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Embryonic growth and the evolution of the mammalian Y chromosome. I. The Y as an attractor for selfish growth factors

LAURENCE D. HURST
Department of Genetics, Downing Street, Cambridge CB2 3EH, U.K.

The fitness of a mammalian zygote is affected by its probability of implantation and of postimplantation maintenance as well as the level of transplacental and transmammary uptake of resources. As with paternally expressed imprinted genes, in a species in which females are not obligately monogamous, a Y-linked sequence that can positively alter any of the above parameters could spread in a population even if it harms the prospects of other embryos. Such a selfish Y-linked gene could act as a sex ratio distorter. In contrast to autosomal imprinted loci, the patrilineal inheritance of the Y ensures that selfish Y-linked growth-promoting genes need not evolve a means to ensure correct parent-dependent expression rules. Thus, as the conditions for both their initial evolution and spread are relatively relaxed, the mammalian Y chromosome is expected to be an attractor for growth-promoting genes. Data from mice and humans indicate that, as expected and in contrast to the Y of flies, the mammalian Y harbours growth factors, sex ratio factors and multiple foetally expressed genes. The accumulation of Y-linked genes may also be explained in terms of sexual antagonism. Sexual antagonism and the model presented here are not mutually exclusive

Keywords: genomic imprinting, selfish genes, Y chromosome.

Introduction

Selfish genetic elements, such as meiotic drive genes and cytoplasmic sex ratio distorters, are components of the genome whose spread within a population inflicts a cost. As a result of this cost the continued spread of the selfish genetic element creates the context for the spread of another gene with an opposing effect. There is said to be a conflict between the selfish element and certain other (typically unlinked) parts of the genome (parts where a suppressor, when present, is capable of spreading).

Recently there has been some debate as to the potential importance to evolution of selfish genetic elements. One of the strongest cases against the notion that conflict is important is that the conditions for the initial creation of a selfish genetic element can be rather restrictive (Wu & Hammer, 1991). In contrast, the conditions for the spread of a selfish gene, once created, can often be quite relaxed and the rate of spread potentially very rapid. Consider for instance the creation of an autosomal meiotic drive gene (Charlesworth & Hartl, 1978; Wu & Hammer, 1991; Hurst & Pomiankowski, 1991). In broad outline two loci are involved, one a *Killer* locus and one conferring insensitivity to *Killer*. The drive chromosome must contain the *Killer* allele and the insensitive allele. These two must be tightly linked so as to avoid the creation of suicide chromosomes through recombination. Once the necessary linkage arrangements are set, and hence the two loci segregate almost as one, then the conditions for spread of the gene complex are quite broad, although in the case of autosomal meiotic drive they are dependent upon the frequency of sensitivity on nondriving homologues. Many selfish genes are believed to involve similar two-locus (killer/insensitive) gene complexes and hence face similar problems with respect to their creation. Do all selfish genetic elements have such restrictive conditions for their initial creation?

Fast replicating mitochondrial genomes (i.e. petite-like mutants) that are often reported in animals, have trivial creation conditions. It seems likely that their deleterious effects and their selfish action (fast replication) are both commensurate upon the deletion of part of the mitochondrial genome. That animal mitochondria have free replication within the cell cycle is thought to be responsible for the immediate replication

advantage of small genomes (Avise, 1991). Nuclear genes are not permitted free replication within the cell cycle and hence are not liable to transform into fast replicating genes. Are there then nuclear selfish genes with trivial creation conditions? Here I note that one class of selfish genetic element, mammalian Y-linked growth factors, has near trivial conditions for both initial evolution and invasion.

Y-linked sequences as selfish foetal growth promoters

If a mother has more than one mate, paternally derived genes in any given foetus will not necessarily be related to genes in fellow brood members or subsequent offspring of that same mother. In contrast, a maternally derived gene in any given foetus has a constant high probability (0.5) that its sibs will contain a clonal copy of it. As Haig (1992) notes, this tripartite asymmetry in relatedness between (i) paternally derived foetal genes, (ii) maternally derived foetal genes and (iii) genes in the mother (and hence in the foetus's sibs) creates a three-way conflict of interest over how much nutrition the foetus should demand from the mother. The mother would 'prefer' to divide resources more-or-less equitably and so maximize her net fitness, not the fitness of any given progeny. In contrast, if the paternally derived genes in any given foetus are not going to be present in the sibs, then any decrement in maternal fitness resulting in reduced offspring production is, at the very least, irrelevant to these paternally derived genes. Paternally derived genes in a given foetus might thus prefer an allocation in excess of that preferred by the mother. The optimal amount of resources that the maternally derived genes in the foetus should require will be intermediate between the optima for the paternally derived genes (a large amount) and the amount the mother should be prepared to provide (a smaller amount).

