

Morphological diversification among pigeon breeds of different aptitudes

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Abstract: - Although DNA studies are nowadays predominant in phylogenetics, morphological approaches are still a widely accepted approach among the taxonomists. In the present study, the authors tried to construct a cladogram among 20 diverse domestic pigeon breeds of different origin (Asia, Europe and United States) and aptitude group (form, hen, crop, colour, drummer, structure, tumblers and meat) based on 30 morphological traits. In the obtained phylogram, groups overlapped, and no pattern according to areas of origin was detected. We hypothesize that artificial selection for similar aptitudes can have had distinct morphological effects, e.g. there can be many possible constructive traits (new phenotypes that are absent in the wild ancestor *Columba livia*) for the same purpose. In any case, this analyses exemplifies the complexities of breed formation in domestic pigeon.

Key-Words: - cladogram; *Columba livia*; doves; morphology; rock pigeon

1 Introduction

The great diversity of pigeon breeds, with striking differences in behaviour, vocalizations, skeletal morphology, feather ornaments, colours, and colour patterns, and with over 350 breeds that exists in the world [1] [2], makes difficult their systematic classification. Moreover, pigeon breeders, with their own breeds or particular interests, have provided partial histories in books and fanciers' magazines; information that is selective and often inaccurate. This is probably why so few comparative studies from morphological characters in pigeon breeds have been performed.

Morphological characters can provide very useful information to complete other investigations about relationships of domestic breeds in general as well as being extremely

important from an anthropological point of view. Statistical techniques such as multivariate analyses and the application of numerical taxonomy to the data derived from morphological traits allow adequate treatment of the information generated in those comparative studies. This statistical treatment has been very much facilitated during last decades because easy-to-run computing packages specially designed for such analyses and because very powerful computers easily available.

In this paper we present a study comprising qualitative and quantitative data analyses for some domestic pigeon breeds of very different origins and purposes. The research is mainly centred in qualitative traits, on which breeders have focused more [2].

2 Materials and methods

2.1 Breeds studied

Twenty pigeon breeds were studied: Archangel (ARC), Barbhan (BAR), Bokhara Trumpeter (BOK), Bombai (BOM), Chinese Owl (CHI), Frillback (FRI), Hungarian Giant (HUN), Indian Fantail (FAN), Indian Tumbler (TUM), King (KIN), Lahore (also known in Iran as Sherazi) [2] (LAH), Lotan (LOT), Kokah (KOK), Mookee (MOO), Parlour Roller (PAR), Pencil Pouter (PEN), Racing Homer (RAC), Runt (RUN), Strasser (STR) and Stargard Shaker (STA). They were grouped according to Müller's groups [1]: form (group I, breeds with striking body and/or head shape: Barbhan, Lahore and Shaker), hen (group III, hen-like breeds: King), crop (group IV, breeds with an ability to inflate their crops far more than normal: Pencil Pouter), colour (group V, breeds with striking colours and markings, without prominent body features except sometimes feathered feet: Archangel and Mookee), drummer (group VI, breeds which do not coo when excited but emit a call which sounds like distant drumming: Kokah and Bokhara Trumpeter), structure (group VII, breeds with special plumage features: Chinese Owl, Frillback, Hungarian Giant and Indian Fantail), and tumblers (group IX, breeds with a typical behaviour, in which they plum from a great height and turn somersaults as they fall: Parlour Roller, Lotan and Indian Tumbler). Meat breeds (Bombai, Runt and Strasser) were classed as a separate group. So all these breeds reflect a collage of defining traits and purposes, and included breeds from Asia. So the heterogeneous spectrum studied provides a geographic anchor to compare geographically separated breeds from Europe, Asia and America.

2.2 Qualitative and quantitative analyses

A total of 30 morphological characters were studied. The characteristics were those described habitually in a breed description and were considered as being informative. Although pigeons show a spectacular range of variation in colour type and pattern, frequently into the same breed, plumage pigmentation phenotypes

were not considered. The set of morphological characters was obtained from breed standards, our own observations and breed descriptions found in the literature. Second author (MAK) was responsible of this part. All character codification was considered to be unordered (that is, change could hypothetically transform freely between any of the described states) and without polarity (no ancestral state is assumed), e.g. all characters were equally weighted for the analysis. The number of states for each character was established depending upon the number of distinguishable phenotypic classes. Coded states were in the range 1 to 5 and unique states in multistate characters were avoided. Discrete characters were described with two (binary) to five potential character states. Continuous characters (body weight) were split into 3 classes. Characters and their states are shown in Table 1. As outgroup we introduced a "multi 0" fiction breed. This is a resource that has been done by other researchers in similar cladistics studies [3].

