**Imprinted green beards: a little less than kin and more than kind**

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Imprinted green beards:

a little less than kin and more than kind

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RNA is complementary to the DNA sequence from which it is transcribed. Therefore interactions between DNA and RNA provide a simple mechanism of genetic self-detection within nuclei. Imprinted RNAs could enable alleles of maternal and paternal origin to detect whether they are the same (homozygous) or different (heterozygous) and thereby provide strategic information about expected relatedness to siblings.

**Keywords:** inclusive fitness, imprinting, siRNA, green beards, relatedness
“The situations in which a species discriminates in its social behaviour tend to evolve and
multiply in such a way that the coefficients of relationship involved in each situation
become more nearly determinate.” [1]

1. Introduction

The probabilities that factor into calculations of relatedness can be parsed into
probabilities given a genealogy and uncertainties of genealogy. Genealogy may
be uncertain, for instance, because a littermate is sometimes a full-sib, sometimes
a half-sib, or because a herd contains kin of different degrees, but members
cannot distinguish the categories [2]. Hamilton proposed that natural selection
favours reduction of genealogical uncertainty. He further proposed that natural
selection favours “discrimination of those individuals which do carry one or both
of the behaviour-causing genes from those which do not.” Here, he considered
the possibility of genes ‘recognizing’ their own copies and directing benefits on
the basis of this privileged information [1].

Dawkins called gene-based discrimination “the Green Beard Altruism
Effect.” He envisaged a gene that encoded both a phenotypic label, the green
beard, and the tendency to be nice to green-bearded individuals [3]. Kinship is a
major cause of identity by kind, but the label is independent of genealogy. Green
beard effects were considered implausible because genetic self-recognition and
altruism were viewed as complex behaviors unlikely to be encoded by a single
gene or tightly-linked cluster of genes. Kinship seemed a much stronger basis for
altruism. The situation is reversed at the genic level. It is much simpler to
imagine a gene, or its products, preferentially interacting with identical genes, or their products, than to envisage a gene that recognizes half-cousins [4, 5]. The interaction between labels of genic identity (green beards) and parental origin (genomic imprinting) makes possible a novel form of discrimination. I first review effects of genomic imprinting on estimates of genic relatedness, then describe the unusual evolutionary properties of imprinted green beards.

2. Parent-specific relatedness

The standard way to calculate the probability that a gene in A has an identical-by-descent copy in B is to multiply by one-half for each generation back from A to a common ancestor C, by one-half for each generation forward from C to B, and then sum these products for all distinct paths linking A to B. Ascending and descending factors of one-half arise from different sources of uncertainty. For each step backward from offspring to parent, a randomly chosen gene in the offspring may come from either mother or father. For each step forward from parent to offspring, the offspring receives one of two alleles in the parent.

Genomic imprinting enables genes to discriminate between matrilineal and patrilineal kin [6]. The factor of one-half for the first backward step resolves into a factor of one or zero when genes have imprinted expression. In the case of sibs, an imprinted gene of maternal origin is definitely present in an offspring’s mother and transmitted to littermates with probability one-half, whereas an imprinted gene of paternal origin is definitely present in the offspring’s father, and transmitted to littermates with probability $p/2$ where $p$ is the chance of
shared paternity. Because expected relatedness to a littermate is lower when
genes are paternally-derived, imprinted genes are predicted to behave more
‘selfishly’ toward littermates when paternally-derived and less ‘selfishly’ when
maternally-derived.

If genes carried imprints of grandparental origin, then factors of one-half
for the first and second backward steps would resolve into factors of either one
or zero [7]. Thus, half-cousins who share a maternal grandmother are related by
one-quarter for genes of maternal grandmaternal origin but are unrelated for all
other genes. As yet, there is no clear evidence for second-order imprints.

3. Imprinted green beards

Complementarity between the strands of a double helix, and between DNA and
the RNA transcribed from its sequence, allow allele-specific interactions within
nuclei between different copies of the same gene. A diverse fauna of small RNAs
participate in a wide variety of regulatory processes. Many of these processes
depend on interactions with complementary DNA or RNA [8]. Because
complementary sequences represent each other, their interaction can be viewed as
a simple form of genetic self-recognition that makes possible intranuclear green
beard effects.

24-nt small-interfering RNAs (siRNAs) of Arabidopsis cause RNA-directed
DNA methylation (RdDM) and transcriptional silencing of DNA sequences with
motifs complementary to the siRNA. The template for synthesis of siRNAs is
probably the sequence subject to RdDM [9]. Dosage-sensitive responses to an
siRNA would allow a sequence to ‘count’ its copies within a nucleus. Imprinted
expression of an siRNA would allow alleles of maternal origin to signal their
presence to alleles of paternal origin, or vice versa. A silent allele can ‘hear’ what
the other allele has to say.

An abundant class of maternally-expressed siRNAs (mesiRNAs) are
expressed from madumnal (maternally-derived) chromosomes of endosperm
[10]. MesiRNAs target genes that delay onset of endosperm cellularization and
prolong endosperm proliferation [11], consistent with theoretical predictions that
maternally-expressed imprinted genes should inhibit endosperm growth [12].

