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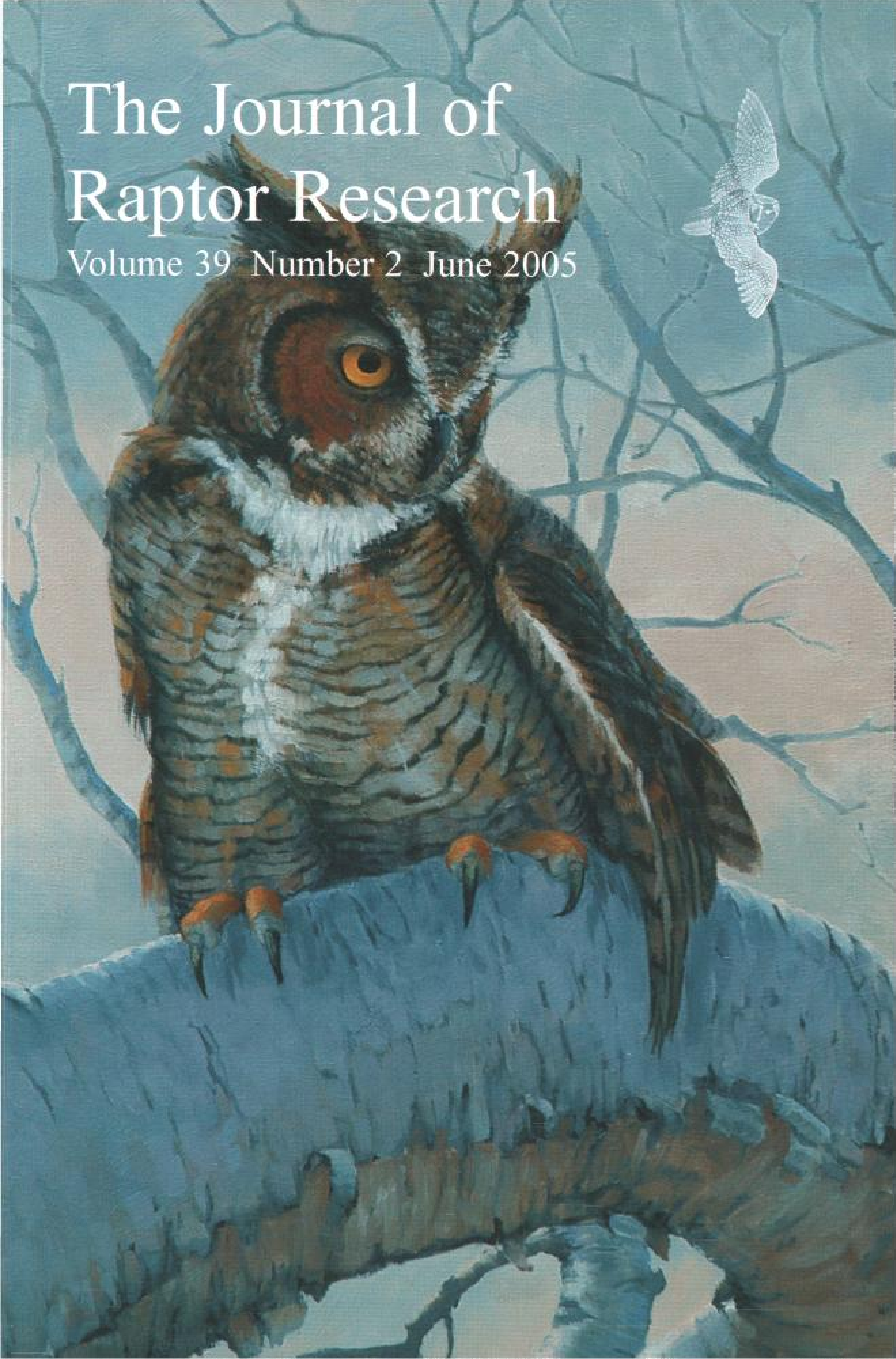

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COVER: Great Horned Owl (*Bubo virginianus*). Oil painting by Eva van Rijn; for more information and wildlife art visit: www.natureartists.com/artists/artist.asp?ArtistID=36

Table 2. Results of the analysis of molecular variance with a between-gender and among-countries arrangement.