Haig and colleagues propose this difference in optima between the maternally and paternally derived genes in a foetus as an explanation for genomic imprinting (Haig & Westoby, 1989; Moore & Haig, 1991; Haig and Graham, 1991; Haig, 1992). This proposition is supported by analysis of one of the best described imprinting systems, namely that of the murine insulin-like growth factor 2 (Igf2) and the Igf2 receptor (alias the mannose-6-phosphate receptor) (see Haig and Graham, 1991, for interpretation and references). Foetally expressed Igf2 is one of the factors that are supposed to promote the acquisition of resources from the mother. Early in mammalian embryogenesis, as expected, paternally inherited genes are expressed that promote the production of Igf2, while maternally inherited genes capable of the same function are not expressed. Instead, again as expected, maternally inherited genes that prevent the action of Igf2 are expressed.

Not all maternal/foetal conflict need be expressed through foetal growth demands. A differential ability to implant and to resist being aborted by the mother may have no effect on foetal growth when compared to other survivors but could affect gene frequencies (Haig, 1993). For instance, in mammals, asynchrony of the uterus and blastocyst development usually decreases blastocyst survival and, after implantation, the endocrinological status of the uterus will change so as to reduce the likelihood of implantation of less well developed blastocysts (Pope, 1988). This situation predisposes to competition between unrelated foetuses to attain early implantation and rapid development. For a fair comparison of two genotypes as regards net growth these aborted/nonimplanted embryos should be included in the equation. In the case of postimplantation survival, some foetally expressed cell surface antigens, such as the Rhesus factors, are involved in immune-mediated maternal/foetal compatibility interactions. Murine severe combined anaemia and thrombocytopenia is due to the action of a selfish gene that acts in the mother to kill foetuses that do not contain a clonal copy of it (Hurst, 1993). Peters & Barker (1993) provide evidence for the effect being immune-dependent. In this paper, when reference is made to growth demands it can be understood, unless otherwise clarified, that growth effects involving pre-implantation activity and implantation maintenance would be equivalent.

Genes on the nonrecombining part of the Y (i.e. the non-pseudoautosomal region: NPAR) are always paternally derived. Hence by minor extension of Haig's logic we would predict that a mutant NPAR Y gene that could manipulate the mother into providing the foetus with extra resources will be able to spread in the population (see Appendix 1). Whereas autosomal selfish resource attractors must not only act to extract more resources, they must also evolve some means to guarantee their appropriate expression (i.e. they must become imprinted). Any NPAR Y gene that simply managed to produce a growth effect would immediately, by virtue of its position on the Y, guarantee appropriate expression. The Y-linked sequence may also act as a sex ratio distorter causing a bias in investment into male progeny. The conditions for invasion of a resource-extracting Y-linked gene in a species in which all sibs are full sibs is a subject left to future study.

As selfish resource acquisition NPAR Y genes do not require differential expression when inherited from

a mother (they never are), it is inappropriate to describe them as being imprinted. However, as the logic behind their spread is very similar to that proposed for imprinted genes with expression off the paternally inherited genome, one might perhaps describe them as being 'neo-imprinted' genes.

If their action was modified dependent upon whether they were maternally or paternally inherited, genes within the pseudoautosomal region (PAR) could also spread as selfish genes. PAR-linked genes that expressed growth demands when inherited from a father, but not when inherited from a mother, would behave in population genetic terms almost identically to standard autosomal imprinted loci.

The eutherian Y codes for growth factors

Several lines of evidence indicate that both in mice and man there are probably multiple Y-linked genes that code for growth factors. The identity of the genes responsible for these effects is unclear. That the Y does code for growth factors has also been noted by Kraak & de Looze (1993) who argue that this feature may be intimately associated with the initial evolution of the mammalian Y chromosome from an ancestral species with environmental sex determination.

