

UNIVERSITI PUTRA MALAYSIA

FINGERPRINTING THE PAINTED STORKS (Mycteria leucocephala PENNANT), MILKY STORKS (Mycteria cinerea RAFFLES), AND THEIR SUSPICIOUS HYBRIDS IN A ZOO IN MALAYSIA

YEE YOKE SIM

FBSB 2018 49



FINGERPRINTING THE PAINTED STORKS (Mycteria leucocephala PENNANT), MILKY STORKS (Mycteria cinerea RAFFLES), AND THEIR SUSPICIOUS HYBRIDS IN A ZOO IN MALAYSIA

By

YEE YOKE SIM

Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, in Fulfilment of the Requirements for the Degree of Master of Science

March 2017

COPYRIGHT

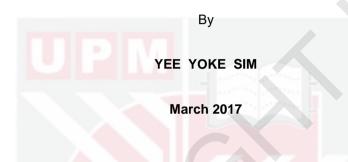
All material contained within the thesis, including without limitation text, logos, icons, photographs and all other artwork, is copyright material of Universiti Putra Malaysia unless otherwise stated. Use may be made of any material contained within the thesis for non-commercial purposes from the copyright holder. Commercial use of material may only be made with the express, prior, written permission of Universiti Putra Malaysia.

Copyright © Universiti Putra Malaysia



Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfilment of the requirement for the degree of Master of Science

FINGERPRINTING THE PAINTED STORKS (Mycteria leucocephala PENNANT), MILKY STORKS (Mycteria cinerea RAFFLES), AND THEIR SUSPICIOUS HYBRIDS IN A ZOO IN MALAYSIA



Chair: Associate Professor Janna Ong Abdullah, PhD. Faculty: Biotechnology and Biomolecular

Painted storks (Mycteria leucocephala) and milky storks (Mycteria cinerea) are large wading birds of southern Asia, and listed as endangered species by IUCN (International Union for Conservation of Nature). Most painted storks inhabit India while milky storks mainly colonise east Sumatra and the west coast of Peninsular Malaysia. In the past decade, no wild milky stork has settled in Peninsular Malaysia. Both species were captive bred at the Zoo Negara for conservation purposes. Yet, storks with intermediate plumage traits between two stork species were observed, and suspected to be their hybrids. Based on the intermediate plumage characteristics, hybrids of two storks were suspected at natural breeding sites of Cambodia, Singapore, and Thailand. However, mere plumage appearances are often insufficient to confirm the bird hybrids, and hence, molecular markers are used. Unbalanced sex ratio in a population could be one of the reasons that two species hybridised. Females and males of both stork species have no differentiation in plumage traits, and therefore, molecularsexing markers are used to identify genders. The objective of this study was to fingerprint individual storks using different classes of DNA markers including sexlinked marker to identify hybrids, and to estimate sex ratio. Based on the plumage characteristics of each stork, blood was sampled systematically onto FTA cards (Whatman, classic) (FTA - fast analysis of nucleic acids). DNA was extracted from a disc of FTA cards (3 mm), and PCR was run with RAPDs (random amplified polymorphism DNA), ISSRs (inter-specific sequence repeat), and cross species microsatellites, electrophoresed on agarose gels and stained with ethidium bromide. Six out of 44 screened primers were selected to fingerprint each stork, and two distinctive sets of banding patterns were

generated, which differentiated pure storks from hybrids. These six markers stork microsatellites WSU09U/WSU09L included two wood and WSU13U/WSU13L), two short RAPDs (Operon D-03 and Operon D-05), one long RAPD (LR7), and one 5'-anchored ISSR (RAM2). The data revealed that most loci of hybrids were combinations of two pure storks, few loci were exclusively found in hybrids alone. The fingerprinting data were compared to plumage characteristics, and it was found out these hybrids possessed six different types of intermediate plumage characteristics between two parental species, and they were not a typical kind of hybrid only. Sex-linked microsatellites P2/P8 was run with PCR, electrophoresed PCR products on 7.5% PAGE gel (non-denaturing) and stained with silver staining. The result showed that sex ratio of female to male in painted stork population was 1 to 5, while all hybrids and milky storks were males, indicating that males were the majority. It can therefore be concluded that stork hybrids were identified through DNA fingerprinting using six selected DNA markers. The hybrids of intermediate plumage traits were confirmed by DNA fingerprinting. Sex ratio in the breed storks was not balanced.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Sarjana Sains

FINGERPRIN BURUNG JONG (*Mycteria leucocephala* PENNANT), BURUNG UPEH (*Mycteria cinerea* RAFFLES), DAN HIBRID SANGSI DALAM ZOO DI MALAYSIA



Pengerusi: Prof Madya Janna Ong Abdullah, PhD. Fakulti: Bioteknologi dan Sains Biomelekul

