Volume 17

The Society News

The Society for the Perpetuation of Desert Bred Salukis

Winter 2021-2022

Running Off Lead-a Free Coursing Primer

Saluki Collars by Sir Terence Clark

True Colors-A Research Article

Society for the Perpetuation of
Desert Bred
Salukis

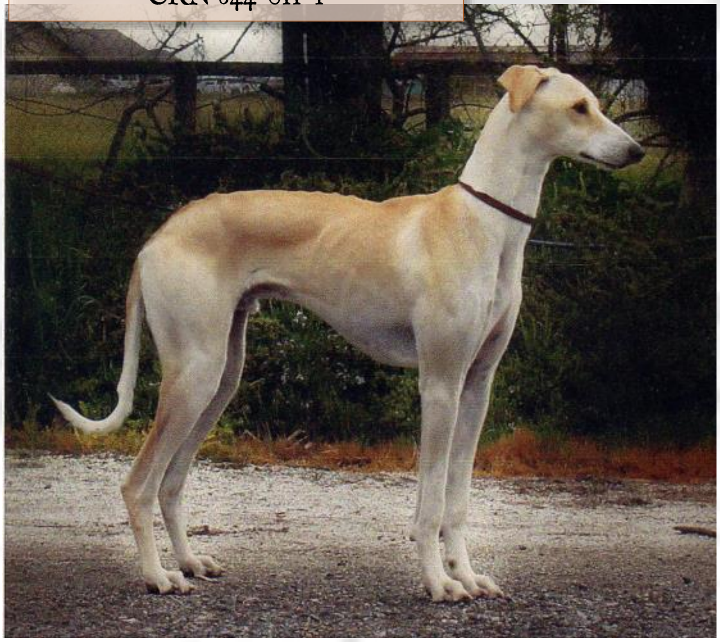
Tallahamra Al Ahad
CRN 64

*Al Melek's Jamila du Liban
CRN 18

Tallahamra Musdiy CC,CM
CRN 198

The Salukis of Tallahamra

Wishbone of Tallahamra
CRN 644-011-1



Tallahamra Abinito
CRN 723-013-2

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A SALUKI IS A SALUKI.
AN UNREGISTERED SALUKI
IS A HUMAN TECHNICALITY
THAT CAN BE OVERCOME.

FROM THE PRESIDENT'S DESK:

As I start my tenure trying to fill the shoes of those who have sat at this desk before me, I find myself contemplating both how things have changed in our world and how they remain the same. Covid continues to have a major impact on all our lives, dividing us by loss of social interactions in person, and political ideologies. Battles the Society has fought in the past have surfaced again. The Centers for Disease Control has stopped importations from our Countries of Origin as the risk of rabies and retail rescue impact directly the homelands of our Salukis.

On the positive side, and it is a BIG positive, AKC has given our Salukis the ability to participate in the PAL program without de-sexing. This allows our imports, Gen 1, and Gen 2 Salukis to be able to compete in all AKC Performance events. We were able to get a critique scheduled over the summer which allowed four Salukis to complete their critiques, two of whom have been entered into the Studbook. It looks like the additional critiques on hold may be able to be completed soon.

Yes, our numbers are down, significantly. With increased opportunities here in the US to import, we see a loss of routine imports from the Middle East. Part of this is our changing world and the urbanization, hence loss of tribal lifestyles, part is the rise of the racing paradigm as hunting is lost throughout the region.

We continue to actively promote the use of FCI in Middle Eastern countries that are now trying to walk the FCI path. We also provide any information or assistance we can as requested. Education on proper vet care, feeding practices, and general Saluki information remains difficult even with the advent of Social Media as language is a barrier.

The latest FCI/AKC acceptance is Bahrain. The AKC BOD voted to accept Bahrain's studbook. Complete pedigrees originating in Bahrain will now go into AKC directly.

As always, if you want to help we have a job for you! We need social media help, web site help, and the Society News can always use help!

Current Doings

Mary Beth Rogers, Editor

2022 is now underway. Sadly, Covid 19 continues to impact all of our lives. That said, we do see progress. Lure Coursing and Open Field Coursing are back underway, although both Covid and Rabbit Hemorrhagic Disease (RHDV2) still impact both sports.

The Open Field hunts have been hampered greatly by the depletion of hares last year, resulting in canceled hunts and no Grand Course for the second year. But, hopefully, hare populations will continue to improve. At the time of this writing the ASFA Lure Coursing standings are out and in the last year our Salukis did quite well. Five Salukis directly from our studbook achieved Top Twenty. One Gen 4 made Top Twenty and one PAL Saluki, who is a neutered rescue from Qatar, made Top Twenty.

The FCI path in Iran is slowly progressing. Registration and pedigrees are a new concept to introduce into an ancient way of life. While urban life in Iran is similar to urban life anywhere in the world, Salukis are generally not appropriate apartment companions. This means convincing the rural hunters and breeders of Salukis that registration and vaccination is of paramount importance. The Society continues to provide information and advice as requested.

From the AKC:

Acceptance of Pedigrees from the Bahrain Kennel Club
The Board reviewed a request from the Bahrain Kennel Club (BKC) to be added to the list of registries with pedigrees acceptable for AKC registration.

The Bahrain Kennel Club (BKC), was established in 1974 by Sheikha Danah Al Khalifa. BKC became a full member of Federation Cynologique Internationale in 2017. BKC is a non-profit organization in the Kingdom of Bahrain which represents the canine community. It's goal as stated on its website is: "To educate the public about responsible dog ownership, provide education and exciting events, where everyone can get together and learn about dogs, their health and welfare."

Following a motion by Mr. Sweetwood, seconded by Mrs. Wallin, the Board VOTED (unanimously) to add the Bahrain Kennel Club (BKC) to the list of registries with pedigrees acceptable for AKC registration.

Secretary's Report

Lauri Domski, Secretary

The 2021 meeting of the Society for the Preservation of Desert Bred Salukis (SPDBS) was called to order at 1:34 PM EST on October 30, 2021, via Zoom. Present were President Mary Beth Rogers, Secretary Lauri Domski, Treasurer Ken Stahli, and Board Members Sir Terence Clark, Susan Schroeder, Kathleen Tigan, Marsha Bradbury, Oksana Belova and Jenna Lowe. Absent was Vice President Elizabeth Dawsari.

The President reported on some of the victories that SPDBS enjoyed this year, including the American Kennel Club's acceptance of SPDBS registered Salukis in all AKC sponsored competitions except conformation, and the spay/neuter requirement shall be waived. We also were updated on the status of the fledgling FCI registry in Iran; while it is progressing, it is still a work in progress.

The secretary reported on no motions proposed or passed during the year.

The treasurer's report is listed elsewhere in the annual newsletter.

The nominating committee presented the candidates for the open seats on the board this year. Susan Schroeder announced that she will step down from the board but will continue her role on the Registrar's committee. All the board members expressed their gratitude for Susan's years of service and dedication.

The membership secretary announced that SPDBS had 70 members at the time of the meeting.

The question of honorary lifetime membership was discussed, and members agreed that honorary membership would include all rights and responsibilities of membership. A motion was made and seconded to confer honorary lifetime membership to Gertrude Hinsch for her years of dedication to the mission of SPDBS.

The Registrar's committee reported that 6 dogs were critiqued over the summer. Two CRN's have been issued.