Burgoyne (1993) has demonstrated the existence of growth promoters on the Y that act to ensure that male mouse embryos, prior to implantation, grow faster than female ones (see also Burgoyne, 1992). A growth difference between XX and XY offspring could have been due to an X effect, but, by following segregating Y chromosomes in between-strain crosses, Burgoyne showed that the effect segregated with the Y and not with the X. This effect is not, however, one ensuring that individuals with a particular Y are larger *per se*, just that they develop faster and hence are more advanced than their competitors. As discussed above, early implanting embryos can reduce the success of other embryos by altering uterine conditions to predispose against further implantation. Even if no interference is witnessed at the preimplantation stage the first implanting embryo may end up larger as it can come to have postimplantation advantages. Further, if at any given time a mother needs to abort some foetuses, she may be more disposed to abort the smaller and hence more slowly developing ones. In sum, any Y-linked mutant that promoted early growth rate could potentially spread because of its ability to out-compete competitors.

The gene(s) responsible for this murine pre-implantation growth effect are unknown. *Ube1y1* is however a good candidate gene. *Ube1y1* codes for a ubiquitin activating enzyme E1 homologue that is known to be involved in the progression of the cell cycle. It is possible that one copy of *Ube1y1* and one of *Ube1x* have a slightly more potent effect than two of the latter. Recently Zwingman *et al.* (1993), confirming the pre-implantation Y growth effect (although they appear to assume there not to be an X effect), claim to show that *Sry* and *Zfy* are transcribed in murine two cell embryos and hence suggest that they may be involved in this pre-implantation growth effect.

Mittwoch (1969, 1989) has consistently argued that not only do XY embryos develop faster than XX embryos but that this growth rate difference is central to the means of sex determination. If so, then *Sry* as the sex determining gene must also be the gene determining growth rate (at least indirectly). Burgoyne (1989, 1992) argues that if there are growth effects associated with sex determination then *Zfy* is a good candidate for these. Potentially then both *Sry* and *Zfy* might also be candidate loci for the pre-implantation growth effects and other Y-linked growth effects (see below). That *Sry* may be a growth factor is also consistent with Kraak & de Looze's (1993) model for the initial evolution of the mammalian Y.

Further evidence for a Y growth effect comes from analysis of individuals with two or more Y chromosomes and from those with deletions. XYY humans are male and typically taller than the average (Varrela & Alvesalo, 1985; Ogata & Matsuo, 1993). Effects on growth assayed by tooth size in XYY individuals also provide direct evidence of a Y effect on tissue growth (Alvesalo *et al.*, 1985; Townsend & Alvesalo, 1985). A large component of the Y effect has been shown to operate between birth and puberty (Ratcliffe *et al.*, 1992) and hence a very large prenatal effect can be ruled out (Chen *et al.*, 1971; Ratcliffe *et al.*, 1992). Because of limited sample sizes, however, a small or moderate prenatal effect cannot be ruled out.

Analysis of individuals with deletions or absence of the Y corroborates the growth effects. Human XO individuals are severely growth-retarded (Ranke *et al.*, 1983). As both human XY males and most XY females are not retarded, it is concluded that the Y must code for some growth factor(s) for which there is a non-dosage compensated X-linked homologue (see Hurst (1994, this issue) for discussion of escape from X-inactivation). This is further supported by the finding that structural abnormalities of the Y often lead to short stature (Simpson, 1975; Buhler, 1980). Deletion analysis indicates that a factor with a growth effect on adult stature is located at Yq11 (long arm) proximal to the gene(s) for spermatogenesis (see Ogata & Matsuo, 1993, for review and also Alvesalo & de la Chapelle,

1981. A growth-related gene has also been localized in the PAR (see Ogata & Matsuo, 1993, for references).

The mechanism(s) of growth effects is uncertain. Ogata & Matsuo (1993) review evidence suggesting that the Y growth effects can be independent of the effects of gonadal sex steroids. Furthermore, a severe (but not mild) lack of androgen has growth retarding effects (Ogata & Matsuo, 1993). Androgen metabolism is at least in part under Y-linked control.