Burung Jong (Mycteria leucocephala) dan Burung Upeh (Mycteria cinerea) adalah burung-burung yang besar di Asia selatan dan disenaraikan sebagai spesies yang terancam oleh IUCN (International Union for Conservation of Nature). Kebanyakan burung Jong mendiami India dan majority burung Upeh mengeduduki Sumatera timur dan pantai barat Semenanjung Malavsia, Dalam dekad yang lalu, tidak ada burung Upeh liar menetap di Semenanjung Malaysia. Kedua-dua spesies ini diternakkan di Zoo Negara bertujuan untuk pemeliharaan. Namun, bulu-bulu bercorak pertengahan diantara dua spesies burung diperhatikan dan disyaki adalah hibrid mereka. Berdasarkan ciri-ciri bulu pertengahan, hibrid kedua spesies burung berkenaan disyaki di tempat semulaiadi Kemboia. Singapura pembiakan dan Thailand. Walau bagaimanapun, observasi ciri-ciri bulu sahaja, selalunya tidak mencukupi untuk mengesahkan hibrid burung dan oleh itu, penanda molekul digunakan. Rasio seks yang tidak seimbang di dalam sesuatu populasi boleh menjadikan salah satu sebab, bahawa dua spesies hibridisasi. Jantan dan betina dari kedua-dua spesies burung Jong dan burung Upeh, tiada pembezaan dalam ciri-ciri bulu dan sebab itu, penanda seks molekul digunakan untuk mengenal pastikan jantina. Objektif kajian ini adalah untuk fingerprintin burung-burung individu menggunakan kelas penanda-penanda DNA yang berlainan, termasuk penanda-seks DNA, untuk mengenal pastikan hybrid-hibrid dan untuk menganggarkan rasio seks. Berdasarkan ciri-ciri bulu setiap ketikan, darah disampel secara sistematik ke kad FTA (klasik). DNA diekstrak daripada disk kad FTA (3 mm) dan PCR dijalankan dengan RAPDs (random amplified polymorphism DNAs), ISSRs (Inter-specific sequence repeat), dan microsatellit spesies berkarabat, elektroforesis pada gel agarose dan diwarnakan dengan

etidium bromida. Enam dari 44 penanda-penanda yang dipilih untuk fingerprin setiap burung dan dua jenis corakan loreng yang berlainan dihasilkan, telah membezakan burung-burung tulen dari hibrid-hibird. Enam penanda-penanda termasuk dua mikrosatellit (WSU09U / WSU09L dan WSU13U / WSU13L), dua RAPDs pendek (Operon D-03 dan Operon D-05), satu RAPD panjang (LR7) dan satu 5'-penambat ISSR (RAM2). Data mendedahkan bahawa kebanyakan loci hibrid adalah gabungan dua spesies burung tulen, beberapa loci eksklusif didapati dalam hibrid-hibrid sahaja. Data fingerprintin dibandingkan dengan ciriciri bulu dan ia mendapati hibrid ini mempunyai enam jenis ciri-ciri bulu pertengahan di antara dua spesies burung, dan mereka bukan hibrid tipikal sahaja. Mikrosatellit seks P2 / P8 dijalankan dengan PCR, produk PCR elektroforesis pada 7.5% gel PAGE (non-denaturing) dan berwarna dengan pewarna perak (silver staining). Hasilnya menunjukkan bahawa rasio seks betina kepada jantan dalam populasi burung Jong adalah 1 hingga 5, manakala semua hibrid dan burung Upeh adalah jantan, menunjukkan bahawa jantan adalah majoriti. Oleh itu, konklusifnya adalah bahawa hibrid stork dikenal pasti melalui fingerprintin DNA menggunakan enam penanda-penanda DNA terpilih. Data berbanding dengan ciri-ciri bulu dan disahkan hibrid-hibrid berbulu variasi. Rasio seks yang tidak seimbang didapati dalam burung-burung berikut.

ACKNOWLEDGEMENTS

The project was initiated by PERHILITAN (Dr. Zainal Zahari), the Zoo Negara (Bird house staff, Doreen Khoo) and Jabatan Kimia (Dr. Chong Lee Kim) with the purpose to find out whether the bred storks were hybrids. Later it was passed to Biotechnology and Biomolecular Faculty of UPM due to short of hands. Thanks to the staff of Bird House of Zoo Negara for providing the information on hybrid plumage characters and the veterinarian team of Forensic and Wildlife Management Department of PERHILITAN and Zoo Negara for sampling the stork blood onto FTA cards.

The project was partially funded by PERHILITAN (Malaysian Wildlife Department), and mainly sponsored by Fundamental Research Grant of the Ministry of Higher Education. It was headed by Prof. Dr. Tan Soon Guan.

A very special thanks to Prof. Dr. Tan Soon Guan, who was my main supervisor, for his guidance and suggestions in this project. He has retired and could not be part of the supervisory committee. Special thanks to Associate Prof Janna who helped me in thesis submission.