The Podcast committee reported that there are several great interviews awaiting production, and what is still needed in that regard. Discussion ensued on the necessity of continuing the interviews and the conclusion that the portion of Saluki history held in the west and the efforts to preserve Country of Origin bloodlines will be of great interest and importance to all Saluki lovers.

We were updated on the status of the SPDBS webstore, the SCOA Specialty booth and the development of other income streams, including sponsorship for the podcast.

The Performance committee expanded on the significance of the acceptance of SPBDS inclusion in AKC events and activities (barring Conformation), and the fact that this has been a long term goal of SPDBS that has been achieved.

Finally, the board discussed the US Center for Disease Control (CDC) shutdown of importation of dogs from the Middle East (with the exception of FCI countries Israel and Bahrain) due to increased incidence of rabies in imports. [The noted exception being Active Duty Military imports with CDC permission]. While these restrictions may be relaxed, these restrictions make importation from countries of origin significantly more difficult. It was also noted that many ancient bloodlines have been lost or diluted by the importation of Salukis with pedigrees from the United Kingdom and other western nations into countries of origin.

The motion to adjourn was made by Susan Schroeder and seconded by Mary Beth Rogers at 2:48 PM EST.

Respectfully submitted,

Lauri Domski

SPDBS Secretary

An image from John D .Whiting. Whiting was born in Jerusalem and lived his life as a noted member of the American Colony. The above image is part of the Library of Congress archive, Prints & Photographs Reading Room. This image is from his 1935 trip to Cappadocia in Turkey. The link will take you to the Library of Congress page that has the entire album. It is interesting to note two of these Saluki are not cropped, the center Saluki does have its ears cropped. The album is a wonderful look at rural life in the region in 1935.

https://www.loc.gov/item/2007675299/

Society for the Perpetuation of
Desert Bred
سلوقي
Salukis

Volume 17

On the back cover:

Ch Abdul Farouk, from the Esther Bliss Knapp collection. The only crop-eared import to the USA in the AKC studbook, also an AKC Champion, is Abdul Farouk. Abdul Farouk was gifted to Esther Bliss Knapp (Pine Paddocks) in 1945 by Colonel Chapman-Walker on the recommendation of the President of the Saluki Club of America, Edward Aldrich. Abdul Farouk was a gift from King 'Abd al-Aziz in Saudi Arabia to Colonel Chapman-Walker in the early 40s after a hunting excursion. This male traveled from Saudi Arabia, to Cairo, Algiers, Naples and on to Washington DC. At the close of the Washington DC assignment Chapman-Walker was to return to England and the required quarantine was considered too hard on Abdul Farouk and Lady Yeled Sarona Ramullah (She was a companion gift from the King of Saudi Arabia). Mrs. Knapp successfully showed Abdul Farouk to his AKC Championship in 1946 and incorporated him into her Pine Paddocks program before AKC allowed him entry into the studbook in 1950.

On the front cover: John Wootton was born c. 1686 in Snitterfield, United Kingdom, died 1764. Wootton is known for his depictions of hunting scenes as well as the dogs and horses of the aristocracy. Trained in his early years by Jan Wyck, a Dutch Baroque painter known for his works on Military subjects, this early exposure brought Wootton to the attention of the British aristocracy gaining the patronage of King George II. Wootton was one of the first of what became known as Sporting Artists, painting hunts in the British landscape.

The painting on the cover is titled *"Lord Harley's Bloody Shouldered Arabian" signed and dated 'JWootton Fecit. 1723' ('JW' linked, lower left) and with inscriptions 'Lord Harley's Bloody Shoulder'd Arabian J.^{n} Wootton.' (lower centre) and inscribed 'L.^{d} Harleys Bloody sh.^{d} Arabian.' (centre right)*
oil on canvas
40½ x 48½ in.

Sold by Christie's July 4, 2011 from the collection of the Duke of Portland. Text compiled from the Christie's auction catalog Old Master & British Paintings-Evening Sale, 2011.

https://www.christies.com/en/lot/lot-5460687

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New Imports

King Soloman's Hunters
Hineha Yafe Dodi Af Na'im

Import from Israel, Generation 2

Bred by Osnat Sitbon Azarzar

Owned by Denise Lynch

Whelped April 19,2021

King Solomon's Hunters Haroe Bashoshanim

Import from Israel, Generation 2

Owned by Daniela Imre

Bred by Osnat Sitbon Azarzar

Whelped April 19,2021

Shiva of Iran at Melik

Import from Iran, Generation 0

Owned by Kathleen Tigan

Bred by Amir Darzi

Whelped January 1, 2019

CRN 0802-016-1 and CRN 0847-020-1

Melik Boorchin Owrang
Bitch. CRN 0802-016-1
Grey/Brown, Feathered
May 22, 2016
Whelped in Milford,VA
Breeder:
George and Mary Beth Rogers
By *Ghobad
CRN 0634-011-0 x
*Qushabee of Boorchin
CRN 0737-013-0
Owner: Cassandra Kraham

Melik Boorchin Pari Ravanbacht
Bitch. CRN 0847-020-1
Black and Grey,Feathered
November 3, 2020
Whelped in Milford VA
Breeder:
Mary Beth and Mary-Wynn Rogers
By *Gare-Qush of Iran
CRN 0830-019-0 x
*Qushabee of Boorchin
CRN 0737-013-0
Owners:
Martina Kissener and Heike Braüer

Nominating Committee Report

As there were no Nominations from the Floor, the Nominating Committee Slate is seated as per our By-Laws.

The Society Board of Directors and Officers are as follows:

SPDBS Board of Directors

President/Registrar– Mary Beth Rogers
president@desertbred.org/spdbs.registrar@gmail.com
Vice–President– Elizabeth Dawsari
Treasurer- Ken Stahli
treasurer@desertbred.org
Secretary-Lauri Domski *secretary@desertbred.org*

