DISTINGUISHING BETWEEN DUCKS, GEESE AND SWANS BY MEANS OF FEATHER MICRO-BIOMETRICS

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SUMMARY

Use of a comparison microscope allows relatively easy separation of ducks from geese from swans because of easily seen differences in relative sizes of feather barbule features. However, such differences are difficult to detect using a single microscope and a simple biometric method is described which separates these groups using three measurements with an accuracy of 88%.

Such a method may also be of use in breaking down the weight ranges of other Orders and examples are discussed.

INTRODUCTION

Basic microscopic identification methods for feather fragments to ordinal level have been described by Chandler (1916), Day (1966) and Brom (1980) and individuals working in the field have developed their own identification keys, which allow the major groups to be separated at least to ordinal level. When attempting to identify birds involved in collisions with aircraft, circumstantial evidence, such as time of year and location etc, can help in determining the species and thereby ascribing the probable weight. However, aero-engine manufacturers are seeking greater accuracy in weight estimates for birdstrike remains identification and this paper describes a biometric method to separate Anseriformes, which are easy to separate from other orders of birds, into ducks (383-3600g), geese (1300-5150g) and swans (4700-11000g) (Brough 1983). Such a method is not usually necessary for those using a comparison microscope as feathers from the different groups can be compared and differences visibly detected. However, any differences are difficult to detect using a single microscope and this method will, therefore, be of use.

METHOD

Basal barbules of basal barbs taken from breast feathers of a number of Anseriformes species of different groups (Table 1) were mounted on microscope slides and the following features were measured using an eyepiece graticule:-

1. The base length, from the base of the barbule ie, where it joins the barb, to the distal end of the first well developed node (Fig 1). The first rudimentary swelling was ignored.

2. The width of the first well developed node, measured at its widest point.

3. The first internode length measured from the end of the first developed node to the distal end of the second developed node.

Barbule length was not used as an identification feature as natural abrasion often resulted in the tip of the barbule breaking off. One hundred measurements of each feature were taken from a number of different feathers, from more than one bird.

These measurements were analysed using SPSS DISCRIMINANT (Nie *et al.* 1975). The aims of this analysis were to determine whether it was possible to discriminate between two or more groups, in this case ducks, geese and swans, using standardized measurements of feather structure base length (BL), node width (NW) and internode length (INL) from samples of known origin and, if it was, to attach confidence limits to the predictive model. For examples of the use of discriminant analysis in biometric studies, see (Green 1982, Wood 1987, and Summers, Nicholl, Underhill and Petersen 1988). The probability of correct classification is expressed as predicted group membership (PGM%). The analysis assumes a normal distribution ie. that the mean value of any variable is distinct between groups and normally, a PGM% of 70% reveals a significant difference between the groups. However, it was decided arbitrarily, to increase the accuracy of the separation, that any PGM% of less than 75% would not be of use as a practical separation tool.

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Having discovered that the three groups were distinct using known feathers, the analysis can be used as a predictive tool to assign one measurement of the three variables of an anseriforme feather of unknown species to one of the three groups using Fisher's linear discriminant functions, automatically produced by the analysis, as the basis of separation equations and the PGM% as a measure of accuracy.

Similar measurements of feathers taken from different areas of a single mallard were used to determine whether individual variation between different feathers would reduce the accuracy of the prediction.

RESULTS

The results revealed a high degree of separation (88.09%) between ducks and geese and swans (Table 1). The measurements clearly separated ducks from geese and swans (PGM% 97.2%), but the geese and swans had less significant classification results indicating that the two could be confused on occasions. Separation of genera and species was less successful with respective PGM% results of 47.43% and 39.26%, showing that the structures measured do not vary sufficiently to provide a worthwhile distinction at these levels.

Examination of feathers from various areas of a single mallard also showed a significant variation with a final PGM% of 76.25% (Table 2). This appears to be related to the size of the feathers since the mean values for each variable show the largest feathers from the back have the largest overall length and the under-wing coverts the smallest. However, when all the data were grouped and compared against the other anseriforme data, the result indicated that all were "ducks". Thus although individual variations occur with feathers from a single species, the main groups are so different that no confusion results.