This thesis was submitted to the Senate of Universiti Putra Malaysia and has been accepted as fulfilment of the requirement for the degree of Master of Science. The members of the Supervisory Committee were as follows:

Janna Ong Abdullah, PhD

Associate Professor Faculty of Biotechnology and Biomolecular Sciences Universiti Putra Malaysia (Chairman)

Ahmad Ismail, PhD

Professor Faculty of Sciences Universiti Putra Malaysia (Member)

Yap Chee Kong, PhD

Associate Professor Faculty of Sciences Universiti Putra Malaysia (Member)

ROBIAH BINTI YUNUS, PhD

Professor and Dean School of Graduate Studies Universiti Putra Malaysia

Date:

Declaration by graduate student

I hereby confirm that

- :
- this thesis is my original work;
- quotations, illustrations and citations have been duly referenced;
- this thesis has not been submitted previously or concurrently for any other degree at any other institutions;
- intellectual property from the thesis and copyright of thesis are fully-owned by Universiti Putra Malaysia, as according to the Universiti Putra Malaysia (Research) Rules 2012;
- written permission must be obtained from supervisor and the office of Deputy Vice-Chancellor (Research and Innovation) before thesis is published (in the form of written, printed or in electronic form) including books, journals, modules, proceedings, popular writings, seminar papers, manuscripts, posters, reports, lecture notes, learning modules or any other materials as stated in the Universiti Putra Malaysia (Research) Rules 2012;
- there is no plagiarism or data falsification/fabrication in the thesis, and scholarly integrity is upheld as according to the Universiti Putra Malaysia (Graduate Studies) Rules 2003 (Revision 2012-2013) and the Universiti Putra Malaysia (Research) Rules 2012. The thesis has undergone plagiarism detection software.

.		
Signature:	Date:	

Name and Matric No: Yee Yoke Sim (GS43344)

TABLE OF CONTENTS

		Page
ABSTR		I
ABSTR		iii
	WLEDGEMENTS	V.
APPRO		vi
DECLA		viii
	TABLES	xi
	FIGURES	xii
LISTOF	ABBREVIATIONS	xiv
CHAPTE		
1	INTRODUCTION	1
	1.1 Objectives of the Study	2
2		3
	2.1 General Information of Painted Storks and Milky Storks	3
	2.2 Geographical Distribution of the Painted Storks and the Milky Storks	5
	2.3 Avian Hybridization	9
	2.4 Various Categories of DNA Markers	10
	2.4.1 Sex-linked DNA Markers of Birds	13
	2.5 Diversity of Markers for Bird Hybrid Zones	14
	2.6 Fingerprinting through Multi- locus Markers	15
	2.7 Conclusion	16
3	MATERIALS AND METHODS	17
	3.1 Materials	17
	3.1.1 Stork Blood Samples	17
	3.2 Methods	17
	3.2.1 FTA Cards and Sampling	17
	3.2.2 DNA Extraction from FTA Disc	18
	3.3.3 PCR and Fingerprinting the Storks	20
	3.2.4 Comparison of Plumage Traits of Pure Storks and Hybrids	27
	3.2.5 Sex Ratio Estimation of Stork Populations by Using P2/P8 Sex-linked Microsatellite Markers	27
		20
4	RESULT	30
	4.1 Fingerprinting Data of Differentiating Pure Storks from Hybrid Storks	30
	4.2 Morphological Data Based On Plumage Patterns and colourations	40
	4.3 Scoring for P2/P8 Sex-linked Microsatellites	51

5	DISC 5.1	USSION Multi-locus Markers and Banding Patterns of the Hybrids	52 52
	5.2	Morphological Traits of the Stork Hybrids	53
	5.3	Molecular Sexing of Painted and Milky Storks	53
6		MARY GENERAL CONCLUSIONS AND OMMENDATIONS FOR FUTURE RESEARCH	55
REFERE BIODAT LIST OF	A OF S	STUDENT	57 64 65



 (\mathbf{C})

LIST OF TABLES

 \bigcirc

Table		Page
2.1	Taxonomy of storks	3
3.1	Information of the screened primers used for screening the DNA markers	23
4.1	Information of six selected markers to fingerprint individual storks	39
4.2	Morphological traits of painted storks, milky storks and hybrids	50

LIST OF FIGURES

Figure		Page
2.1	Photograph of Mycteria storks	4
2.2	Distribution map of the painted storks	5
2.3	Distribution map of the milky storks	6
2.4	Juveniles of milky stork and painted stork	8
3.1	Photographs of FTA cards (classic,Whatman)	18
3.2	Gel image of electrophoresis of DNAs extracted from a FTA disc (3mm)	20
4.1	Diagrammatic representation of electrophoresis for the locus WSU09U /WSU09L	31
4.2	Diagrammatic representation of electrophoresis for the locus WSU13U / WSU13L	32
4.3	Diagrammatic representation of electrophoresis for the locus D-03	34
4.4	Diagrammatic representation of electrophoresis for the locus D-05	35
4.5	Diagrammatic representation of electrophoresis for the locus LR7	37
4.6	Diagrammatic representation of electrophoresis for the locus RAM2	38
4.7	Milky stork in the bird house at Zoo Negara	41
4.8	Painted storks	42
4.9	Hybrid 1 at Zoo Negara	43
4.10	Hybrid 2 at Zoo Negara	44
4.11	Hybrid 3 at Zoo Negara	45
4.12	Hybrid 4 at Zoo Negara	46
4.13	Hybrid 5 at Zoo Negara	53