Board of Directors

Oksana Belova
Marsha Bradbury
Sir Terence Clark

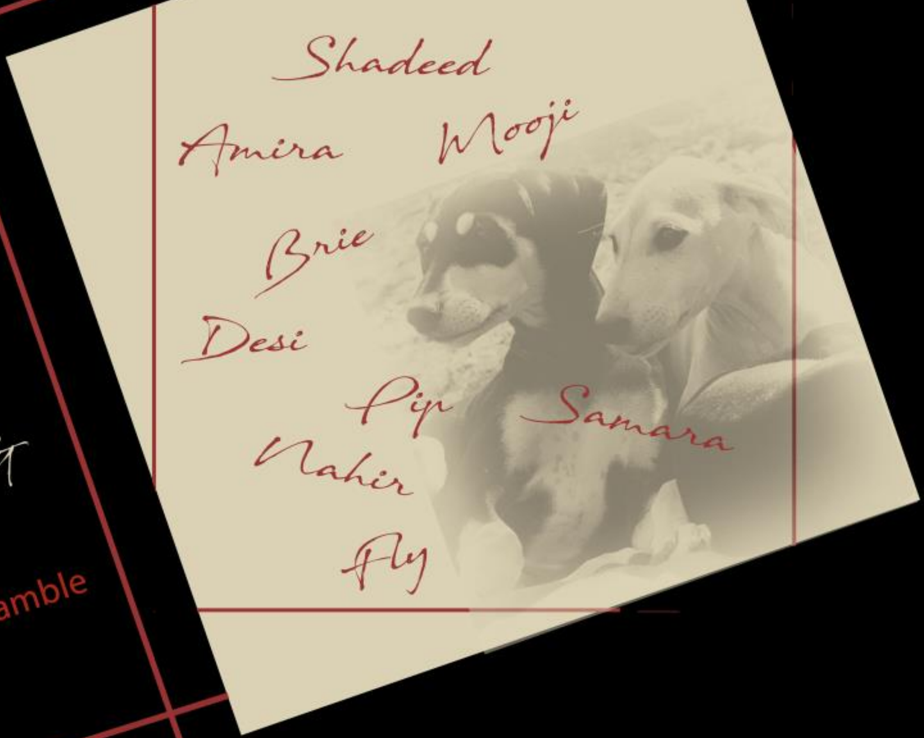
Paul Domski
Jenna Lowe
Kathleen Tigan

Melik Boorchin Parisa at Shahbaaz

*Atash de Boorchin of Iran

Looking to the Future◆Honoring the Past

The Perez Family



Wishing everyone
a New Year
Rich in wonders
Peace, Love Et
Joy !

Stephanie & Brad Gamble
Daniela Imre

Yazi

Yamadan

Stephanie & Brad Gamble
Yamadan14@gmail.com

BRED BY STEPHANIE & BRAD GAMBLE & DANIELA IMRE

Fly

Gen.3

Yamadan's Midnight Flight for Tallahamra (Tallahamra Abinitio x El Jabri Nedjma Yamadan)

Daniela Imre
daniela-is@live.com

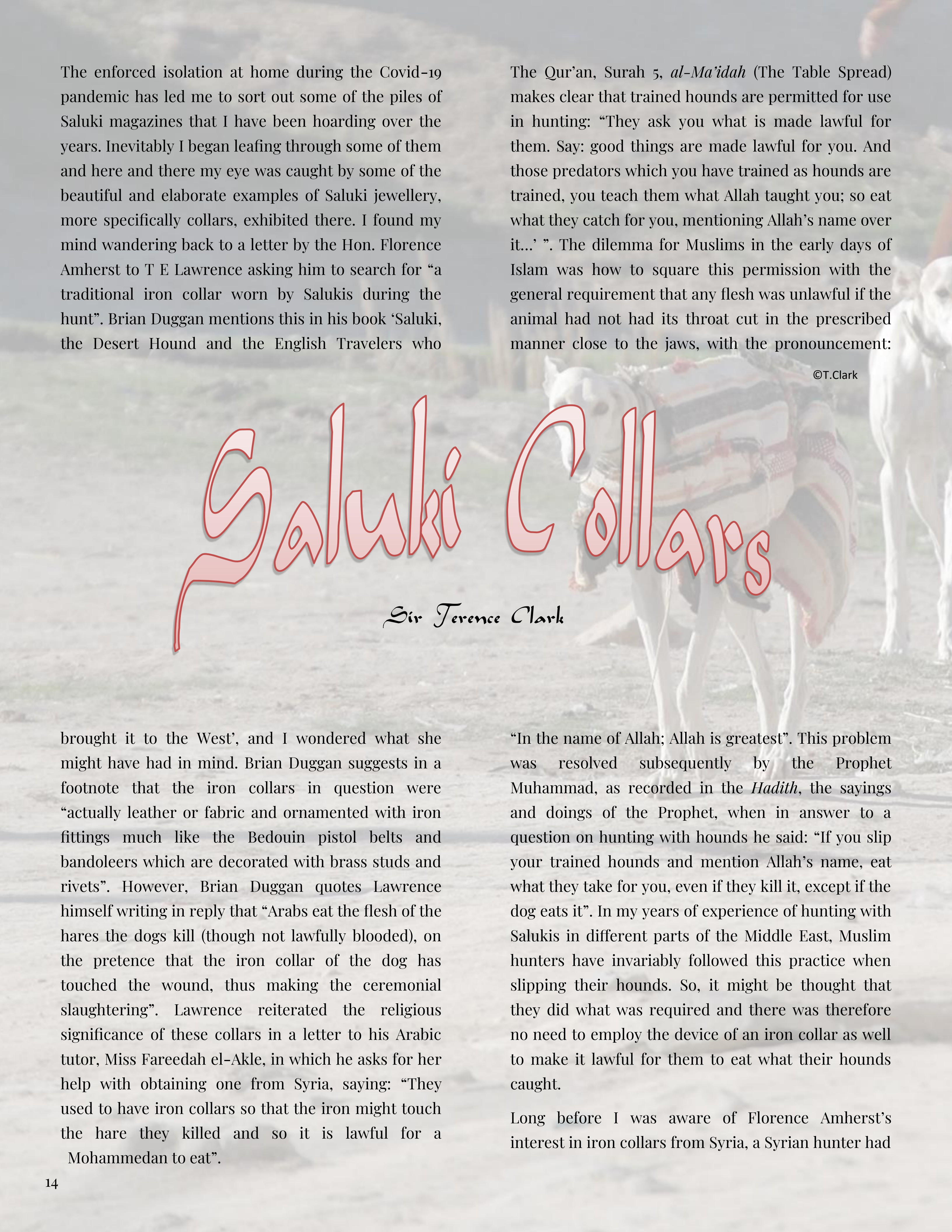
Shepherd

My Beloved is
Mine and
I am his
The Shepherd
In the Roses

Song of Solomon 2:16

Gen. 2

King Solomon's Hunters Haroe Bashoshanim; whelped in Haifa, Israel, 04/19/2021
Breeder: Osnat Sitbon Azarzar
Owner: Daniela Imre Contact: Daniela-is@live.com



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Saluki Collars

Sir Terence Clark

The enforced isolation at home during the Covid-19 pandemic has led me to sort out some of the piles of Saluki magazines that I have been hoarding over the years. Inevitably I began leafing through some of them and here and there my eye was caught by some of the beautiful and elaborate examples of Saluki jewellery, more specifically collars, exhibited there. I found my mind wandering back to a letter by the Hon. Florence Amherst to T E Lawrence asking him to search for "a traditional iron collar worn by Salukis during the hunt". Brian Duggan mentions this in his book 'Saluki, the Desert Hound and the English Travelers who brought it to the West', and I wondered what she might have had in mind. Brian Duggan suggests in a footnote that the iron collars in question were "actually leather or fabric and ornamented with iron fittings much like the Bedouin pistol belts and bandoleers which are decorated with brass studs and rivets". However, Brian Duggan quotes Lawrence himself writing in reply that "Arabs eat the flesh of the hares the dogs kill (though not lawfully blooded), on the pretence that the iron collar of the dog has touched the wound, thus making the ceremonial slaughtering". Lawrence reiterated the religious significance of these collars in a letter to his Arabic tutor, Miss Fareedah el-Akle, in which he asks for her help with obtaining one from Syria, saying: "They used to have iron collars so that the iron might touch the hare they killed and so it is lawful for a Mohammedan to eat".