The original matrix of morphological resemblances for each breed is shown in Table 2. Analysis was based on the parsimony principle, and the criterion was to find the heuristic tree (cladogram) that required the least number of changes. The method used was Fitch parsimony, in which characters are reversible and unordered, meaning that all changes have equal cost. The heuristic algorithm used was "Subtree Pruning and Regrafting" (SPR). Two informative indexes for the cladogram were obtained: the per-character Consistency Index (CI) and the per-character Retention Index (RI). CI is defined as m/s , where m is the minimum possible number of character changes (steps) on any tree, and s is the actual number of steps on the current tree [4]. CI varies from one (no homoplasy) and down towards zero [4] (a lot of homoplasy -a trait has been gained or lost independently in separate breeds). RI is defined as $(g-s)/(g-m)$, where m and s are as for the consistency index, while g is the maximal number of steps for the character on any cladogram [4]. RI measures the amount of synapomorphy -a trait present in the ancestral species and shared exclusively (in more or less

modified form) by its descendants- on the tree, and varies from zero to one [4].

All analyses were performed using the PAST computing package (Paleontological Statistics Software Package for Education and Data Analysis) [5].

3 Results

The cladogram resulting from the application of the Fitch parsimony method to the morphological traits is shown in Figure 1, which evaluated 5,400 trees. The values in the tree indicated the number of replicates from the bootstrap analysis (loosely, the width of the confidence interval). Fitch parsimony needed 168 steps (total length of the tree) to rearrange the characters to obtain the minimum parsimonious tree. The obtained cladogram must be viewed merely as a group tree concerning mere morphological relationships, no phylogenetic relationships. Anyway, it did not reflect common behaviours, physical appearance, and/or related geographic origin, as group-breeds (both for origin as according to aptitude groups) overlapped, and no pattern according to areas of origin was neither detected. This lack of clustering may indicate traits that are not shared by grouped breeds rather than not have sampled the closest relatives.

Their similarities between groups must not be used to group like with like in descending order of specificity. The CI was 0.506 and the RI was 0.464. These similar homoplasy and synapomorphy values would indicate similar actions both for conserving existing traits as for constructing new traits. Moreover for us it is clear that it must exist a certain correlation among body parts, which ultimately impact phenotypic diversification. Figure 2 represents the strict-rule consensus tree formed after 100 bootstrap replicates. The strict consensus of these trees recovers a monophyletic tree, relative to the outgroup. The parsimony tree and the strict rule consensus tree were very similar.

4 Conclusion

Domesticated animals can give an important insight in the vastly slower process of natural selection, as it accomplishes in generations what normally takes thousands of years. One species in particular, the pigeon (*Columba livia*), is central to the understanding of the evolution and diversification of natural species, as it provides an analogous and accelerated window into that process, in which artificial selection has been the primary force driving pigeons' breed diversification.

We suggest that formation for each breed must be studied as mechanism in which attributes that can characterize each breed are not necessarily the same in spite of similar purpose selection. Each breed has been subjected to a different mode of combinations between those factors, such genetic, reproductive, behavioural, ecological and cultural conditions. In other words, each aptitude group is not evolutionary, in the sense that they do not create the same identity for all traits, so being no similar evolutionary tendency. In other words: breeds' groups are not phenetic groups as each breed for a same aptitude can be distinct, sharing few common traits.

But the evolution of pigeon breeds as well as those of other domestic animals is far from being completed. Moreover new types will be developed, as this happens inevitably in the course of incessant creative (and destructive) human activities with respect to those species which have been tamed.

5 Competing interests

The authors are not conversant of any memberships, financial holdings or affiliations that could raise a conflict of interest.

6 Availability of data

Additional information and biological datasets can be requested directly to first author.

7 Authors' contributions

Kabir collected all morphological data. Parés was responsible of data treatment and discussion of results.

References:

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Table 1. Characters and their states, used for the construction of the morphological resemblance matrix.

Weight	660-770g	240-370g	430-550g		
	1	2	3		
Size	Small	Medium	Big	Very small	
	1	2	3	4	
Chest	Narrow	Medium	Wide	Very wide	
	1	2	3	4	
Legs length	Short	Medium	Large		
	1	2	3		
Legs thickness	Fine	Medium	Thick		
	1	2	3		
Legs feather	Muff	No	Grouse		
	1	2	3		
Relative head size	Small	Medium	Big		
	1	2	3		
Head shape	Rounded	Squared			
	1	2			
Crest	Wild type	Peak	Breast frill	Shell	Rose
	1	2	3	4	5
Beak bulkiness	Fine	Medium	Thick		
	1	2	3		
Beak length	Short	Medium	Very short		
	1	2	3		
Beak form	Slightly curved	Straight			
	1	2			
Nose wattle	Little	Slightly	Developed		
	1	2	3		
Aspect of	Fine	Rough			
	1	2			
Chin wattle	Without	Fine			
	1	2			
Eye cere	Fine	Developed	Well developed		
	1	2	3		
Globe seize	Little	Medium	Well developed		
	1	2	3		
Globe form	Slight	Oval	Rounded		
	1	2	3		
Hanging of crop	Not hanging	Pendulous			
	1	2			