6

4.14	Hybrid 6 at Zoo Negara	54
4.15	Lesser adjutant (<i>Leptopilus javanica</i>)	55
4.16	Banding pattern for female and male of painted stork revealed by silver staining of the locus P2/P8	58



 \bigcirc

LIST OF ABRREVIATIONS

APS	Ammonium persulfate (NH ₄) ₂ S ₂ O ₈
bp	base pairs
DNA	Deoxyribonucleic Acid
FTA	Fast Technology Analysis of nucleic acid
dNTP MIX	deoxy-N-triphosphate (N = A / T / C / G) (A - adenosine, T - thymine, C - cytosine, G-guanine)
F1	Felial 1 (offspring of parental species)
F2	Felial 1 cross with felial 1 to give felial 2 offspring
F3	Felial 2 cross with felial 2 to give felial 3 offspring
нсон	Formaldehyde
MgCl ₂	Magnesium chloride
NaOH	Sodium hydroxide
PAGE	Polyacrylamide Gel Electrophoresis
PCR	Polymerase Chain Reaction
RNA	Ribonucleic acid
10XTBE	Tris-base(1mM), Boric Acid(1mM), Na₂EDTA(20mM)
1X TBE	Tris-base(0.1mM), Boric Acid(0.1mM) Na₂EDTA (2mM)
1XTE	Tris-Cl(10mM), Na ₂ EDTA(1mM)
TEMED	N,N,N',N'-tetramethylethylenediamine

G



CHAPTER 1

INTRODUCTION

The painted stork (*Mycteria leucocephala*) and the milky stork (*M. cinerea*) are large migratory birds of southern Asia and listed as endangered species by IUCN (International Union for Conservation of Nature). The largest population of painted storks is found in India but their numbers are declining significantly primary due to deforestation (Kalam and Urfi, 2008, Urfi, 2011). Milky storks, on the other hand, are found mainly in east Sumatra, Indonesia and at one time, on the west coast of Peninsular Malaysia (Verhrught, 1987; Iqbal, 2008). However, in the past decade, no wild milky stork population has been detected in Peninsular Malaysia (Li et al., 2006). Both stork species are captive-bred at the Zoo Negara in Malaysia for conservation purposes. According to the breeders of the Zoo Negara, the breeding programme has been successful, and these storks now inhabit the breeding site. Both species have similar body sizes and shapes but are distinguished by plumage colourations and patterns. Yet, storks with intermediate plumage traits between two stork species have been observed at the Zoo Negara, and these are suspected hybrids. The breeders separated hybrids from pure storks according to feather traits, as they had discovered that the fertility of hybrid storks was uncertain and some hybrids could even be barren (Schilthuizen et al., 2011), hence, identification of these hybrids is important. Although bird hybrids are frequently detected by their feather characteristics, yet in many cases, mere physical appearances are insufficient to ascertain the hybrids. Therefore, molecular markers have become main approach to distinguish hybrids from pure breeds (Stenzler et al., 2004; Huang et al., 2004; Gonzalez et al., 2005). Combination of genetic data and morphological data was recommended for hybrid identification (Jorstad et al., 2007, Irwin et al., 2009). Hybridization of birds is commonly in the wild and bird hybrids are often spotted through feather traits or songs (Randler, 2002). Based on intermediate plumage traits, hybridisation between painted storks and milky storks was suspected at the Thailand National Park, the Cambodian National Park, and the Singapore National Zoo (www.thainationalparks.com/species.paintedstork).The sex ratio of a population plays an important role in hybridisation (Backström & Välli, 2011). Two different species with compatible mating behaviour tend to hybridise. especially when opposite sex number is low (Mallet, 2007). Thus, a balanced sex ratio is crucial to prevent hybridisation in breed populations. There is no feather differentiation between females and males of painted storks, and of milky storks, hence, molecular-sexing method is used to identify genders of these storks. The results of DNA fingerprinting, plumage characteristics and sex ratio were provided the breeders of Zoo Negara, for separating hybrids from pure storks, and improving the breeding programme. In this study, there were two sections of DNA fingerprinting, the first one was identifying the hybrids by using selected DNA markers and the second one was molecular-sexing of the storks through sex-linked DNA marker.