The Qur'an, Surah 5, *al-Ma'idah* (The Table Spread) makes clear that trained hounds are permitted for use in hunting: "They ask you what is made lawful for them. Say: good things are made lawful for you. And those predators which you have trained as hounds are trained, you teach them what Allah taught you; so eat what they catch for you, mentioning Allah's name over it…' ". The dilemma for Muslims in the early days of Islam was how to square this permission with the general requirement that any flesh was unlawful if the animal had not had its throat cut in the prescribed manner close to the jaws, with the pronouncement: "In the name of Allah; Allah is greatest". This problem was resolved subsequently by the Prophet Muhammad, as recorded in the *Hadith*, the sayings and doings of the Prophet, when in answer to a question on hunting with hounds he said: "If you slip your trained hounds and mention Allah's name, eat what they take for you, even if they kill it, except if the dog eats it". In my years of experience of hunting with Salukis in different parts of the Middle East, Muslim hunters have invariably followed this practice when slipping their hounds. So, it might be thought that they did what was required and there was therefore no need to employ the device of an iron collar as well to make it lawful for them to eat what their hounds caught.

Long before I was aware of Florence Amherst's interest in iron collars from Syria, a Syrian hunter had presented me with a beautiful collar at the end of one of our excursions into the desert near Hama. It was made of padded cloth artistically decorated with hundreds of tiny beads, with small designs and the hound's name – *Barood* or Gunpowder – picked out in different colours. It was made to go over the head without a buckle and a slip lead could be attached to the metal rings hanging from the metal fastenings joining the two ends together. I was told that such collars were made by prisoners in Hama jail to earn a little money during their incarceration. At the time I attached no particular importance to the fastenings, as they seemed a purely practical device.

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Over the course of succeeding years and further hunting trips with my Arab and Kurdish friends from Hama, I was given other beaded collars. The colours of the beads and the designs of the decorations are all different but the metal fastenings are similar, consisting of a metal ring at each end of the collar from which one or two plaited wire elongated loops

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extend, joined if necessary in the middle by a plaited wire ring. Two plaited wire rings also hang from each loop, through which a slip cord could be threaded.

Out of curiosity, I asked one day why the collars had these metal fastenings, when a buckle and a ring would have been more practical. It was then that I heard for the first time of their religious significance. The hunters were not only making the pronouncement: 'In the name of Allah: Allah is greatest', when they slipped their hounds, but were also reinsuring the lawfulness of eating what they caught by the metal fastenings replacing symbolically the slaughterer's knife. These were clearly the sort of iron collars that Florence Amherst had sought a century ago.

T E Lawrence's above-mentioned letter to Fareedah el-Akle also says: "These collars used to have little blue beads also on them, to keep off the evil eye". Although the colour blue is believed to have this power and blue beads or a blue eye in glass or a blue ceramic hand, representing the hand of Fatima, the Prophet Muhammad's daughter, may be attached as protective amulets to children or animals or the doorway of a house, most of the Saluki collars that I saw were not decorated with blue beads specifically for this purpose, if there were any beads at all or merely cowry shells. This might help to explain why T E Lawrence could not find any and never sent any examples to Florence Amherst, though he did of course have many other preoccupations at the time.

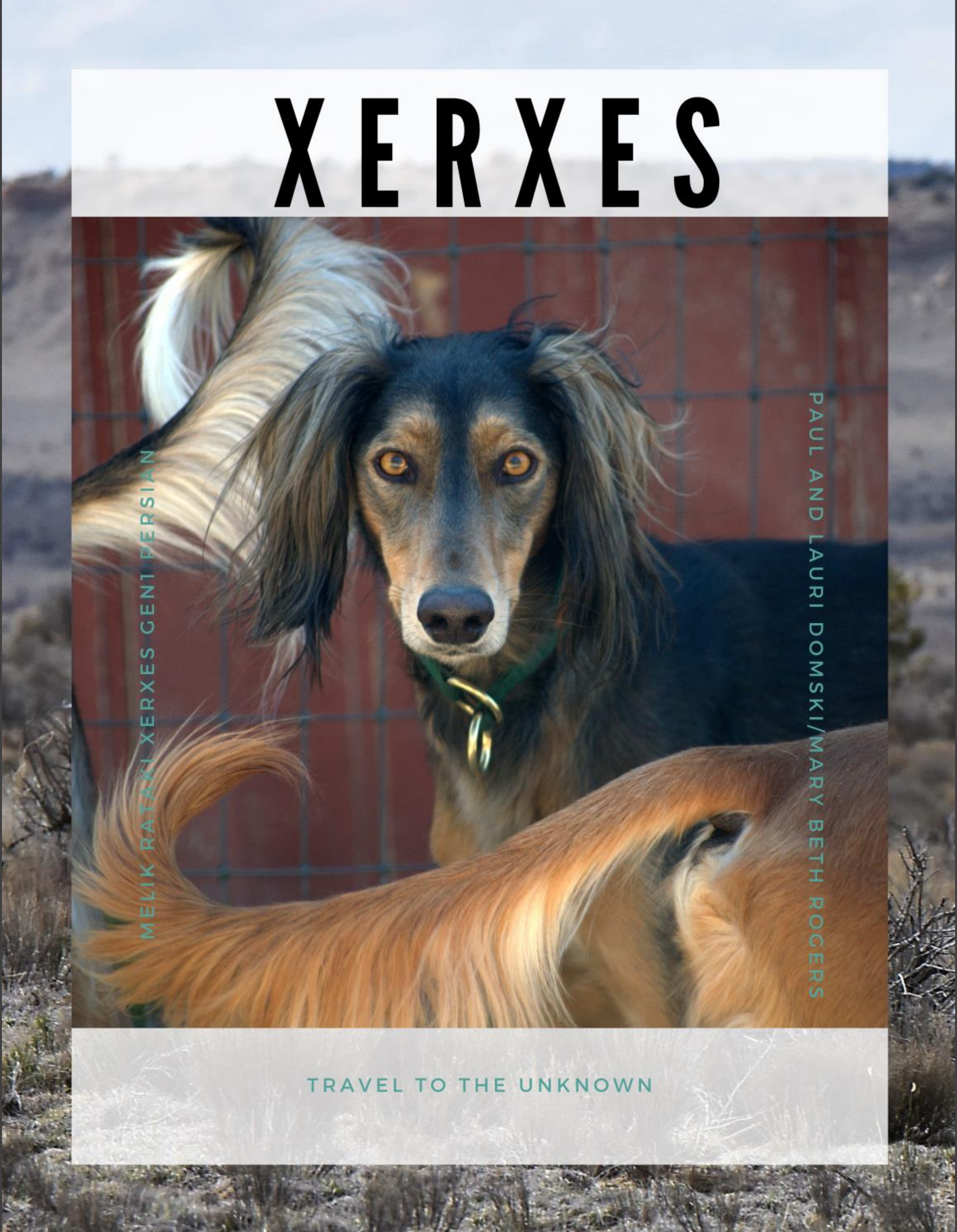
Like so much of Saluki lore in the Middle East, the original purpose of certain practices is often forgotten and they have become merely customary. This may well be the case with these ‘iron collars’, which incidentally I have come across only in northern Syria and southern Turkey. However, one thing is clear: the decorative collars of today with their special metal fastenings are worn specifically for hunting. At home, where the hounds are often chained up for much of the day, a plain collar with a robust metal ring is the norm.