Early embryonic growth and post-meiotic gene expression

Zygotic and early embryonic growth effects need not involve gene expression (transcription) coincidental with the growth effects. Postmeiotic gene expression in spermatids is unusual (Erickson, 1989) but has been reported for proto-oncogenes (Propst *et al.*, 1988). This late expression may be to prime the sperm with transcripts/proteins that will be necessary for early postfertilization development (Propst *et al.*, 1988). Moore & Haig (1991) suggest that these proto-oncogenes may exercise selfish effects. By definition genes that are expressed in spermatogenesis will be paternally derived if they are to be inherited. Hence a proto-oncogene that mutates so as to enable it to have expression in late spermatogenesis is liable to spread if the expression can have concomitant growth effects in the zygote. It is thus significant that, like these proto-oncogenes (and hence putative growth-related factors), *Zfy* (Kalikin *et al.*, 1989), *Ube1y1* and *Sry* (Hendriksen *et al.*, 1993) also have postmeiotic gene expression. As noted above, a Y-linked mutant that promoted early growth rate could potentially spread because of preferential implantation. That gene expression is found in spermatids (Hendriksen *et al.*, 1993) suggests that the transcripts may be maintained within the sperm that produced them (i.e. a haploid specific effect). If foetal competition is between full sibs, as well as between paternally unrelated individuals, then haploid specificity would be required. If only the latter, then haploid specificity would be irrelevant.

Both *Zfy* (Koopman *et al.*, 1991) and *Ube1y1* (Kay *et al.*, 1991) cannot be excluded as having some role in spermatogenesis. However, even if *Zfy* and *Ube1y1* are involved in spermatogenesis the boost in transcription of the latter at the spermatid stage (Hendriksen *et al.*, 1993) is enigmatic. *Sry*'s testicular expression is of unknown function. As *Sry* transcripts in sperm are not associated with polysomes (Capel *et al.*, 1993) it is possible that translation is not achieved during spermatogenesis. Similarly, many of the spermatid-expressed proto-oncogenes also do not associate with polysomes (Propst *et al.*, 1988). However, protamine transcripts go through a phase in which they are not attached to polysomes. These genes are, however, used in late spermatogenesis for the packaging of DNA. Hence a lack of polysome attachment at any given stage in spermatogenesis does not imply a complete absence of translation (Propst *et al.*, 1988). It might, however, be conjectured that the circularity of *Sry* transcripts (Capel *et al.*, 1993) could be a device to prevent premature translation. That human *Sry* is not circular would suggest that either the circular nature of murine *Sry* is of no particular importance (Capel *et al.*, 1993), or that human *Sry* has achieved the same end by an alternative route. Note also that two X-linked genes, *Ube1x* and the human homologue of *RAD6* (*HHRA*^{MM}), also have spermatid gene expression (Hendriksen *et al.*, 1993) and hence these might be suspected as being selfish imprinted-like genes (again note the paternal specific nature of genes expressed in spermatogenesis).

Genes on the Y are capable of acting as sex ratio distorters

The resource extraction model predicts not only that males with the selfish Y should be larger than ones without, but also that the selfish Y could be associated with a sex ratio effect (meaning both a sex bias in investment and a bias in the absolute number of individuals). This sex ratio effect should be found in organisms with multiple zygotic implantations per pregnancy. Any such sex ratio effect could be associated with a growth effect but need not be. If a Y-linked sequence could simply act to ensure that competitors received less nutrition than they ought to, and hence were aborted or died early, then a net growth effect would not be found in the survivors but a sex ratio effect could be seen.

Weir (1976) (see also Weir, 1960) has demonstrated that mice of strain PHH and PHL differ in their sex ratio, and that this effect is Y-linked and mediated by the action of the Y on non-Y sequences. It is unknown which gene(s) is responsible for this effect. However, the strains of mice in which a Y-linked sex ratio effect has been found have also been shown to have a Y-linked pubertal testosterone titre effect (Jutley & Stewart, 1985). Further, female rodents positioned within the uterus between two males become androgenized through the import of testosterone that has passed out of the males and into the female (see Clark *et al.* (1993) for references). The level of exposure to androgen *in utero* slows the development of the females and they achieve puberty later than nonandrogenized controls (see Clark *et al.*, 1993, for references). Furthermore, the androgenized females in turn produce male biased progeny sex ratios (Clark *et al.*, 1993). This may simply be because poor quality females typically produce male-biased broods. It is

unclear whether the androgenization of females is itself directly responsible for the growth retardation. It could be that testosterone forces increased resources to be diverted to the males and hence nearby females competing for the same resources are starved of nutrition. Alternatively, androgenized females may demand fewer resources. Either way, the slowing of female development suggests that the males of such broods might be receiving more resources (assuming net investment is not decreased in line with the decreased demands of the females). Males exposed to high intrauterine testosterone develop to be reproductively more successful than those exposed to low testosterone titres (Clark *et al.*, 1992).