1.1 Objectives of the Study

The main objective of this study was to carry out fingerprinting of individual storks for identifying hybrids, and molecular-sexing. Identification of hybrids was the main part while the molecular-sexing was the minor part of the project. The sub-objectives were:

- 1. To screen a range of different classes of DNA markers, searching for suitable DNA markers that generating different banding patterns between hybrids, and pure storks. Selected DNA markers were used to fingerprint individual storks of each population, and to differentiate the hybrids from pure storks.
- 2. To collect morphological data based on plumage colourations and patterns of pure storks and hybrids. The fingerprinting data were compared to plumage characteristics, and separated pure storks and hybrids accordingly.
- 3. To estimate the sex ratio of the stork populations by using P2/P8 sex-linked microsatellite markers.

REFERENCES

- Aliabadian, M. and Nijman, V. (2007). Avian hybrids: Incidence and geographic distribution of hybridisation in birds. *Contributions to Zoology:* 76 (1) 59-61.
- Amaral, A. J., Silva, A. B., Grosso, A. R., Chikhi, L, Bastossilveira, C. and Dias, D. (2007). Detection of hybridisation and species identification in domesticated and wild quails using genetic markers. *Folia Zoology* 56(3): 285 – 300.
- Ausubel, F. M., Brent, R., Kingston, R. E., Moore, D. D. Seidman, J. G., Smith, J.A.and Struhl, K. (1999). Non-denaturing polyacrylamide gel electrophoresis. *Short protocol in molecular biology, 2nd edition.* (pp. 2.13 – 2.16, 2.21 – 2.23). Harvard Medical School, Wiley International Publisher.
- Backström, N. and Väli, Ü. (2011). Sex and species biased gene flow in a spotted eagle hybrid zone. *BMC Evolutionary Biology* 11:100.
- Barbanera, F., Negro, J. J., Giuseppe, G. D., Bertoncini, F., Cappelli, F. and Dini.F.,(2005). Analysis of the genetic structure of red-legged partridge (*Alectoris rufa, Galliformes*) populations by means of mitochondrial DNA and RAPD markers: a study from central Italy. *Biological Conservation* 122: 275–287.
- Barilani, M., Deregnaucourt, S., Gallego, S., Galli, L. Mucci, N., Piombo, R. Puigcerever, M., Rimondi, S., Rodríguez-Teijeiro, J. D., Spanò, S., and Randi, E. (2005). Detecting hybridisation in wild (*Coturnix c. coturnix*) and domesticated (*Coturnix c. japonica*) quail populations. *Biological Conservation* 126: 445–455.
- Barilania, M., Bernard-Laurentb, A., Muccia, N., Tabarronic, C., Karkd, S., Jose' Antonio Perez Garridoe, J. A. P. and Randia, E. (2007). Hybridisation with introduced chukars (*Alectoris chukar*) threatens the gene pool integrity of native rock (*A. graeca*) and red-legged (*A. rufa*) partridge populations. *Biological Conservation* 137: 57 69.
- Bello, N. and Sänchez, A. (1999). The identification of a sex-specific DNA marker in the ostrich using a random amplified polymorphic DNA (RAPD) assay. *Molecular Ecology* 8: 667 – 669.
- Bensch, A., Helbig, A.J., Salomon., M. and Seibold, I. (2002). Amplified fragment length polymorphism analysis identifies hybrids between subspecies of warblers. *Molecular Ecology* 11: 473-481.
- Bonin.A., Ehrich.D and Manel.S.(2007). Statistical analysis of amplified fragment length polymorphism data: a tool for molecular ecologists and evolutionists. *Molecular Ecology* 16: 3737 3758.