MELIK BAANU-ABEE E SHEYDA LAA YUDAANI

GENERATION 3
AKC POINTED
SUPERB TREE CLIMBER, SQUIRREL HUNTER,
LOVER OF LIFE

Jan Isley and Carola Butler
Marietta Georgia

XERXES



MELIK RATAKI XERXES GEN1 PERSIAN

PAUL AND LAURI DOMSKI/MARY BETH ROGERS

TRAVEL TO THE UNKNOWN

The Bloody Shoulder'd Arabian : Many Tales

by Elizabeth Al-Hazzam Dawsari

Did a flesh and blood prototype for the bloody shouldered Arabian legend ever exist? Of course! From where did the notion emanate? Tales abound, with documented and graphic evidence of such a horse's existence dating from the early 1700s, perhaps much, much earlier, all the way to the proliferation of modern versions repeated in print and on the Internet, each with a little different twist. The common thread of all retelling links a skirmish, or battle in the desert, followed by a rider's flight slumped across his trusty war mare, his dried blood indelibly staining her shoulder and becoming a part of her DNA. Pierced by a bullet in some stories, a lance in others, even a sword in one or two, the mortally wounded rider is borne home. The story never ends there. The mare foals, often said to be on the same night as her return, delivering a colt similarly marked by the rider's blood as seen dried upon his dam's shoulder. Subsequent descendants, generation after generation, manifest the marking. This is the substance of the legend.

Is there any truth to it, or is the blood red stain more likely associated with grey horses born chestnut? The fact remains, grey Arabians exist today with a variety of rusty red markings on their shoulders or elsewhere on their bodies. There's even a Breyer Horse model celebrating such a horse. But let's look at a few of this story's iterations.

In September of 1982, *Arabian Horse World* published a version of the story. In this recitation, the "most prized possession" of a Bedouin chieftain by the name of Ahmed, "was a beautiful grey mare renown as the fleetest and most beautiful horse in the world that kings and chieftains had tried to acquire." Of course Ahmed had to scour the desert in the quest of a mate suitable for his mare and, naturally, he "bred her to the Sultan's premier stallion." What other stallion would be worthy of her? Here's where the story touches upon the essence of the earliest iteration of the legend associated with John Wootton's 1724 painting (or was it really in 1723?) discovered thus far, the 1719/20 record of Captain Oliver. (But more about the Captain later.) According to the Captain, our chieftain, Ahmed, ran into a band of robbers. According to the *Arabian Horse World*, shot and mortally wounded by the robbers, Ahmed "fell over the neck of his beloved mare, who never slowed. She carried him to his tents on this final ride," his blood drying as it ran down her shoulder. That night, she foaled a "perfect specimen of the Arabian breed" that carried the same bloody mark on his shoulder. And that colt's descendants to this day carry the same insignia. Please make note of the reference to "perfect specimen of the Arabian breed." There's political and cultural significance to that statement when one examines Wootton paintings of *The Bloody Shoulder'd Arabian* and when the tale is recounted in modern times.

Quite a gripping story, no? Another unfolding of the Bloody Shouldered Arabian story was written by Carol Deegan in the May 2000 issue of *Arabian Horse World* on page 132. In this later version, the Bedouin isn't named nor are robbers or bullets mentioned. However, the Bedouin is mortally wounded in battle, and his mare "went for days without food or water to return her master to his family." The mare was in foal, and when her colt was born, he "also bore the identical 'bloody shoulder' that his mother had from her master's blood." Now here's where this story touches upon another possible source for the legend, this one attributable to Shia iconography, specifically to Zuljenah, Husayn's grey horse with his bloody shoulder and mortal wounds from arrows. (Who's Husayn? Later.) Carol Deegan's story continues, " It was then that the tribe realized that Allah had rewarded this mare and their tribe for their courage, loyalty and faith and that the bloody shoulder was a reminder of His favor. … graced by God with the bloody shoulder. … a sign of Allah's favor." That fact is repeated for emphasis.

Where does this legend come from? Nobody can say for certain, at least not yet, but there are two potential sources. The first is associated with the Wootton painting, *The Bloody-Shoulder'd Arabian*, and the second is related to the death of Husayn Ibn 'Ali with his faithful horse, Zuljenah, in the Battle of Karbala in 680.

This version of The Bloody Shouldered Arabian is believed to have been executed in 1724.

Wootton really liked the horse. Instead of engravings, he painted multiple but similar versions of the Bloody Shouldered Arabian, an Arabian stallion imported into England from Aleppo. Donna Landry writes, "The horse had arrived in England by sea in the spring of 1719/1720, shipped home by Nathaniel Harley, an English merchant at Aleppo, for his nephew, Edward, Lord Harley (1689-1741), who in 1724 would succeed his father, Robert Harley, and become the second Earl of Oxford. Wootton painted hundreds of horse portraits, and he painted this particular horse more than nine times, more than he painted any other horse." (Landry, page 51)

Nathaniel Harley, a merchant, sailed to Aleppo in 1686. Correspondence among Thomas Trench, Sir Edward Harley, Lady Harley, and Nathaniel Harley appears in *The Manuscripts of His Grace the Duke of Portland at Welbeck Abbey*. On February 15, 1714-15, Nathaniel Harley writes to his brother, Edward Harley, "Aleppo—By this ship I have sent a cargo of great value, which I take the liberty to recommend to your care. The hawks are both long winged, but of different kinds, and such as we fly at antelopes ; and if they show you as good sport in England as they have done here I flatter myself that they will not be unworthy of Lord Harley's acceptance. If they arrive, it is impossible but that they must be in very bad condition, which together with the forwardness of the season will render it necessary to put them immediately into the mew. I send also a little greyhound bitch of this country that has been used to the hawks." Nathaniel Harley's letter continues, referring to the horse that has "been more taken notice of than I desired, and has had the honour of being visited by the Turk himself incognito, who would have him for the Grand Signior's [sic] own stable. … I shall not be easy till I hear he is on board ship. … Now that I have dispatched away my horses, my dogs, and my hawks, you may be sure I shall not remain long here …" (*The Manuscripts*, page 255)

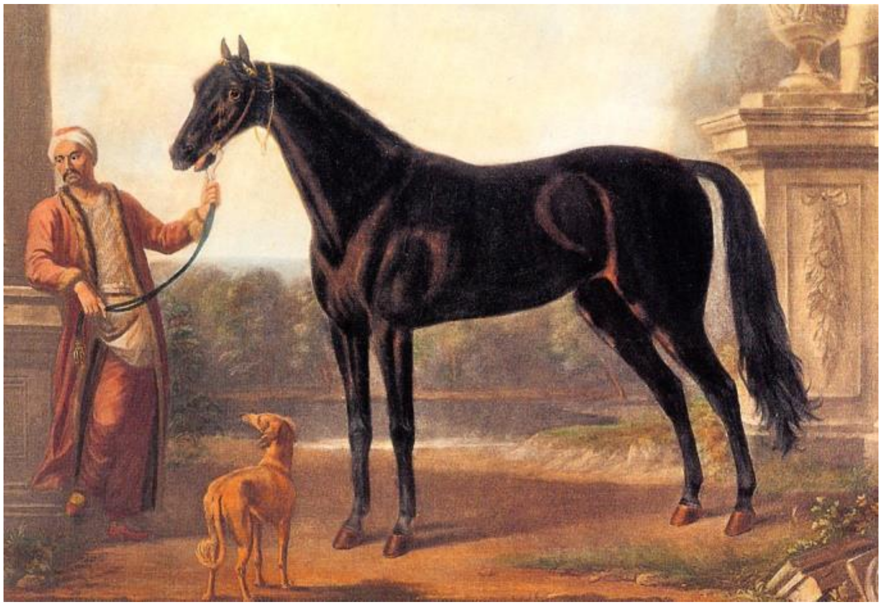
In a 1716 letter to his nephew, Robert Harley, Nathaniel Harley details a several days hunt in pursuit of antelope, or gazelle, with hawks and hounds, a colorful recounting published on pages 258 and 259 of