USE IN BIRDSTRIKE REMAINS IDENTIFICATION

The relatively simple method described above shows that, by using a single microscope, remains from a birdstrike involving an anseriforme species can be identified to a group with a reasonable degree of accuracy thus reducing the large possible weight range of the original Order.

Fisher's linear discriminant functions (Table 3), provide the basis of separation equations. These can be computed manually from one set of measurements of the anseriforme barbule, or the single set of measurements can be assigned to the correct group using the Basic programme at Appendix 1.

REDUCING THE WEIGHT RANGES OF OTHER ORDERS

Due to the success in breaking down the Order Anseriformes into smaller weight range groups of ducks, geese and swans, students working with the Aviation Bird Unit have used similar methods in attempts to sub-divide other orders with large weight ranges.

Passeriformes (song or perching birds) are being increasingly submitted for identificaiton as aerodrome staff are becoming more interested in the task and in finding the relatively small remains, especially from *en route* birdstrikes. The possible weight range in the UK with this Order is 9-1150g, which again is of little use to engineers attempting to correlate damage with bird weight and aircraft speed.

Using four measurements; base length (BL), internode length (INL), node width (NW) and barbule width (BW) (Fig 2), no separation into families was possible. However, it was found that the Order could be split into corvids, the heaviest birds with a weight range of 160-1105g, and other passerines weighing 9-160g, with an accuracy of 78.16%. The Basic programme for this technique is at Appendix 2.

Unfortunately, there has been no success using similar techniques to separate gulls (Laridae), which is the group of birds most frequently involved in UK birdstrikes, or pigeons (Columbidae), which are increasingly struck *en route*, into weight categories.

ACKNOWLEDGEMENTS

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Figure 1. DIAGRAMMATIC STRUCTURE OF A TYPICAL ANSERIFORMES BARBULE, SHOWING MEASUREMENTS TAKEN