	df	SS	MS	VARIANCE COMPONENT	Φ_{ST}	P[a]
Hungary						
Between genders	1	21.15	21.15	00.966 (7.2%)	0.07	<0.001
Among individuals/within genders	18	222.55	12.36	12.364 (92.8%)		
Switzerland						
Between genders	1	57.91	57.91	2.637 (14%)	0.14	<0.001
Among individuals/within genders	30	476.28	15.88	15.876 (86%)		
Pooled (all females vs. all males)						
Between gender	1	49.30	49.30	1.278 (7%)	0.07	<0.001
Among individuals/within gender	50	843.50	16.87	6.870 (93%)		
Pooled (all Hungarian vs. all Swiss)						
Among countries	1	114.92	114.92	4.04 (21%)	0.21	<0.001
Among individuals/within countries	50	777.89	15.56	15.56 (79%)		

[a] Nonparametric randomization test with 1000 permutations.

21% (Table 2) and the estimated number of migrant individuals between the Swiss and Hungarian populations is 0.96 per generation. The pair-wise Φ_{ST} values gave the same results as the between-sexes arrangement (Table 3). Moreover, the among-males (0.32) and the among-females values (0.20) suggest a higher genetic difference of males between populations. From these data we estimated that 0.53 males and 1.01 females migrate between populations each generation (Nm values).

DISCUSSION

Genetic differentiation among breeding females was greater than among breeding males in both Hungary and Switzerland. The differential dispersal distances of the sexes, males being more philopatric than females, may explain this differentiation. Therefore, males are genetically more similar to each other within a population. This scenario, based on sex-specific dispersal, may also explain the greater among-males differentiation between populations (about twice as many females as males appear to emigrate). Because males do not emigrate as much as females, they preserve the genetic features of their population to a greater degree. This is further supported by the fact that the estimate of migrants per generation (based on genetic data) gave the same result as the ringing data: greater male philopatry (Taylor 1994). Previous studies suggested that, from Hungary, a greater percentage of individuals move toward central Europe than in the opposite direction (Mátics 2003); i.e., the Hungarian population was more of a "source" than a "sink" population. As a consequence, gender- and population-differentiation is greater in Switzerland than in Hungary, because the exchange of individuals is *guttata-* and female-biased. These results were concordant with the fact that both phenotypic and genotypic variability of individuals were greater in the middle of a transition zone than on the edges (Arnold 1997, Roulin 2003). This proposal could be tested with data from other localities such as from western European Barn Owl populations.

Table 3. Pairwise genetic distances of the populations (Φ_{ST} between pairs of populations). Above diagonal is the probability that random distance (Φ_{ST}) > observed distance; (number of iterations = 1000; H = Hungary, CH = Switzerland).

	CH MALE	CH FEMALE	H MALE	H FEMALE
CH male	—	0	0	0
CH female	0.14	—	0	0
H male	0.32	0.29	—	0
H female	0.25	0.20	0.07	—

The between-gender differentiation of the species detected using RAPDs (7%, 14%) seem to be disproportionally high. Using the random priming technique the sexual differentiation was expected to be between 1–2%, as the Barn Owl has 92 chromosomes (Belterman and De Boer 1984). This higher value of gender differentiation could be due to the relatively large size of sexual chromosomes in birds (Stevens 1991). The sexual differentiation of autosomal markers caused by sex-biased dispersal is instantaneous because the next generation receives a random set of alleles from both parents. On the other hand, sex-chromosomal markers preserve the differentiation for longer time and when gene flow occurs continuously, this differentiation could be detected permanently. Differentiation detected in this study therefore may be associated with markers located on sex-chromosomes.

Although only two populations were analyzed, the Φ_{ST} value of 0.21 indicated a substantial genetic substructuring among our study populations. The results of another RAPD study gave Φ_{ST} values of 0.048 and 0.103 for island species (two populations of both the Puerto Rican Vireo [*Vireo latimeri*] and Jamaican Vireo [*V. modestus*], respectively), and 0.015 for a migratory continental species (three populations of the White-eyed Vireo [*V. griseus*]; Zwartjes 1999). For the Greater Rhea (*Rhea americana*) a Φ_{ST} value of 0.0637 was found among four wild and a captive population (Bouzat 2001), which is a low value given that this species is flightless. The special mating system of the Greater Rhea could play an important role in producing this low genetic substructuring. The male rhea establishes a territory and builds a nest. He will then attract a group of about three to six females with whom he mates and they lay ca. 20–30 eggs in his nest. While the females go off to mate with other males, the male will incubate the eggs and look after the chicks on his own. The relatively strong substructuring of the Barn Owl populations could be explained by at least three factors: (1) nonmigratory behaviour, (2) the socially monogamous mating system of the species, and (3) the presence of a geographic barrier (Alps) between the populations analyzed. The Nm value of roughly one is the minimum amount of gene flow that prevents differentiation at neutral loci among populations by genetic drift (Wright 1931).