The Manuscript. It is his next letter wherein the Bloody Shouldered Arabian appears for the first time. On February 21, 1716-17, Nathaniel Harley writes to his brother, Edward, "Aleppo.—I have sent down to Scanderoon a horse to be shipped aboard the *Ohslow* (hard to read this word in the text). I cannot tell whether he can be got off, the prohibition being very strict at present. He is a Gordeen horse, one of the best among them. I bought him from under the Bey of the mountains." (*The Manuscripts*, page 259) On May 18, Nathaniel Harley writes that the horse has been returned to him, perhaps because the Captain was unwilling to encumber himself with a horse on ship board due to the war with Sweden. (*The Manuscripts*, page 260).

Documentation accompanying the horse is attributed to Captain Oliver, who apparently was responsible for shipping the horse. According to what the Captain was told, robbers (remember them?) attacked and wounded the owner of the colt's dam, and it was that man's blood that dried on her shoulder. Her colt bore the same marking, as painted by Wootton. The owner and seller of the stallion claimed he was of the rare "Gordeen" breed which subsequently has been identified as Seglawi Jedran—a strain well known to today's Arabian breeders.

The Bloody Shouldered Arabian was scarcely the first Eastern horse to appear in England. Landry cites the gift, in the year 1121, of an Eastern horse by King Alexander of Scotland to a church. In the years between 1660 and 1750, more than two-hundred Oriental horses were imported into England. Now, there are political and cultural ramifications attributed to the stain on the Bloody Shouldered Arabian—a stain which only appeared on Arabians or their descendants at that time. The concept of "purity" was associated with imported Eastern horses, i.e., Arabs, Barbs, etc., into England. According to Landry, "… something significant happened to horse breeding and horse culture in these years. … a certain degree of magical thinking associated with pedigrees in a society with a ruling aristocracy like England's should be expected, as 'the parallels between … the human obsession with title, hereditary position and social caste … are too obvious to need emphasis.'" (Landry, page 43)

Horses imported into England from the East did not belong to just anyone. Upon arrival, they became the provenance of England's aristocracy. Landry writes that "If titled aristocrats possessed the lion's share of Eastern equine bloodstock during the eighteenth century, there were by 1750 many land gentlemen of smaller means who owned horses descended (please note the word "descended" meaning part bred. E.D.) from Eastern blood as well as paintings and engravings of them as the ideal of equine beauty. The horse portrait was an eighteenth-century innovation, and sporting art was the definitive eighteenth-century English contribution to



The Byerly Turk after John Wootton (Snitterfield c.1682 – London 1765). One of a set of three prints of racehorses. This horse (c.1684-1706) was the earliest of three stallions that were the founders of the modern Thoroughbred horse racing bloodstock (the other two are the Godolphin Arabian and the Darley Arabian). The stallion is believed to have been captured by Captain Robert Byerley at the Battle of Buda (1686), served as Byerley's war horse when he was dispatched to Ireland in 1689 during King William's War and saw further military service in the Battle of the Boyne. This a wonderful rendition of the Saluki often seen in Wooton's work.

the history of painting." (Landry, page 42). An interesting feature in paintings of the Bloody Shouldered Arabian, for instance, is that his head is carried aloft, above the attendant's head, unlike paintings of Continental royals whose mounts are depicted as severely curbed, their heads held considerably below those of their masters.

All sorts of symbolism and coded messages abound in these paintings. "In one sense, the Bloody Shouldered Arabian's Eastern origins are very much on the surface of his portrait, and yet a certain Englishing of him has taken place. The stream in Wootton's nine paintings symbolizes importation—coming across the water. The architecture in the background is Eastern, and the attendant is garbed either as a Turk or an Arab. Interestingly, the Saluki also represents the East. Not only does the horizontal strip of water appear in the multiple versions of the portrait, reminding viewers of the stallion's importation, but the horse is usually accompanied by a man in Turkish or Arab dress and by a Saluki, an Eastern greyhound. (Nathaniel Harley had, in the winter of 1714/15, shipped home to England a Saluki that probably came into the possession of his nephew, Lord Harley.)" (Landry, page 56)


"The Evening of 'Ashura" painted by Mahmud Farshchiyan, an Iranian artist.

After the death of Husayn Ibn Ali in the Battle of Karbala.

What inspired the importation of Eastern horses, stallions for the most part? Mares were nearly impossible to secure due to their owners reluctance to sell coupled with the fact that mares were jointly owned by multiple parties. This prompted the landed gentry to breed native English mares to the imports in order to acquire descendants of these stallions.

Racing. It was all about racing. Speed—the suitability of Oriental horses to travel at sustained high speed over rough terrain. The proof of the pudding is in equine portraiture. As Landry states, "… the first English equine portraits were painted of imported Eastern horses—Arabians, Turks, and Barbs—and their racing progeny. It was Newmarket racing that first inspired horse portraiture, beginning with the Restoration of Charles II in 1660. Between 1710 and 1730, horse portraits became common, with Wootton the leading exponent." (Landry, page 54)

So where do Husayn Ibn Ali and his horse, Zuljenah, enter the picture? Allegedly, the Prophet Muhammad, the grandfather of Husayn, bred the horse. Thus far I have not read *Kitab Maqtal Al-Husayn*, the Karbala narrative written by the Kufan historian Abu Mikhnaf, the primary source documenting the Battle of Karbala, nor have I as yet seen any original source substantiating the claim that the Prophet Muhammad actually bred the horse. But the story of Zuljenah has been repeated, much as the legend of the Bloody Shouldered Arabian has oft been told. What is a fact is that representations of this horse appear even today in Shia commemorations of Husayn's martyrdom. Is this root of Carol Deegan's reference to Allah in her Bloody Shouldered Arabian account? (Landry. *Noble Brute*, page 120).

I don't know.

Sources:

LANDRY, DONNA. "The Bloody Shouldered Arabian and Early Modern English Culture." Criticism, vol. 46, no. 1, Wayne State University Press, 2004, pp. 41–69.

"If titled aristocrats possessed the lion's share of Eastern equine bloodstock during the eighteenth century, there were by 1750 many land gentlemen of smaller means who owned horses descended from Eastern blood as well as paintings and engravings of them as the ideal of equine beauty. The horse portrait was an eighteenth-century innovation, and sporting art was the definitive eighteenth-century English contribution to the history of painting. (page 42).