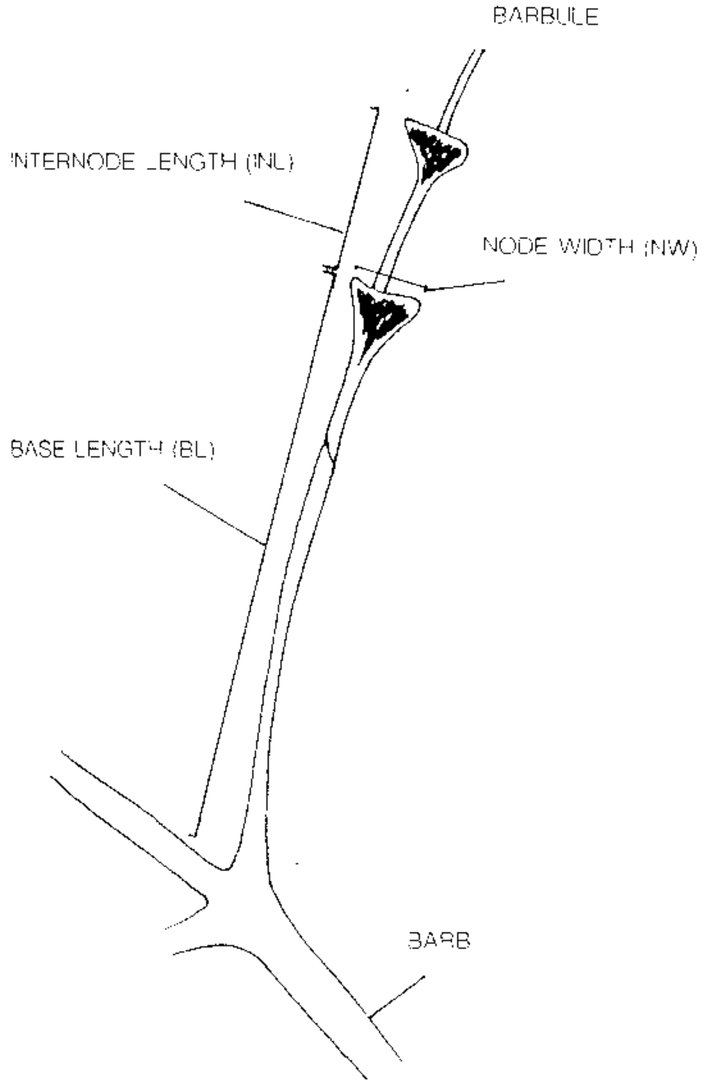

Figure 2. DIAGRAMMATIC STRUCTURE OF A TYPICAL PASSERIFORMES BARBULE, SHOWING MEASUREMENTS TAKEN

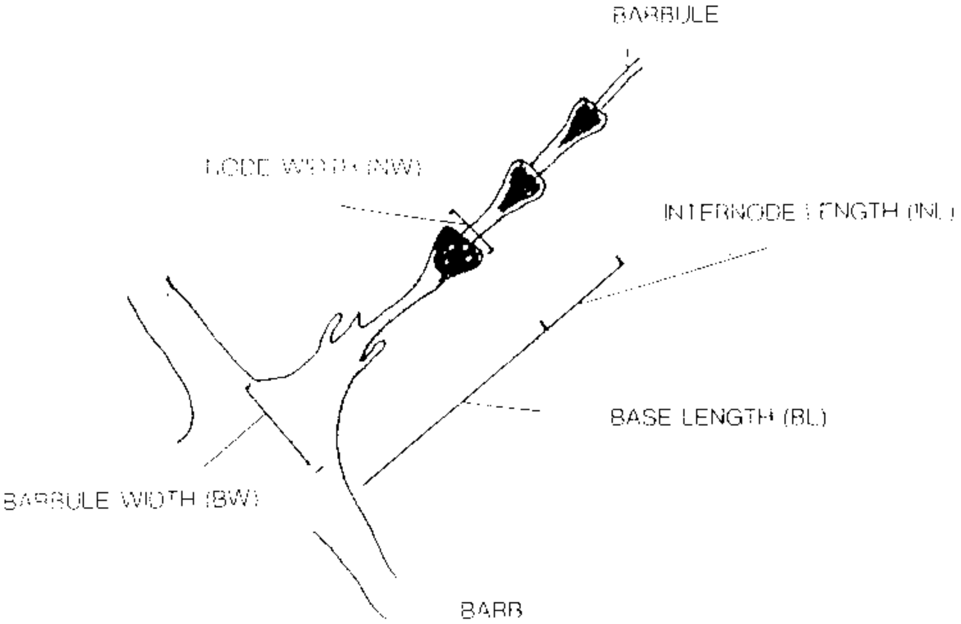

Table 1:

GROUP	P
DUCK	9
GOOSE	79
SWAN	69

OVERALL PREDIC

Table 1: DISCRIMINANT ANALYSIS RESULTS ATTEMPTING TO SEPARATE ANSERIFORMES INTO GROUP, GENUS AND SPECIES

GROUP	PGM%	GENUS	PGM%	SPECIES	PGM%
DUCK	97.2	ANAS	51.5	Teal *A. crecca*	[illegible]
				Shoveler *A. clypeata*	[illegible]
				Wigeon *A. penelope*	[illegible]
				Mallard *A. platyrhynchos*	[illegible]
		TADORNA	41.0	Shelduck *T. tadorna*	[illegible]
		AIX	49.0	Mandarin *A. galericulata*	[illegible]
		SOMATERIA	27.0	Eider *S. mollissima*	[illegible]
		AYTHYA	42.5	Pochard *A. ferina*	[illegible]
				Tufted duck *A. fuligula*	[illegible]
		MELANITTA	40.0	Scoter *M. nigra*	[illegible]
		BUCEPHALA	22.0	Goldeneye *B. clangula*	[illegible]
		MERGUS	46.0	Red-breasted merganser *M. serrator*	[illegible]
				Goosander *M. merganser*	[illegible]
GOOSE	79.3	ANSER	37.3	Pink-footed goose *A. brachyrhynchus*	[illegible]
				White-fronted goose *A. albifrons*	[illegible]
				Greylag *A. anser*	[illegible]
		BRANTA	59.7	Brent goose *B. bernicla*	[illegible]
				Barnacle goose *B. leucopsis*	[illegible]
				Canada goose *B. canadensis*	[illegible]
		CHLOEPHAGA	27.0	Upland goose *C. picta*	[illegible]
SWAN	69.0	CYGNUS	85.3	Whooper Swan *C. cygnus*	[illegible]
				Mute Swan *C. olor*	
				Bewick's swan *C. columbianus*	[illegible]