Vertical crease	No	Yes			
	1	2			
Neck length	Short	Medium	Long		
	1	2	3		
Neck thickness	Fine	Medium	Thick		
	1	2	3		
Back	Flat	Slightly	Arched		
	1	2			
Garland	No	Yes			
	1	2			
Number of rectrices	12	30			
	1	2			
Tail length	Short	Medium	Long		
	1	2	3		
Tail form	Flat	Arched			
	1	2			
Rump width	Narrow	Medium	Broad		
	1	2	3		
Position of wing	Below	Upon the tail			
	1	2			
Station	Horizontal	Vertical			
	1	2			

Table 2. Morphological resemblance matrix. Breeds abbreviations in the text.

	Station	Position of wing upon the tail	Rump width	Tail form	Tail length	Number of rectrices	Number of rectrices	Garland	Back	Neck thickness	Neck length	Vertical crease in the globe	Hanging of the globe	Globe form	Globe seize	Eye cere	Chin wattle	Aspect of nose wattle	Nose wattle	Beak form	Beak length	Beak bulkiness	Crest	Head shape	Relative head size	Leg feather	Legs thickness	Legs length	Chest	Size	Weight					
K	1	3	4	1	3	2	3	2	1	3	2	1	1	2	3	3	1	1	2	1	1	2	2	1	1	2	3	2	3	2	1					
M	2	2	2	2	2	2	3	2	2	3	2	2	1	1	2	2	1	1	1	2	1	1	2	2	2	2	3	2	2	2	2	1				
A	2	2	2	2	2	2	3	1	2	1	2	1	1	1	2	1	1	1	1	2	2	2	2	2	3	1	2	2	2	2	2	2	1			
B	3	3	2	3	2	1	3	2	5	2	1	2	1	1	1	1	1	1	1	1	2	1	2	1	2	5	2	1	2	1	2	1	3			
K	2	2	2	2	1	2	2	2	2	2	2	1	1	1	2	1	1	1	2	2	1	2	2	2	2	2	2	2	2	2	2	2	2	1		
C	2	1	2	1	1	2	1	1	3	3	3	2	2	1	1	2	1	1	1	2	2	2	2	2	1	3	3	3	2	2	2	2	2	1		
F	3	2	4	2	2	1	2	1	2	3	2	2	2	2	2	1	1	1	2	2	2	2	2	2	1	2	3	2	2	2	2	2	2	1		
F	2	2	2	2	2	1	2	1	4	2	2	2	1	1	2	1	1	1	2	1	2	2	2	2	1	4	2	2	2	2	2	2	2	2	1	
H	1	3	4	2	3	1	2	2	4	1	1	1	2	1	1	1	1	1	1	2	1	1	1	2	4	1	1	1	1	1	1	1	1	1		
S	2	4	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
B	3	3	2	2	3	2	3	2	1	3	1	1	3	1	2	3	1	2	3	1	2	3	1	3	1	3	1	1	1	1	1	1	1	1	1	
L	3	3	4	3	3	3	3	1	1	2	2	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	
L	2	1	2	2	2	2	2	2	2	2	2	2	2	1	1	1	2	1	1	1	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1
T	2	2	2	2	2	2	3	1	1	1	2	1	1	1	1	1	1	2	2	1	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1
P	2	2	2	1	2	2	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
P	2	4	2	3	2	2	2	2	1	1	2	2	2	1	1	2	3	3	2	1	2	2	2	2	1	2	2	2	2	2	2	2	2	2	2	2
R	3	3	4	2	3	2	2	2	1	3	2	1	3	1	1	2	3	3	1	1	2	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1
R	1	3	4	2	3	2	2	2	1	3	1	2	3	1	1	3	3	2	1	1	1	2	3	1	1	1	1	1	1	1	1	1	1	1	1	1
B	2	2	3	2	2	2	3	2	4	2	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
S	1	3	4	1	3	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	2	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1