"In the years between 1660 and 1750 alone, at the same time that gentlemen began turning down their boot-tops and shortening their stirrups to achieve a forward—"hunting" or "jockey"—seat, more than two-hundred horses designated as Oriental in origin were imported into England. In fact, so-called Oriental horses had been imported into the British Isles for centuries, but in very limited numbers. The first recorded instance may be the Arab horse presented by Alexander, King of Scotland, to a church in 1121." (page 43)

"… something significant happened to horse breeding and horse culture in these years. … a certain degree of magical thinking associated with pedigrees in a society with a ruling aristocracy like England's should be expected, as "the parallels between … the human obsession with title, hereditary position and social caste … are too obvious to need emphasis." (page 43)

"In the many existing versions of his portrait, the Bloody Shouldered Arabian is always the same, though his circumstances and attendants vary." (page 50)

"The horse had arrived in England by sea in the spring of 1719/1720, shipped home by Nathaniel Harley, an English merchant at Aleppo, for his nephew, Edward, Lord Harley (1689-1741), who in 1724 would succeed his father, Robert Harley, and become the second Earl of Oxford. Wootton painted hundreds of horse portraits, and he painted this particular horse more than nine times, more than he painted any other horse." (page 51)

"There is no record how much Wootton was paid for the Bloody Shouldered Arabian's portrait, but other horse portraits were billed at the rate of twenty-six pounds and five shillings (for Lord Harley's *Dun Arabian*, painted sometime before 1720 … a larger picture than *The Bloody Shoulder'd Arabian*, but referred to as a 'sketch'), and as much as forty guineas for *The Countess of Oxford's Dun Mare, with Thomas Morton the Groom,* also from 1715 … a picture 'as big as ye life.'" (pages 52-53)

In 1914, the Duke of Portland purchased an almost exact replica of the Harley-commission portrait of the Bloody Shouldered Arabian, signed by Wootton and dated 1723, bringing the total of Wootton's pictures in the 1936 catalogue to twenty-one. Painted a year before Harley's version was painted, the 1723 version is likely to be the earliest of Wootton's multiple portraits of the horse, unless both derive from an earlier—and currently unknown—original." (page 53)

"… the first English equine portraits were painted of imported Eastern horses—Arabians, Turks, and Barbs—and their racing progeny. It was Newmarket racing that first inspired horse portraiture, beginning with the Restoration of Charles II in 1660. Between 1710 and 1730, horse portraits became common, with Wootton the leading exponent." (page 54)

"In one sense, the Bloody Shouldered Arabian's Eastern origins are very much on the surface of his portrait, and yet a certain Englishing of him has taken place. Not only does a horizontal strip of water appear in the multiple versions of the portrait, reminding viewers of the stallion's importation, but the horse is usually accompanied by a man in Turkish or Arab dress and by a Saluki, an Eastern greyhound. (Nathaniel Harley had, in the winter of 1714/15, shipped home to England a Saluki that may have come into the possession of his nephew Lord Harley.) (page 56)

LANDRY, DONNA.Noble Brutes:*How Eastern Horses Transformed English Culture*. Baltimore, Md. : Johns Hopkins University Press, c2009.

"'His lordship's Arabian,' a phrase often heard in eighteenth-century England, described a new kind of horse imported into the British Isles from the Ottoman Empire and the Barbary States of North Africa. Noble Brutes traces how the introduction of these Eastern blood horses transformed early modern culture and revolutionized England's racing and equestrian tradition. More than two hundred Oriental horses were imported into the British Isles between 1650 and 1750. With the horses came Eastern ideas about horsemanship and the relationship between horses and humans. Landry's groundbreaking archival research reveals how these Eastern imports profoundly influenced riding and racing styles, as well as literature and sporting art. After only a generation of crossbreeding on British soil, the English Thoroughbred was born, and with it the gentlemanly ideal of free forward movement over a country as an enactment of English liberties. This radical reinterpretation of Ottoman and Arab influences on horsemanship and breeding sheds new light on English national identity, as illustrated in such classic works as Jonathan Swift's 'Gulliver's Travels' and 'George Stubbs' portrait of Whistlejacket'."

(source: Nielsen Book Data)

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"293. ARABHORSE, WITH ATTENDANT IN A LANDSCAPE. J. WOOTEN. 1724.

White Arab horse with Eastern attendant in red, wearing a turban, leaning on a low wall to right; a greyhound [sic] seated in the foreground, landscape background with architecture.

Signed on wall to right, 'J. WOOTON FECIT 1724.' Canvas, 40 ¾ in. H x 50 ½ in. W.

Cat. 1747. Vestibule No. 8. 'The Bloody Shoulder'd Horse, sent over from Aleppo with the Turk & his Dog.'

Exhibited at Manchester. Cat. No. 9. Modern Masters." (page 82)

Taunton, Thomas Henry. *Portraits of Celebrated Race Horses of the Past and Present Centuries, in Strict Chronological Order, Commencing in 1702 and Ending in 1870, Together with Their Respective Pedigrees and Performances Recorded in Full.* In Four Volumes. London: Sampson Low, Marston, Searle & Rivington, 1887.

According to Taunton, "No authenticated record exists for the history of the Bloody-Shouldered Arabian. He was, however, a stallion of high repute, and the sire of several noted racers, foremost among which was the Duke of Bolton's famous chestnut horse, Sweepstakes, bred by Mr. Snell in 1772, and sold to his Grace. ... The Bloody-Shouldered Arabian was likewise the sire of Sir Nathanial Curzon's Brisk, the winner of several Royal Plates, and beating most of the best horses of his time. On the point of the shoulder in the print, will be seen the bright red mark from which this Arabian acquired his name. In the same way, the celebrated grey stallion, Bloody-Buttocks, derived his name from a scarlet patch on his hind-quarter." (page 4, volume 1)

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Historical Manuscripts Commission. Thirteenth report, appendix, part II.

Calendar of the Manuscripts of the Duke of Portland. Nathaniel Hartley letters start @ page 240.

Society for the Perpetuation of
Desert Bred سلوقي Salukis

Daughters of the Wind
https://daughterofthewind.org/al-hamdaniah/

Famous Godolphin Arabian painting for auction (scroll down ... keep reading)
https://www.horsetalk.co.nz/news/2011/07/035.shtml

For Thursday Art Day
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https://rkd.nl/en/explore/images/244615

The Legend of the Bloody Shoulder Arabian
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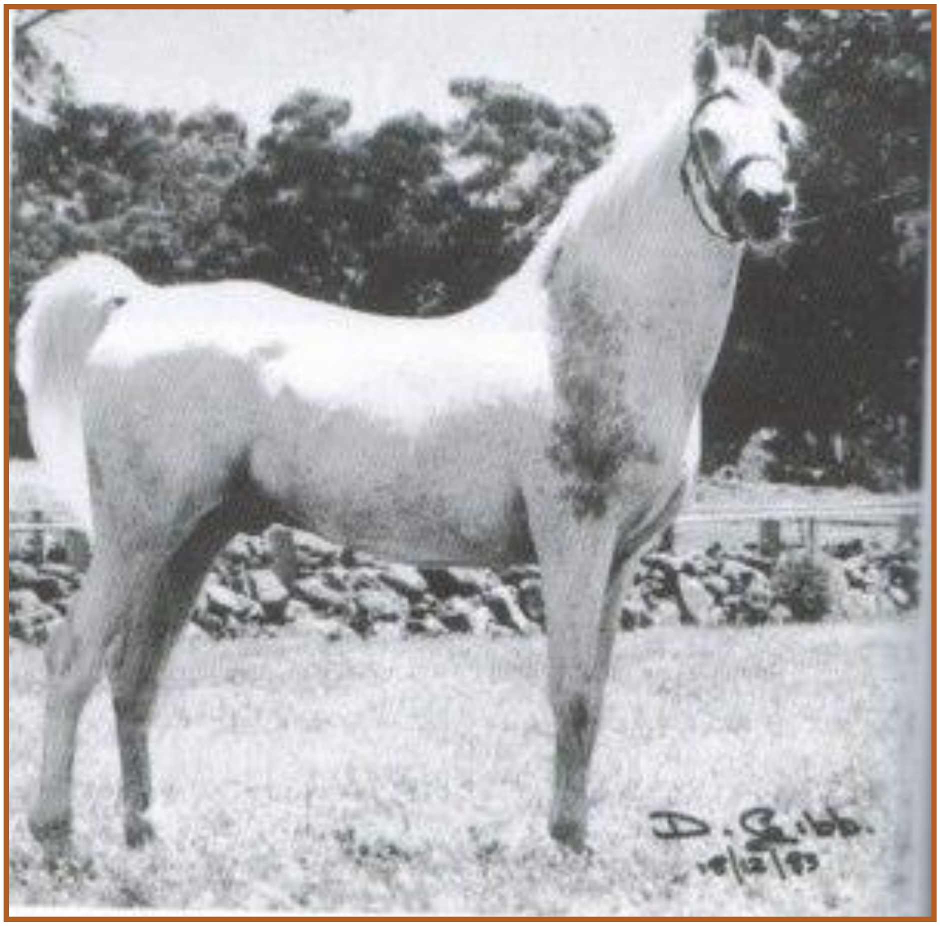
Old Master & British Paintings
https://www.christies.com/en/lot/lot-5460687