OVERALL PREDICTED GROUP MEMBERSHIP:-

GROUP :- 88.09%
GENUS :- 47.43%
SPECIES:- 39.26%

Table 2: GROUP MEANS FROM DIFFERENT AREAS OF A SINGLE MALLARD

LOCATION	BASE LENGTH (microns)	NODE WIDTH (microns)	INTERNODE LENGTH (microns)
BREAST	678.1	17.6	34.8
BACK	927.3	18.2	35.5
NECK	767.0	17.7	32.8
UNDER-WING COVERTS	657.6	14.8	36.1

Predicted Group Membership:- 76.25%

Table 3:

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Group means:-

DUCK
GOOSE
SWAN

Fisher's line

BASE LENGTH
NODE WIDTH
INTERNODE LENG
CONSTANT

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Table 3: RESULTS FROM A DISCRIMINANT ANALYSIS OF FEATHER PARAMETERS USED TO SEPARATE DUCKS FROM GEESE AND FROM SWANS

Group means:-

	BASE LENGTH +/-SD (microns)	NODE WIDTH +/-SD (microns)	INTERNODE LENGTH +/-SD (microns)
DUCK	578.79+-177.36	16.47+-2.81	32.34+- 6.43
GOOSE	390.68+- 71.10	13.22+-2.66	62.77+-13.05
SWAN	284.64+- 62.09	13.16+-2.42	49.54+- 8.68

Fisher's linear discriminant functions:-

	DUCK	GOOSE	SWAN
BASE LENGTH	2.35377×10^{-2}	1.844289×10^{-2}	1.280905×10^{-2}
NODE WIDTH	2.140961	1.779903	1.660221
INTERNODE LENGTH	4.211884×10^{-1}	7.596760×10^{-1}	5.921977×10^{-1}
CONSTANT	-32.23771	-40.07710	-28.29570

Percent of "grouped" cases correctly classified = 88.09%

Appendix 1.

BASIC PROGRAMME USED TO SEPARATE DUCKS, GEESE AND SWANS

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10 REM ANSERIFORMES IDENTIFICATION PROGRAMME
20 PRINT "INPUT BL, GW, INL, IN MICRONS, SEPARATED BY COMMAS"
30 INPUT A, B, C
40 X= (0.[illegible]*A) + (2.[illegible]*B) + (0.4211884*C) - 31.[illegible]
50 Y= (0.018[illegible]*A) + (1.[illegible]9903*B) + (0.7596790*C) - 40.077[illegible]
60 Z= (0.01280905*A) + ([illegible].660221*B) + (0.591977*C) - 28.2957
70 IF X>Y AND X>Z GOTO 100
80 IF Y>X AND Y>Z GOTO 120
90 IF Z>X AND Z>Y GOTO 140
100 PRINT "DUCK":X
110 GOTO 150
120 PRINT "GOOSE":Y
130 GOTO 150
140 PRINT "SWAN":Z
150 END
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Appendix 2.

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10 REM PASSERI
20 PRINT "INPU
30 INPUT A, B,
40 Y= (0.33504
      20.3087
50 Z= (0.50520
      29.9028
60 IF Y>Z GOTO
70 IF Z>Y GOTO
80 PRINT "OTHE
90 GOTO 120
100 PRINT "COR
120 END
```

Appendix 2.

BASIC PROGRAMME FOR PASSERIFORMES SEPARATION

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10 REM PASSERIFORMES IDENTIFICATION PROGRAMME

20 PRINT "INPUT TNL, BL, NW, BW SEPARATED BY COMMAS"

30 INPUT A, B, C, D

40 Y= (0.3350435*A) + (0.09216676*B) + (2.55595*C) - (0.1233225*D) -
      20.30879

50 Z= (0.5052046*A) + (0.0978210*B) +  (3.04599*C) - (0.1040325*D) -
      29.9028

60 IF Y>Z GOTO 80

70 IF Z>Y GOTO 100

80 PRINT "OTHER PASSERINE (9-160g)";Y

90 GOTO 120

100 PRINT "CORVID (160-1105)";Z

120 END
```