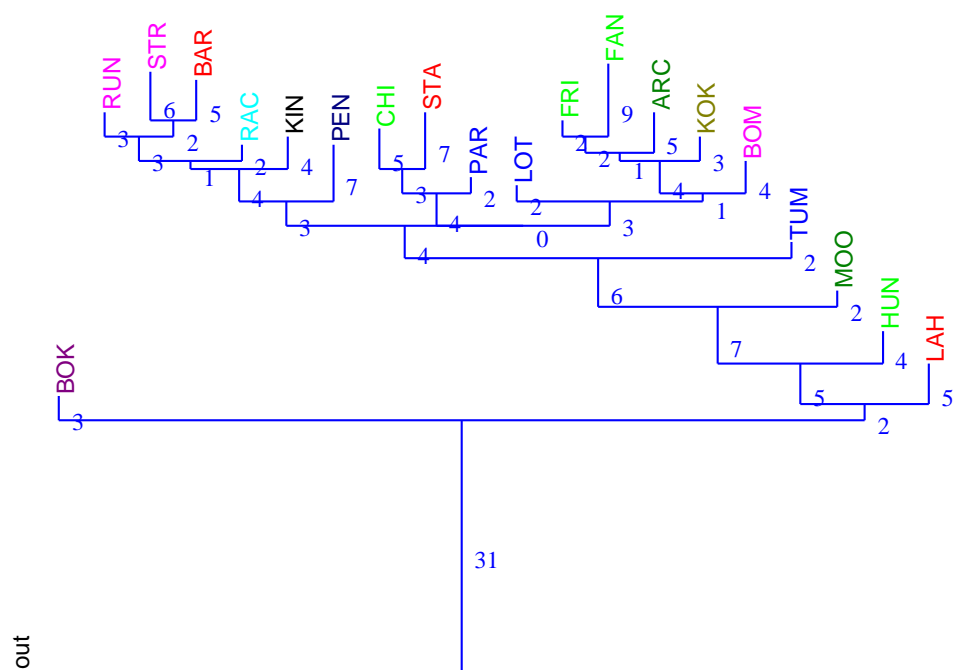


Figure 1. Phylogram resulting from the application of Fitch parsimony method and SPR (Subtree Pruning and Regrafting) heuristic algorithm. Fitch parsimony evaluated 5,400 trees. The values in the tree indicated the number of replicates from the bootstrap analysis (loosely, the width of the confidence interval). Fitch parsimony needed 168 steps (total length of the tree) to rearrange the characters to obtain the minimum parsimonious tree. Breed acronyms in the text. The outgroup (out), from which the dendrogram was computed, was an arbitrarily designed hypothetical breed, in which all traits were assumed to be zero.

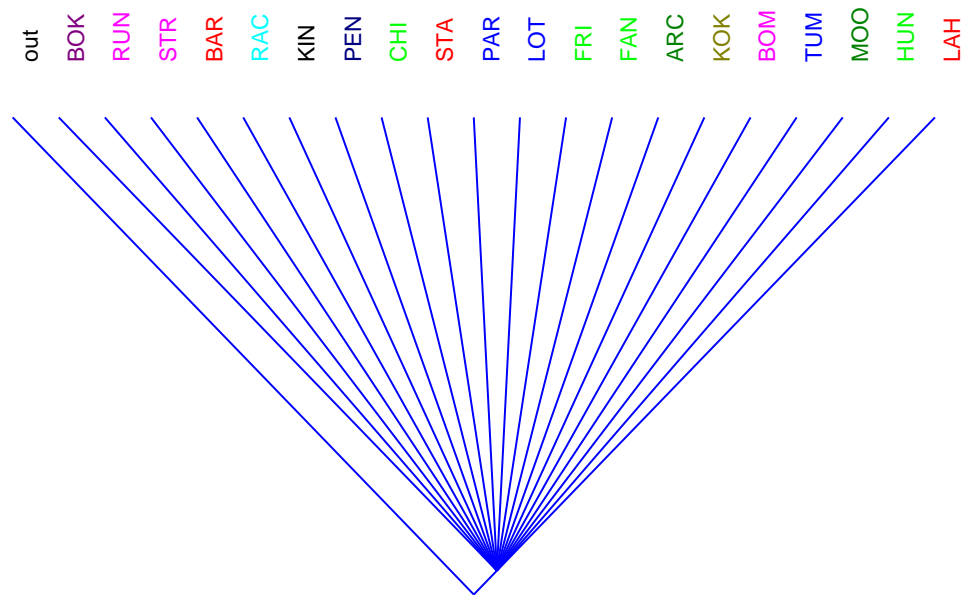


Figure 2. Strict-rule consensus tree from morphological data formed after 100 bootstrap replicates. Acronyms in the text. The outgroup (out), from which the dendrogram was computed, was an arbitrarily designed hypothetical breed, in which all traits were assumed to be zero.