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RESEARCH HIGHLIGHT

Social dominance hierarchy: toward a genetic and evolutionary understanding

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In social animals, the formation of dominance hierarchy is essential for maintaining the stability and efficacy of social groups. A study by Wang and colleagues employ a combination of comparative genomic and functional approaches to shed new light on both the genetic mechanisms and the evolutionary histories of dominance behavior.

Many animals display social behavior of one sort or another, ranging from the relatively simple (e.g., food sharing in wolf packs) to the extremely complex (e.g., the formation of human societies). While social behavior is widespread up and down the animal kingdom, there is a clear evolutionary trend wherein the more derived species on the phylogenetic tree such as placental mammals tend to display more sophistication in their social behavior.[1] This trend reflects the fact that positive Darwinian selection generally favors greater sociality as it tends to confer enhanced fitness to the species.

A prevailing theme in highly social animals is the formation of social groups. Within-group cooperation on many activities such as the search for food, procurement of shelter, and provision of common defense, can enhance the fitness of all group members. Social groups are commonly structured as a dominance hierarchy based on a ranking system whereby higher-ranked individuals have better access to valuable resources such as food and mates but they also tend to assume greater responsibilities in providing leadership and maintaining order.[2,3] The formation of a hierarchical ranking system requires the dominant-subordinate relationship to be established between individual group members. This can be achieved by physical fights, proxy contests such as sizing each other up and visual displays of strength, and in cognitively advanced animals, political maneuvers. Importantly, in order for a hierarchy to remain stable, each individual needs to remember and follow its dominance rank vis-à-vis other members of the group until such time when challenging the established rank is deemed beneficial.

The first scientific investigation of dominance behavior can be traced to Thorleif Schjelderup-Ebbe about a century ago, when he used the now popular colloquial term "pecking order" to describe the dominance hierarchy in domestic chickens.[4] He noted that dominance in chickens is asserted by various types of behavior, including pecking by the dominant chickens on the subordinate ones, which he used as a measure of dominance rank. He proposed that such a hierarchy, while arising from and maintained by some degree of conflict (e.g., pecking), could enhance social stability and actually reduce overall conflict.

To date, the study of social dominance has mostly focused on the neurocircuitry and neurochemicals underlying dominance behavior.[3] Many brain regions have been associated with social decision-making including dominance behavior such as the prefrontal cortex and the amygdala. Several hormones and neurotransmitters such as testosterone, dopamine and serotonin have also been implicated. By contrast, not much is known about the genetic basis of dominance behavior and how it evolved.

A recent paper in *Cell Research* by Wang et al. offers a nice inroad into the genetics and evolution of dominance behavior.[5] This study took a somewhat unusual approach. The authors began by performing a whole-genome sequence comparison across 16 amniotes (12 placental mammals, one marsupial, two birds and one reptile) to screen for genomic regions exhibiting accelerated evolution in the common ancestral lineage leading to placentals. The most accelerated region identified in the screen was named placental-accelerated sequence 1 (PAS1). Among the 16 species used in the original screen plus three additional species added to the comparison (two marsupials and one monotreme), PAS1 is found to be strongly conserved in the placentals and be also well conserved among the non-placentals, but shows substantial divergence between placentals and non-placentals. This indicates dramatically accelerated evolution of this otherwise highly conserved region in the ancestral placental lineage. Indeed, PAS1 displays a rate of sequence change in this lineage that is over one order of magnitude greater than the null expectation of constant rate.

PAS1 is a putative enhancer located upstream of the *LIM homeobox 2* (*Lhx2*) gene. *Lhx2* is a key regulator of embryogenesis including brain development.[6] The authors confirmed the enhancer activity of PAS1 on *Lhx2* expression in the embryonic nervous system, and showed that PAS1 orthologs from different species can drive different patterns of gene expression in cell culture and in transgenic mice. They then generated three modified PAS1 alleles in mice, including knockout of endogenous PAS1 ($PAS1^{-}$), knockin of wallaby PAS1 to replace the endogenous copy ($PAS1^{w}$), and knockin of chicken PAS1 ($PAS1^{c}$). The authors measured the dominant-subordinate relationship of mice carrying various combinations of these modified PAS1 alleles and the wild-type allele ($PAS1^{m}$) using the classic tube test. In this test, two rodents are allowed to enter a tube from opposite ends. When they meet in the middle, the animal that manages to push forward in the tube is scored as being dominant, whereas the animal that retreats is considered subordinate.[7] $PAS1^{w/m}$ mice are found to be more dominant than $PAS1^{w/w}$, whereas $PAS1^{c/m}$ mice are less dominant than $PAS1^{c/c}$. It is important to note that in these mice, once a dominance rank is established between two individuals, it is stably maintained over time as would be expected in nature.

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Interestingly, tests of PAS1$^{-/m}$ against PAS1$^{-/-}$ mice showed that they failed to establish a stable dominance rank. One mouse could be dominant over another on one day, but the relationship could change on the next day. The authors concluded that PAS1, through its enhancer function on *Lhx2*, acts as an essential regulator of social dominance behavior, and furthermore, PAS1 has played a role in the evolution of social hierarchy in amniotes.

The authors suggested that the accelerated evolution of PAS1 in the ancestral lineage leading to placentals might have contributed to the emergence of social hierarchy broadly observed in placentals. While this is a reasonable hypothesis, it should be pointed out that sociality is not a clear-cut defining trait demarcating placentals from non-placentals as prolonged gestation. While a high degree of sociality is found in many placentals, it is far from universal as many placental species are solitary. Additionally, some non-placentals are quite social, such as kangaroos and chickens. As such, there may be alternative interpretations for the accelerated evolution of PAS1 in the ancestral placental lineage. Another caveat of the study is that, even though the authors generated multiple PAS1 alleles in the mouse that could potentially give rise to many genotype combinations, only a few genotypes were used in the assessment of dominance rank (i.e., PAS1$^{w/m}$ vs PAS1$^{w/w}$, PAS1$^{c/m}$ vs PAS1$^{c/c}$, and PAS1$^{-/m}$ vs PAS1$^{-/-}$). This could be due to the difficulty in performing large amounts of animal breeding and testing. Nevertheless, with limited genotypes used in the study, it is difficult to interpret how PAS1 in different species modulates dominance behavior.

Notwithstanding the above caveats, the study is significant in that it provides the first example of an enhancer involved in the modulation of social dominance and it hints at the tantalizing possibility that the sequence evolution of this enhancer could have contributed to the phenotypic evolution of social dominance behavior in amniotes. Future studies are needed to bring more granular insights into the functional and evolutionary significance of this enhancer.

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