If the Weir effect is mediated by testosterone levels it might be possible that the same testosterone variation should have a growth effect. The variation in testosterone level described by Jutley & Stewart (1985) in the PHH and PHL mice (see above) does not, however, result in significant variation in organ weight of those tissues responsive to testosterone. Jutley & Stewart (1985) argue that this is paradoxical but postulate that endogenous testosterone levels are likely to be above the dose range at which a Y-effect on organ weight could be seen in intact animals. In humans severe androgen deficiency does lead to growth defects (Ogata & Matsuo, 1993).

As *Sry* and Y-linked steroid sulfatase (*Sts*) are both involved in testosterone production their involvement in the Weir effect might be suspected. *Sry* is slightly further implicated as its expression is also associated with prostate cancer (Tricoli *et al.*, 1993, but see also Tricoli and Bracken (1993) for the involvement of *Zfy*) and prostate cancer is associated with a sex ratio effect as well. The sex ratio of the progeny of human males with prostate cancer is significantly higher than the overall sex ratio expected on the basis of live birth sex ratios ($P<0.05$) (James, 1987). From subsequent analyses, James (1990) reports that of two independent studies, one found a significant effect (0.516:0.454, $P<0.05$, $n=142$ individuals with prostate cancer), whilst the other, though also finding a higher sex ratio in males with prostate cancer (0.487:0.469), found no significant difference with the control group ($n=142$). The mechanism of this effect is unknown and it is unclear why cancer in the male should communicate to a sex ratio effect in the progeny. A connection between androgen titre and sex ratio has, however, been noted previously (James, 1992, and references therein).

For the above connection between *Sry* and a sex ratio effect to be coherent it is probably necessary to suppose that a mutant form of *Sry* could modify testosterone titre without compromising sex determination. Is this reasonable? SRY seems to have two principle effects. First, it prevents the formation of female tissues; second, it promotes the production of male tissues (possibly by inhibiting an inhibitor of male differentiation: McElreavey *et al.*, 1993). These effects are possibly mediated (but the evidence is far from conclusive) by *Sry* promoting the production of Mullerian inhibiting substance (MIS) and down-regulating P450 aromatase (see Haqq *et al.*, 1993, for references). MIS is a member of the transforming growth factor β family. P450 aromatase catalyses the conversion of testosterone to oestradiol. Down-regulation of P450 aromatase could thus maintain a high level of testosterone. MIS also blocks the conversion of testosterone to oestradiol.

One human pedigree supports the notion that strong Y-linked sex ratio distorters may exist. Harris (1946) identifies a human pedigree of 34 individuals over 10 generations. Only two of the progeny in this pedigree were female. This case history is regarded as one of the two unambiguous cases of sex ratio distortion in a human lineage (Stern, 1973). This pedigree is consistent with a Y-linked sex ratio effect. It is, however, unknown whether the effect is prezygotic or postzygotic, although most evidence supports the former. Suggestive of a prezygotic effect is the finding that the male's sperm, though plentiful, had a very small head size. In favour of a hormonally mediated effect, possibly androgenic, was the finding that the male had low libido. This low libido is consistent with the small average family size (only 2.125 offspring per generation). Hormone/androgen mediated effects on the sex ratio have been extensively described (James, 1990, 1992 and references therein) and may, as discussed, also be the explanation of the above murine effect. Were the effect prezygotic this could still be indicative of involvement of selfish genes (e.g. a Y-linked meiotic drive gene).

Interpretation of the sex ratio and growth effects

The finding of growth factors and sex ratio factors associated with the Y chromosome of mammals, while consistent with the proposed model, is not proof that the model is correct. Rice (1992) has experimentally shown that in *Drosophila* a pseudo-Y chromosome can accumulate sexually antagonistic genes. If growth and sex ratio factors are sexually antagonistic (as indeed they may be) then the existence of Y-linked growth effects has at least two potential explanations. The two hypotheses (conflict and sexual antagonism) are, however, mutually compatible. Hence, the demonstration of a Y-linked growth factor in salmon (Forbes *et al.*,

1994), a species without parental care, while supportive of sexual antagonism as a force in the evolution of the Y, does not exclude conflict as a potential force in the evolution of the mammalian Y chromosome.

