also similar: it has little effect on ASR change or extinction time, but it makes the starting system destabilize slightly earlier than when no C_R is present. The only difference is that C_R never spreads.