The conversion of F_{ST}-related values into Nm is problematic for several reasons, including that it is based on isolation-by-distance models. In this study, we could not test for correlations between genetic and geographic distance. Furthermore, population size and dispersal rates are not constant over time and space and assumptions of demographic and genetic equilibrium and uniformity are unrealistic (Whitlock and McCauley 1999). Many assumptions of the models used are violated, so that results cannot be interpreted as direct measures. In addition, other evolutionary forces contribute in establishing differentiation (Bossart and Prowell 1998). Finally, we suggest that drift should play an important role in the microevolution of the Barn Owl as this species of tropical origin (Voous 1988) goes frequently through bottlenecks in the suboptimal European area in hard winters (Taylor 1994).

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LITERATURE CITED

ARMSTRONG, J., A. GIBBS, R. PEAKALL, AND G.F. WEILLER. 1994. RAPDistance: random amplified polymorphic DNA analysis. http://life.anu.edu.au/molecular/software/rapid.html.

ARNOLD, M.L. 1997. Natural hybridisation and evolution Oxford Univ. Press, Oxford, U.K.

BAGLIACCA, M., A. VALENTINI, AND I. CAPPUCCIO. 1997. RAPD molecular markers to study populations of Black Grouse *Tetrao tetrix* in the Alps. *Wildl. Biol.* 3: 269.

BAUDVIN, H. 1975. Biologie de reproduction de la chouette effraie (*Tyto alba*) en Cote d'Or: premiers résultats. *Jean. Blanc* 14:1–51.

BELTERMAN, R.H.R. AND L.E.M. DE BOER. 1984. A karyological study of 55 species of birds, including karyotypes of 39 species new to cytology. *Genetica* 65:39–82.

BOSSART, J.L. AND D.P. PROWELL. 1998. Genetic estimates of structure and gene flow: limitations, lessons, and new directions. *Trends Ecol. Evol.* 13:202–206.

BOUZAT, J.L. 2001. The population genetic structure of the Greater Rhea (*Rhea americana*) in an agricultural landscape. *Biol. Conserv.* 99:274–284.

EXCOFFIER, L., P.E. SMOUSE, AND J.M. QUATTRO. 1992 Analysis of molecular variance inferred from metric distances among DNA haplogroups: applications to human mitochondrial DNA restriction data. *Genetics* 131:479–491.

GLUTZ VON BLOTZHEIM, U.N. AND K.M. BAUER. 1980 Handbuch der Vögel Mitteleuropas. Vol. 9. Akademische Verlagsgesellschaft, Wiesbaden, Germany.

GOUDET, J., N. PERRIN, AND P. WAER. 2002. Test for sex-biased dispersal using b-parentally inherited genetic markers. *Mol. Ecol.* 11:1103–1114.

Greenwood, P.J. 1980. Mating systems, philopatry, and dispersal in birds and mammals. *Anim. Behav.* 28: 1140–1162.

Haig, S.M., J.M. Rhymer, and D.G. Heckel. 1994. Population differentiation in randomly amplified polymorphic DNA of Red-cockaded Woodpeckers *Picoides borealis. Mol. Ecol.* 3:581–595.

Harrison, R.G. (Ed.). 1993. Hybrid zones and the evolutionary process. Oxford Univ. Press, New York, NY U.S.A.

Horn, P.L., J.A. Rafalski, and P.J. Whitehead. 1996. Molecular genetic (RAPD) analysis of breeding Magpie Geese. *Auk* 113:552–557.

Huff, D.R., R. Peakall, and P.E. Smouse. 1993. RAPD variation within and among natural populations of out crossing buffalograss (*Buchloe dactyloides Nutt. Engelm.*). *Theor. Appl. Genet.* 86:927–934.