The model evoking sexual antagonism need not suppose Y-linked genes to be foetally expressed whereas it is a prediction of the conflict hypothesis. It would be instructive to know whether the mammalian Y (particularly the eutherian Y) is unusual in having so many foetally expressed genes (see also Hurst, 1994, this issue). Comparison with the only other well described Y chromosome, that of *Drosophila melanogaster* (Lindsley & Zimm, 1992, for review), reveals it to be significantly different from the mammalian Y. Whereas for instance the mammalian Y has numerous genes that are active during foetal development, the *Drosophila* Y-linked genes typically have expression restricted to events during or just prior to spermatogenesis. Only the *bobbed* locus (the rDNA repeats that constitute the nucleolar organizer region) seem to be an exception to this rule in having somatic expression as well. The author can find no evidence for the existence of Y-mediated growth effects (either positive or negative) on the *Drosophila* Y. This difference between mice and flies, however, might simply reflect a difference in the means of sex determination and the fact that female flies are larger than males.

Kraak & de Looze (1993) present the argument that growth factors on the mammalian Y may be what initially defined the Y. They argue that in species with environmental sex determination, growth rate is often the determiner of sex. In species with large males they thus argue that a growth factor would often find itself in a male and could even become the male-determining gene; hence it would define the sex chromosome. This model for the initial evolution of the mammalian Y is hence complementary to the one presented here for the future evolution of the Y due to the spread of mutant forms of the sex/growth determining genes.

The Y as a vulnerable chromosome

The absence of recombination between X and Y (except in the pseudo-autosomal region) ensures that any selfish gene that requires linkage disequilibrium between two potentially polymorphic genes is more likely to evolve on the Y than on the autosomes or the X, all other things being equal (Hurst & Pomiankowski, 1991). Meiotic drives genes are, for instance, of this nature and Hamilton (1967) postulates that the inactivity of the Y may be as a response to the presence of Y-linked drivers. This hypothesis is dismissed by Charlesworth (1991) as not being particularly mechanistically feasible. However, genes on the Y are also particularly vulnerable to becoming selfish resource extractors. This is for the simple reason that, by virtue of their position, they need not evolve any special means to ensure expression only when inherited from a father. Following Hamilton's logic, Y inactivity might in part be a counter to such selfish growth promoters. However, if these growth factors also exercise their effects in the same act as their normal function (e.g. sex determination) then Y inactivation would not be a viable counter to these selfish genes. Genes that are involved in a necessary function and that exercise developmentally early growth effects might thus be expected to accumulate on the Y because of the Y's singular transmission genetics. That Y-linked genes can easily become selfish resource extractors thus provides a novel understanding of the evolution of the mammalian Y and of the genes which might be found on it. In the following paper (Hurst, 1994, this issue) I address how the above model might also explain why some Y-linked genes are fast evolving, why they may vary in copy number and how they interact with their X-linked homologues.

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Appendix

Consider a mammal in which a female has either one (probability $= x$) or two (probability $= 1 - x$) mates but always produces N male progeny. N may vary between species but is assumed to be constant within any given one. Let us assume that the female has only one brood and allocates resources independently to sons and daughters. Allocation is dependent upon a growth signal from the foetus. Let us assume the situation to be at equilibrium; that is, all foetuses are demanding resources at some set level and all foetuses hence receive the same titre of resources.

Consider now a mutant Y chromosome that has a growth factor on it and hence the foetus bearing it demands more resources. The increment in demand is δ at a cost U. The net allocation to an individual demanding $1 + \delta$ resources is a simple function of the total resource demand. If the brood contains n male progeny sired by a father with the mutant Y and the remaining $N - n$ progeny sired by a male without the mutant Y then the net relative demand (D_δ) by any mutant-bearing foetus is

$$D_\delta = (1 + \delta)/(n(1 + \delta) + (N - n)) \quad (1)$$

whereas that of the wild-type in a such mixed brood is

$$D_{-\delta} = 1/(n(1 + \delta) + (N - n)). \quad (2)$$

It shall be assumed that the average size of the offspring is not dependent upon brood size. This assumption is made to allow comparison between theoretical species with different fixed brood sizes. Size (S) of offspring is hence proportional to ND. The effect of size on fitness (F) is assumed to be a diminishing function such that