- Borštnik, B. and Pumpernik, D. (2002). Tandem repeats in protein coding regions of primate genes. *Genome Research* 12: 909-915.
- Buschiazzo, E and Gemmell, N. J. (2006). The rise, fall and renaissance of microsatellite in eukaryotic genomes. *BioEssays* 28:1040-1050.
- Bussche, R. A. V. D., Harmon, S. A., Baker, R. J., Bryan, A. L. Jr., Rodgers, J. A. Jr., Harris, M. J. and Brisbin, I. L. Jr. (1999). Low levels of genetic variability in North American population of the wood stork (*Mycteria americana*). *The Auk* 116(4): 1083 – 1092.
- Byun, S. O., Fang, Q., Zhou, H. and Hickford, J. G. H. (2009). An effective method for silver-staining DNA in large numbers of polyacrylamide gels. *Analytical Biochemistry* 185: 174-175.
- Callejas, C., Velasco, A., Gobbi, A., Beiti, F. and Ochando, M. D. (2005). Fast discrimination (RAPD-PCR) of the species forming the pest complex *Aleurodicus* disperses-*Lecanoideus floccissimus* (Hom:*Aleyrodidae*). *Journal of Entomology And Nematology* 129(7):382 -385.
- Charlesworth, B. and Charlesworth, D. (2016). Population genetics from 1966 to 2016. *Heredity 2016*: 1-8.
- Delph, L. F. and Demuth, J. P. (2016). Haldane's rule: Genetic bases and their empirical support. *Journal of Heredity 2016*: 383 391.
- Dubiec, A. and Zagalska-neubauer, M. (2006). Molecular techniques for sex identification in birds. *Biological Letter* 43(1):3-12.
- Dutton, G. (2005). Thinking outside the icebox on DNA storage. *The Scientist* 28 (14): 28 30.
- Fisher, P. J., Gardner, R. C. and Richadson, T. E. (1999). Single-locus microsatellites isolated using 5'-anchored PCR. *Nucleic Acid Research* 24 (21): 4369 4371.
- Fridolfsson, A-K., Cheng, H., Copeland, N. G, Jenkins, N. A., Liu, H-S., Raudsepp, T., Woodage, T., Chowdhary, B., Halverson, J. and Ellegren, H. (1998). Evolution of the avian sex chromosomes from an ancestral pair of autosomes. *Proceeding of National Academic of Science USA* 95: 8147 – 8152.
- Fridolfsson, A-K. and Ellegren, H. (2000). Molecular evolution of the avian CHD-1 genes on the Z and W Sex Chromosome. *Genetics* 155: 1903 1912.
- Gonzalez, E. G., Castilla, M. and Zardoya, R. (2005). Novel polymorphic microsatellites for the red-legged partridge (*Alectoris.rufa*) and crossspecies amplification in *A.graeca. Molecular Ecology Notes* 5: 449 – 451.

- Griffiths, R., Double, M. C., Orr, K. and Dawson, R. J. G. (1998). A DNA test to sex most birds. *Molecular Ecology* 7: 1071 1075.
- Haig, S. M., Mace, T. R. and Mullins, T. D. (2003). Parentage and relatedness in polyandrous comb-crested Jacana using ISSR's. *Journal of Heredity*94 (4): 302 – 309.
- Heredity Editorial (2014). Genomic imprinting : Theories and data. *Heredity* 113: 93–95.
- Irwin, D. E., Brelsford, A., Toews, D. P. L., MacDonald, C. and Phinney, M. (2009). Extensive hybridization in a contact zone between MacGillivray's warblers *Oporornis tolmiei* and mourning warblers *O. Philadelphia* detected using molecular and morphological analyses. *Journal of Avian Biology* 40: 539 552.
- Iqbal, M. and Hasudungan, F. (2008). Observations of milky stork (*Mycteria cinerea*) during 2001 -2007 in South Sumatra. *Birding Asia* 9: 97 99.
- Iqbal, M., Mulyono, H., Riwan, A. and Takari, F. (2012). An alarming decrease in the milky stork *Mycteria cinerea* population on the east coast of South Sumatra province, Indonesia. *Birding Asian* 18: 68 - 70.
- Jiggins, C. D. and Mallet, J. (2000). Bimodal hybrid zones and speciation. *Trends In Ecology and Evolution.* 15 (6): 250 – 255.
- Jorstad, K. E., Produhl, P. A., Agnalt, A. L., Hughes, M., Farestveit, E., Ferguson, A.G.(2007). Comparison of genetic and morphological methods to detect the presence of American lobster, *Homarus. american* H.Milne Edward 1837 (*Astacidae nephropidae*) in Norwegian waters. *Hydrobiologia* 590: 103-114.
- Kalam, A. and Urfi, A. J. (2008). Foraging behaviour and pray size of the painted stork. *Journal of Zoology* 274(2): 198 204.
- Kahn, N. W., John, J. S. and Quinn, T. W. (1998). Chromosome-specific intron size differences in the avian CHD gene provide an efficient method for sex identification in birds. *The Auk* 115: 1074 1078.
- Kannan, V. and Manakadan, R. (2007). Nocturnal foraging by painted storks (*Mycteria lecucocephala*) at Pulicat Lake, India. *Indian Birds* 3(1): 25 26.
- Ke, L., Sun, Y., Liu, P., and Yang, G. (2004). Identification of AFLP fragments linked to one recessive genic male sterility (RGMS) in rapeseed (*Brassica napus.L.*) and conversion to SCAR markers for markeraided selection. *Euphytika* 138(2): 163-168.
- Kingston, S. E. Jernigan, R. W., Fagan, W. F., Braun, D. and Braun, M. J. (2012). Genomic variation in cline shape across a hybrid zone.

Ecology and Evolution 2(11): 2737 – 2748.