Hwang, S.Y., H.W Lin, Y.-S. Kuo, and T.-P. Lin. 2001. RAPD variation in relation to population differentiation of *Chamaecyparis formosensis* and *Chamaecyparis taiwanensis. Bot. Bull. Acad. Sin.* (Taipei) 42:173–179.

Mátics, R. 2003. Direction of movements in Hungarian Barn Owls (*Tyto alba*): gene flow and barriers. *Diver. Distr.* 9:261- -268.

——— and G. Hoffmann. 2002. Location of the transition zone of the Barn Owl subspecies *Tyto alba alba* and *Tyto alba guttata* (*Stringiformes: Tytonidae*). *Acta Zool. Cracov.* 45:242–250.

———, ———, T. Nagy, and A. Roulin. 2002. Random pairing with respect to plumage coloration in Hungarian Barn Owls. *J. Ornithol.* 143:493–495.

Negro, J.J., M.J. Torres, and J.A. Godoy. 2001. RAPD analysis for detection and eradication of hybrid partridges (*Alectoris rufa × A. graeca*) in Spain. *Biol. Conserv.* 98:19–24.

Nei, M. and W. Li. 1979. Mathematical model for studying genetic variance in terms of restriction endonucleases. *Proc. Natl. Acad. Sci. U.S.A.* 76:5269–5273.

Park, R.L., S.S. Xiong, J.O. Richards, J.C. Shaw, R.P. Evans, and R.N. Thwaits. 1997. Identification of RAPD markers linked to the W-chromosome in the Ostrich using segregant bulks. Scherago International Inc., San Diego, CA U.S.A.

Plomion, C., N. Bahrman, C.E. Durel, and D.M. O'Malley. 1995. Genomic mapping in *Pinus pinaster* (Maritime pine) using RAPD and protein markers. *Heredity* 74:661–668.

Prugnolle, F. and T. de Meeus. 2002. Inferring sex-biased dispersal from population genetic tools: a review. *Heredity* 88:161–165.

Roulin, A. 1999. Nonrandom pairing by male Barn Owls (*Tyto alba*) with respect to a female plumage trait. *Behav. Ecol.* 10:688–695.

———. 2003. Geographic variation in sexually selected traits: a role for direct selection or genetic correlation? *J. Avian Biol.* 34:251–258.

———, C. Dijkstra, C. Riols, and A.L. Ducrest. 2001 Female- and male-specific signals of quality in the Barn Owl. *J. Evol. Biol.* 14:255–266.

Sambrook, J., E.F. Fritsch, and T. Maniatis. 1989. Molecular cloning: a laboratory manual. Cold Spring Harbor Laboratory Press, Cold Springs, NY U.S.A.

Schönfeld, M. 1974. Ringfundauswertung der 1964–72 in der DDR beringter Schleiereulen *Tyto alba guttata* Brehm. *Jahresber. Vogelwar. Hidden.* 4:90–122.

Shao, J. and D. Tu. 1995. The jackknife and bootstrap. Springer-Verlag, New York, NY U.S.A.

Stevens, L. 1991. Genetics and evolution of the domestic fowl. Cambridge Univ. Press, Cambridge, U.K.

Taylor, I. 1994. Barn Owls. Cambridge Univ. Press, Cambridge, U.K.

Vitalis, R. 2002. Sex-specific genetic differentiation and coalescence times: estimating sex-biased dispersal rates. *Mol. Ecol.* 11:125–138.

Voous, K.M. 1950. On the distributional and genetical origin of the intermediate populations of the Barn Owl in Europe. Verlagsgesellschaft Geest Portig, Leipzig, Germany.

———. 1988. Owls of the northern hemisphere. W. Collins Sons & Co. Ltd., London, U.K.

Wang, X.H. and C.H. Trost. 2001. Dispersal pattern of Black-billed Magpies (*Pica hudsonia*) measured by molecular genetic (RAPD) analysis. *Auk* 118:137–146.

Whitlock, M.C. and D.E. McCauley. 1999. Indirect measures of gene flow and migration: $Fst \neq 1/(4Nm+1)$. *Heredity* 82:117–125.

Wright, S. 1931. Evolution in Mendelian populations. *Genetics* 16:97–159.

———. 1951. The genetical structure of populations. *Annals. Eugenics* 15:323–354.

Zwartjes, P.W. 1999: Genetic variability in the endemic vireos of Puerto Rico and Jamaica contrasted with the continental White-eyed Vireo. *Auk* 116:964–975.

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