$$F = (1 + \alpha)S/(1 + \alpha S) \quad (3)$$

which, as S tends to infinity, has an asymptote at

$$F = (1 + \alpha)/\alpha.$$

The fitness due to demand δ is F_δ. The fitness of wild-type individuals sharing a womb with individuals demanding δ is $F_{-\delta}$. Fertilization is random. Hence a mother with N progeny will produce a variable n with the mutant Y. The net output of offspring containing the selfish Y is a function of Ω, where

$$\Omega = \sum_{n=0}^{n=N} n.\, F_\delta (0.5)^N.\, {}^N C_n / N. \quad (4)$$

Likewise, the output of the same mother of individuals with the wild-type Y is a function of ψ where

$$\psi = \sum_{n=0}^{n=N} (N - n) F_{-\delta} (0.5)^N.\, {}^N C_{N-n}) / N. \quad (5)$$

The frequency of the mutant Y chromosome in the next generation (p') relative to this generation (p) is then given by

$$Wp' = (1 - U)p[x + (1 - x)(p + 2(1 - p)\Omega)] \quad (6)$$

where

$$W = (1 - U)p[x + (1 - x)(p + 2(1 - p)\Omega)] + (1 - p)[x + (1 - x)((1 - p) + 2p\psi].$$

Invasion is possible when

$$dp'/dp > 1 \text{ at } p = 0$$

which resolves to the condition that

$$U < 1 - 1/(x(1 - 2\Omega) + 2\Omega) \quad (7)$$

must be satisfied for invasion. It follows that, for invasion, $x < 1$, $N > 1$, $\alpha < \infty$ and $\delta > 0$ must all be satisfied. The graphical solution for this is given in Figs