- Kumar, V. (2003). Isolation, characterization and application of DNA microsatellite markers in mungbean (*Vigna radiate L. W. lczek*) and either selected legumes. PhD Thesis, UPM.
- Li, Z. W., Yatim, S. H., Howes, J., and Illies, R. (2006). Status overview and recommendation for the conservation of milky storks (*Mycteria cinerea*) in Malaysia. Final report of the 2004/2006 milky stork field surveys in the Matang Mangrove forest, Perak, Malaysia. Wetland International and Development of Wildlife and National Parks, Kuala Lumpur, Malaysia.
- Liu, Z. J. and Cordes, and J. F. (2004). DNA marker technologies and their applications in aquaculture genetics. *Aquaculture* 238: 1–37.
- Mallet, J. (2007). Hybrid speciation. Nature 446 : 279 283.
- Mank, J. E., Nam, K. and Ellegren, H. (2010). Faster-Z evolution is predominantly due to genetic drift. *Molecular Biology Evolution* 27(3):661–670.
- Mebert, K. (2008). Good species despite massive hybridization: Genetic research on the contact zone between the water snakes *Nerodia* sipedon and *Nerodia.fasciata* in the Carolinas, USA. *Molecular Ecology* 17:1918 1929.
- Megannathan, T. and Urfi, A. (2009). Inter-colony variations in nestling ecology of painted stork (*Mycteria leucocephala*) in the Delhi Zoo (North India). *Waterbirds* 32(2): 352 – 356.
- Morinha, F., Carvalho, M., Ferro, A., Guedes-pinto, H., Rodrigues, R. and Bastos, E. (2011). Molecular sexing and analysis in wild common quail (*Coturnix c.coturnix*) and domesticated Japanese quail (*Coturnix c. japonica*). Journal of Genetics Online Resource 90: e39 – e 43.
- Mueller, U. G. and Wolfenbarger, L. L. (1999). AFLP genotyping and fingerprinting. *Trends In Ecology And Evolution.* 14 (10): 389 394.
- Moiseyeva, I. G., Romanov, M. N., Nikiforov, A. A., Sevastyanova, A. and Semyenova, S. K. (2003). Evolutionary relationship of red jungle fowl and chicken breeds. *Genetic Selection Evolution* 35: 403 – 423.
- Morales, H. E., Pavlova, A., Joseph, L. and Sunnuck, P. (2015). Mitochondrial genomes (mitogenomes). *Molecular Ecology* 24: 2820-2837.
- Negro, J. J., Torres, M. J. and Godoy, J. A. (2001). RAPD analysis for detection and eradication of hybrid partridges (*Alectoris rufa* and *A. graeca*) in Spain. *Biological Conservation* 98:19 24.
- Nesje, M. and Røed, K.H. (2000). Sex identification in falcons using microsatellite DNA markers. *Heriditas* 132:261-263.

- Ng, W. L. and Tan, S. G. (2015). Inter-simple sequence repeat (ISSR) markers: Are we doing it right? *A.S.M. Science Journal* 9(1):30 33.
- O'Hanlon, P. C., Peakall, R and Briese, D. T (2000). A review of new PCRbased genetic markers and their utility to weed ecology. *Weed Research* 40: 239 – 254.
- Ong, H. K. A. and Subramaniam, V. (2008). An evaluation of CHD specific primer sets for sex-typing of birds from feathers. *Zoo Biology* 27: 62 – 69.
- Ong, H. K. A., Chinna, K., Khoo, S. K., Ng, W. L., Wong, B. Y., Chow, K. L., Chong, L. K., Pillai, K. and Subramaniam, V. (2011). Morphometric sex determination on milky and painted storks in captivity. *Zoo Biology* 30: 1-10.
- Patten, M. A., Rotenberry, J. T. and Zuki, M. (2004). Habitat selection, acoustic adaptation and the evolution of reproductive isolation. *Evolution* 58(10): 2144 2155.
- Primmer, C. R., Møller, A. P. and Ellegren, H. (1996). A wide-range survey of cross-species microsatellite amplification in birds. *Molecular Ecology* 5: 635 378.
- Primmer, C. R., Painter, J. N., Koskinen, M. T., Palo, J. U. and Merilä, J. (2005). Factors affecting avian cross-species microsatellite amplification. *Journal of Avian Biology* 36: 348 360.
- Randler, C. (2002). Avian hybridization, mixed pairing and female choice Animal Behaviour 63: 103 – 119.
- Randler, C. (2008). Hybrid waterfowl in central Europe an overview. *Waterbirds* 31(1): 143-146.
- Rheindt, F. E. and Edwards, S. V. (2011). Perspective in ornithology genetic introgression: An integral but neglected component of speciation in birds. *The Auk* 128(4): 620 – 632.
- Roewer, L. (2013). DNA fingerprinting in forensics: past, present, future. *Investigative Genetics* 4(22): 1 – 10.
- Roldán, V. A., Navarro, J. L., Gardenal, C. N. and Martella, M. B. (2011). Many captive populations of great rhea (*Rhea americana*) act as genetic reservoirs in Argetina? *Zoo Biology* 30: 65 – 70.
- Rubinsztein, D. C, Amos, B. and Cooper, G. (1999). Microsatellite and trinucleotide-repeat evolution: evidence for mutational bias and different rates of evolution in different lineages. *Philosphical Transactions of The Royal Society of London B* 354: 1095-1099.