Consider the introduction of mesiDNA (a motif that encodes mesiRNA)
into a previously unimprinted gene encoding a growth enhancer. Transcription
of A, the established allele without mesiDNA, is expected to be a compromise
between a lower level favoured as a madumnal allele and higher level favoured
as a padumnal (paternally-derived) allele. In contrast, A’, the initially rare allele
with mesiDNA, will be transcribed at the same level as A when it is a padumnal
allele, because the siRNA is not expressed, but at lower levels than A when it is a
madumnal allele, because the siRNA is expressed. Thus, A’ behaves as a
padumnally-expressed, madumnally-silent allele when heterozygous. It will
increase in frequency at the expense of A because it makes finer discriminations
of relatedness.

By contrast to its behavior in heterozygotes, A’ mRNA is transcribed from
neither allele in homozygotes, because both alleles are silenced by the mesiRNA.
The siRNA produced by madumnal A’ informs padumnal A’ that the seed
contains an A’A’ embryo rather than an AA’ embryo and that the mother carries
at least one copy of A’. Therefore, at least half of other embryos will receive A’
from their mother (in addition to those that receive A’ from their father). Thus,
mesiRNA signals a doubling of ‘relatedness’ to self and increased ‘relatedness’ to littermates ($r_L$). If $r_L$ more than doubles, the balance of benefits to self and costs to littermates for padumnal $A'$ shifts in favour of production of less growth enhancer, as occurs in the presence of mesiRNA.

Whether $r_L$ is doubled will depend on allele frequencies, the frequency of selfing, and the number of fathers per brood. A complete analysis of this problem is beyond the scope of this letter, although some insight can be gained by considering effects when $A'$ is rare. In an outbreeding population, $A'$ will be transmitted predominantly by $AA'$ parents with padumnal $A'$ expressed when mothers are $AA$ but inhibited by mesiRNA in 50% of seeds when mothers are $AA'$. MesiRNA signals a doubling of $r_L$ for single paternity of a mother’s offspring and more than doubling for multiple paternity. Therefore a reduction in seed size, with concomitant increase in seed number, would appear to benefit $A'$. MesiRNA functions as a ‘secret hand-shake’ that allows padumnal $A'$ to recognize its allelic partner as self and to reduce its own transcription for the benefit of madumnal $A'$ in littermates.

MesiRNA could also function as an adaptive signal of self-fertilization. Selfing shifts the optimal trade-off between seed size and number for genes expressed in filial tissues to smaller seeds [13]. If mothers sometimes self, padumnal $A'$ will be more likely to encounter mesiRNA in selfed seeds than outcrossed seeds, especially when $A'$ is rare. Therefore, padumnal $A'$ will promote smaller seeds on selfing and larger seeds when outcrossed.

$A'$ produces less mRNA in homozygotes than is optimal for an unimprinted allele expressed in offspring. Therefore, near fixation of $A'$, rare alleles (such as $A$) that are expressed more than $A'$ will be favoured by natural
selection. This suggests $A$ and $A'$ will be maintained at a polymorphic equilibrium.

Green-beard altruism is vulnerable to 'cheats' who flaunt the label, receive its benefits, but do not reciprocate [14]. $A^\circ$, a version of $A'$ that retains mesiRNA but is insensitive to its inhibitory action, would increase in frequency at the expense of $A'$ because madumnal $A^\circ$ induces padumnal $A'$ to reduce demand, benefiting $A^\circ$, but $A^\circ$ does not reciprocate when madumnal and padumnal roles are reversed. Once $A^\circ$ eliminates $A'$, the population is primed for the introduction of $A^*$, an allele that possesses a beard of a different colour (new mesiRNA) [15]. Such an iterative process (Figure 1), in which successively-introduced mesiRNAs are only transiently effective, could explain the diversity of mesiRNAs, their rapid evolutionary turnover, and mild effects [10, 16].

Imprinted gene clusters of mammals contain many non-coding RNAs [17]. DNA–DNA associations and RNA–DNA interactions within these clusters may be facilitated by somatic pairing of madumnal and padumnal chromosomes [18, 19]. MicroRNAs processed from maternally-expressed antiPeg11 cause mRNA degradation of paternally-expressed Peg11 [20]. Mutations of madumnal Rasgrf1 silence the padumnal copy of a neighboring non-coding RNA [21]. Disruption of madumnal Ube3a upregulates padumnal Ube3a-antisense [22]. Such examples suggest the possibility of green beard effects at mammalian imprinted loci.
References


Figure 1: The mesiRNA ratchet. A population initially fixed for allele $A$ (upper left) is successively invaded by an allele $A'$ that also encodes a mesiRNA; an allele $A^\circ$ that retains the mesiRNA but is insensitive to its effects; and an allele $A^*$ that encodes a new mesiRNA (lower right). Subscripts $m$ and $p$ indicate madumnal and padumnal alleles. Squares represent the coding sequence of an mRNA. Circles and triangles represent coding sequences of mesiRNAs. Filled symbols are expressed. Unfilled symbols are silent. Homozygotes lie on the main diagonal. Off-diagonal elements are heterozygotes.