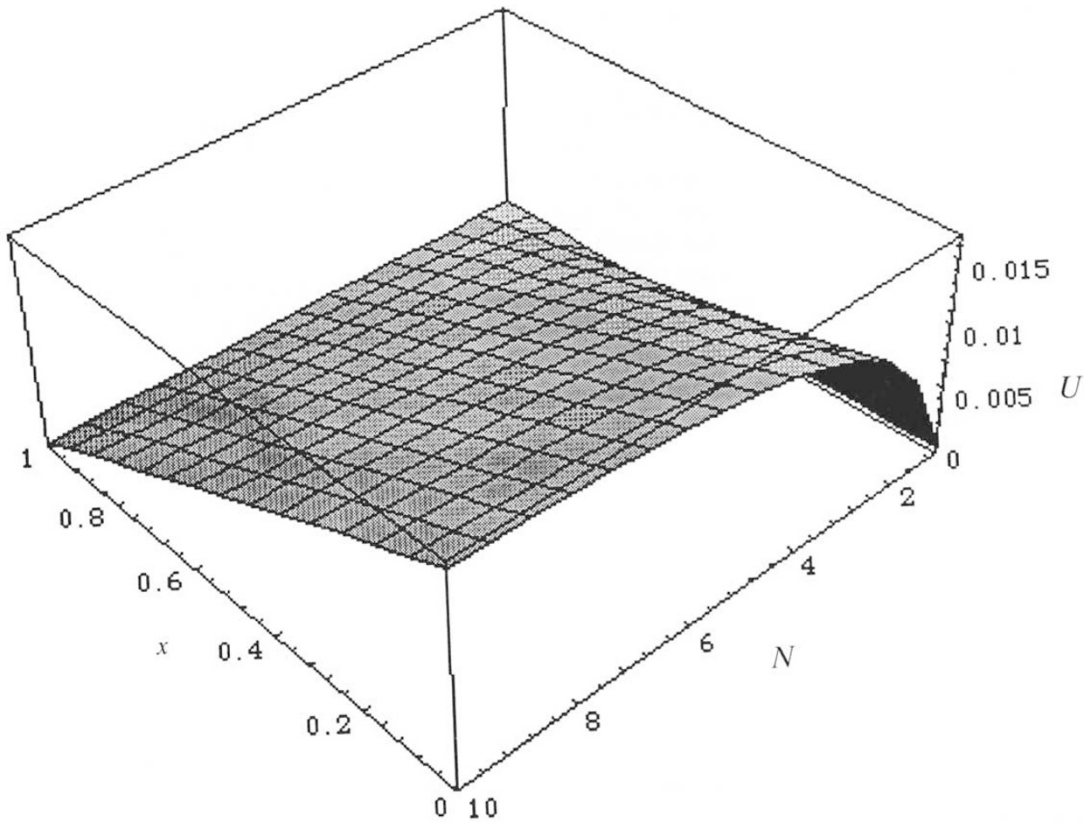

Fig. 1 Cost of the signal (U) permitted to allow invasion of the growth-demanding Y chromosome as a function of the probability of a single mating (x) and the number of male brood mates (N). The parameter values are $\alpha = 1.5$ and $\delta = 0.1$. The value of U must be below the surface for invasion to be possible. Note the two limiting conditions: if $x = 1$ all females are monogamous, and hence a selfish Y cannot share a womb with a nonselfish Y. Similarly, if N (number of sons) is unity, the womb can never be shared with another male.

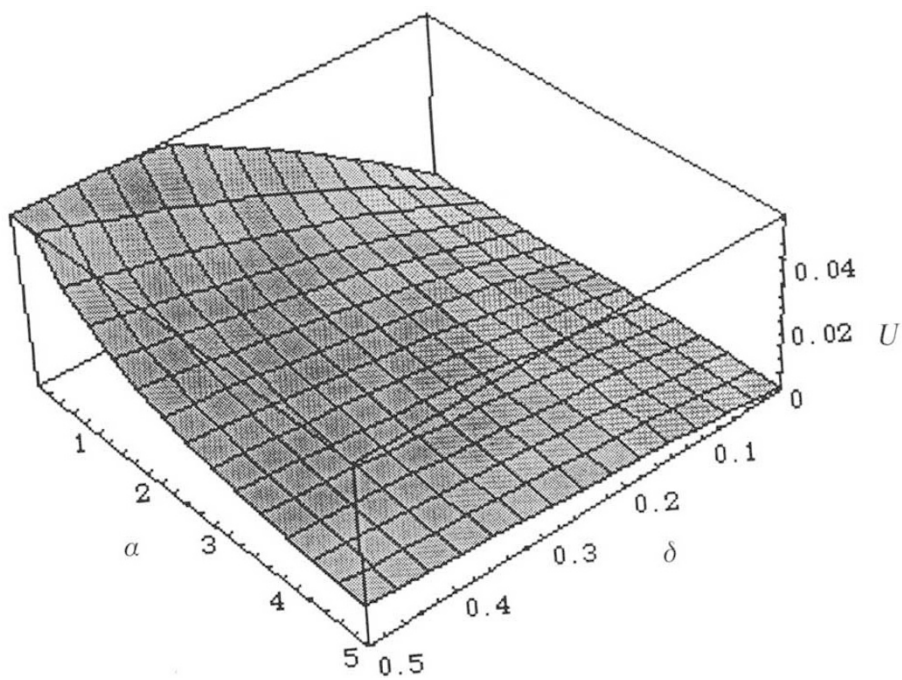

Fig. 2 Cost of the signal (U) permitted to allow invasion of the growth-demanding Y chromosome as a function of the strength of the signal (δ) and the parameter of the fitness trade-off curve (α). The parameter values are $N = 5$ and $x = 0.5$. The value of U must be below the surface for invasion to be possible. Note the two limiting conditions: if $\delta = 0$ the selfish Y gains no advantage (it is not selfish, only costly). Similarly, as α tends to infinity, so the fitness gain tends towards zero.

1 and 2. Solving $p' = p$ reveals that equilibria occur at

$$p^* = 0,\ p^* = 1 \text{ and } p^* = \frac{(2 + x - 2x)(1 - U) - 1}{(x - 1)(2 - 2\Omega - 2\psi - U + 2U)}. \quad (8)$$

Graphical solution (not presented) demonstrates that, just so long as the invasion conditions are satisfied (eqn 7), the above term (eqn 8) is never greater than zero. Invasion must hence be followed by fixation.

The model is designed to provide the most stringent conditions for invasion of the selfish Y. Therefore (i) sons cannot utilize resources intended for daughters, (ii) mothers are semelparous, hence sons cannot increase the total resource provisioned to a brood as they might in iteroparous organisms, and (iii) N is constant, hence if $N = 1$ a male can never share a womb with another male. A limitation of the above model is that it does not consider the possible trade-off between signal intensity (δ) and cost (U); it simply derives the maximum value that U may take for any given value of δ.