- Saetre, G-P., Borge, T., Lindroos, K, Haavie, J., Sheldon, B. C., Primmer, C. and Syvänene, A-C. (2003). Sex chromosome evolution and speciation in *Ficedula* flycatchers. *The Proceeding of Royal Society of London (Serial B)* 270: 53-59.
- Schilthuizen, M., Giesbers, MCWG. And Beukeboom, L.W. (2011). Haldane's rule in the 21st Century. *Heredity* 107: 95 102.
- Stenzler, L. M. Fraser, R. and Lovette, I. J. (2004). Isolation and characterization of twelve microsatellite loci from golden-winged warblers (*Vermivora chrysoptera*) with broad cross-taxon utility In Emberizine songbirds. *Molecular Ecology Notes* 4: 602 -604.
- Su, Y. Liu, C. W., Ye, C. H., Cao, W. Q., Huang, Y.Q., Zheng, J., Cai, D. Y., and Olowofeso, O. (2006). Studies on genetic variation of different Chinese duck populations with random amplified polymorphic DNA analysis. *Asian-Australian. Journal of Animal Sciences*.19 (4): 475 – 481.
- Tejedor, M. T., Monteagudo, L. V. and Arruga, M. V.(2008). Microsatellite markers for the analysis of genetic variability and relatedness in redlegged partridge (*Alectoris rufa*) farms in Spain. *Research in Veterinary Science* 85: 62–67.
- Tomasulo-seccomandi, A. M., Schable, N. A., Bryan, A. L. Jr., Brisbin, I. L. Jr., Del-Lama, S. N. Jr. and Glenn, T.C. (2003). Development of microsatellite DNA loci from the wood stork (Aves, Ciconiidae, Mycteria americana). Molecular Ecology Notes. 3(4): 563 567.
- Urfi, A.J. (1993). Breeding patterns of painted storks (*Mycteria leucocephala*) at Delhi Zoo, India. *Colonial Waterbirds* 16: 95 – 97.
- Urfi, A. J. (2011). Foraging ecology of the painted stork (*Mycteria leucoephala*). *Waterbirds* 34(4): 448 456.
- Urfi, A. J. and Kalam, K. (2006). Sexual dimorphism and mating pattern in painted storks. *Colonial Waterbirds* 29(4): 489 496.
- Usmani, S. (2002). Isolation, characterization and application of microsatellite markers in the Southern Asia river catfish (Baung) *Mystus nemurus* (C&V). PhD Thesis, UPM.
- Valera, M. A., González-tizón, A., Mariñas, L and Martínez-lage, A. (2007). Genetic divergence detected by ISSR markers and characterization of microsatellite regions in *Mytilus* mussels. *Biochemical Genetics* 45: 565 -578.
- Vallender, R., Robertson, R. J., Friesen, V. L. and Lovette, I. J. (2007). Complex hybridization dynamics between golden-winged and bluewinged warblers (*Vermivora chrysoptera* and *Vermivora pinus*)

revealed by AFLP, microsatellite, intron and mtDNA markers. *Molecular Ecology*16: 2017–2029.

- Verhrught, W.J.M.(1987). Conservation status and action program for the milky storks (*Mycteria cinerea*). Colonial Waterbirds 10: 211 220.
- Vigfúsdóttir, F., Pálsson, S. and Ingólfsson, A. (2008). Hybridisation of glaucous gull (*Larus hyperboreus*) and herring gull (*Larus argentatus*) in Iceland: mitochondrial and microsatellite data. *Philosophical Transactions of the Royal Society B* 363: 2851–2860
- Walsh, J., Shriver, W. G., Olsen, B. J. and Kovach, A. I. (2016). Differential introgression and the maintenance of species boundaries in an advanced generation avian hybrid zone. *BMC Evolutionary Biology* 16:65-70.
- Wang, J. (2015). Individual identification from genetic marker data: Developments and accuracy comparisons of methods. *Molecular Ecology Resources* Page 1-7.
- Watson, M. M. C., Berg, M. and Søreide, K. (2014). Prevalence and implications of elevated microsatellite alterations at selected tetranucleotides in cancer. *British Journal of Cancer* 111:823-827
- Wink, M. (2006). Use of DNA markers to study bird migration. *Journal of Ornithology* 147:234 244.
- Yang, L., Fu, S., Khan, Md. Asaduzzaman. , Zeng, W. and Fu, J. (2013). Molecular cloning and development of RAPD-SCAR markers for Dimocarpus longan variety authentication. Springer Plus 2:501 (<u>http://www.springerplus.com/content/2/1/501</u>
- Zane, L., Bargellon, L. and Patarnello, T. (2002). Strategies for microsatellite isolation: a review. *Molecular Ecology* 11: 1- 16.
- Zhang, D and Hewitt, G. M. (1996). Nuclear integrations: challenges for mitochondrial DNA markers. *Trend in Ecology and Evolution* 11(6): 247 – 251.