What Do We Know About Zuljanah (Horse_)?
Sayed Ammar Nakshawani
https://www.youtube.com/watch?v=jiFoZQ-j5QQ

Cheffins Autumn Sale October 2020
https://www.cheffins.co.uk/fine-art/lot-view,john-wootton-british-c-16821764_63261.htm



Greylight , Arabian Stallion foaled in 1959
(Bright Shadow/Royal Radiance)

CH’IEN HAN SHU *(The beginnings of west to east trade)* *Iranicaonline.org*

CH’IEN HAN SHU (*Qian Han shu*) “History of the Former Han Dynasty,” a historical work which includes information on Iran. It was originally simply called the *Han shu* and is often still referred to by that name. It is the second of the series of *Twenty-four Standard Histories*. Its author, Pan Ku (Ban Gu), revised and continued a work begun by his father Pan Piao (Ban Biao; d. a.d. 54), and his own work was completed by his sister, Pan Chao (Ban Zhao), after his death in 92. It covers the period from the founding of the dynasty in 206 b.c. to the death of the usurper, Wang Mang, in a.d. 23. The most important part for providing information on Iran is the “Monograph on the Western Regions” (chap. 96). Other material is found in the “Monograph on the Hsiung-nu (Xiongnu)”(chap. 94) and in the biographies of envoys and generals who were involved in Han relations with the west.

One of Ten Prized Hounds From the National Palace Museum in Taiwan “Lang Shining (Giuseppe Castiglione, 1688-1766), Qing dynasty . Emperor Qianlong was well known for his love of hunting and kept large kennels. He was particularly fascinated with the hunting sighthound of the Middle East .

In the early part of the work, down to about the beginning of the first century b.c., Pan Piao and his son mostly based themselves on the *Shih-chi* (*Shiji*) of Ssuma Ch’ien (Sima Qian), making only minor changes of wording for stylistic reasons. The matter is complicated, however, by the claim that has been made that certain parts of the *Shih-chi* were lost and later restored from the *Ch’ien Han shu*, including the “Monograph on Ta yüan (Dayuan)” in the *Shih-chi*, which corresponds to the “Biographies of Chang Ch’ien (Jung Qian) and Li Kuang-li (Li Guangli)” (chap. 61) and substantial parts of the “Monograph on the Western Regions” (Hulsewe, 1975, 1979). For arguments supporting the contrary opinion, that the present text of the *Shih-chi* is the primary source for the corresponding parts in the *Ch’ien Han shu*, see Pulleyblank (1970, 1981).

The first Chinese contacts with the Iranian world that are recorded in the *Ch’ien Han shu* came about through the famous mission of Chang Ch’ien (Zhang Qian) in search of the Yüeh-chih (Yuezhi), who had migrated westward after being defeated by the Hsiung-nu and whom the Chinese hoped to enlist as allies against their nomadic enemies. In about 126 b.c.e., on the banks of the Oxus, Chang Ch’ien found the Yüeh-Chih, who had conquered the Greek kingdom of Bactria. His return to China was followed by a period of intense Chinese diplomatic and military activity in the west; the Silk Road across Central Asia was opened, and in 104-101 b.c.e. expeditions were led by Li Kuang-li against Ta-yüan (probably located in Sogdia proper, rather than Ferghana, as is usually said) to obtain “blood-sweating heavenly horses.” A protector-general of the Western Regions was appointed in 59 b.c.e. to bring under control the states of the Tarim basin, which had previously been subject to the Hsiung-nu. Much of the material in the “Monograph on the Western Regions” probably comes from information gathered at his headquarters. In 38 b.c.e. there was a second Chinese military expedition to the far west, described in the “Biographies of Ch’en Tang (Chen Tang) and Kan Yen-shou (Gan Yenshou)” (chap. 70), this time to K’ang-chü (Kangju; Tashkent), against the dissident Hsiung-nu chieftain Chih-chih (Zhizhi), who had established himself as overlord in that region. There is reason to believe that some information about Afghanistan and Sogdia was added from a report by Pan Ku's brother, Pan Ch'ao (Ban Chao), on his return from a military expedition to Khotan and Kashgar in 74-75 c.e. (Pulleyblank, 1968, p. 251).

After an introduction summarizing Chinese relations with the west during the Former Han period, "The Monograph on the Western Regions" outlines an itinerary along the southern route through the Tarim basin from Lou-lan to Khotan, across the Hanging Pass to Chi-pin (Jibin; Kashmir), and beyond to Wu-i-shan-li (Alexandria = Kandahar or Herat?) and An-hsi (Anxi; Parthia). More distant countries that are mentioned include T'iao chih (Tiaochi; Seleukia; see Wu, 1977) and Li-chien (Lijian; probably originally Hyrcania, later confused with Ta-ch'in/Daqin, the Roman Orient). The route then turns north and east via Great Yüeh-chih (Bactria), K'ang-chü, and Ta-yüan (Sogdia; the locations and relative strengths of these countries were not constant throughout the period). Re-entering the Tarim basin via the Pamirs, the route passes through Shu-le (Kashgar) and, after an account of the nomadic Wu-sun at the western end of the T'ien-shan (Tienshan), proceeds eastward back to China along the northern side of the Tarim basin.


Kublai Khan on a traditional Mongol hunting expedition. Painted by Liu Guandao, 1280. Now located in the National Place Museum in Taipei.

In addition to brief descriptions of the Iranian inhabitants of Parthia, Bactria, Transoxania, and the city states at the western end of the Tarim basin (Kashgar and Khotan), the *Ch'ien Han shu* has references to the Iranian Sai (Sakas) both as invaders of Chi-pin, when they moved south under pressure from the Yüeh-chih, and as inhabitants of small states in the Pamirs. It has also sometimes been claimed that the Yüeh-chih, who had originally migrated from Kansu (Gansu), were Iranians; in the opinion of the present author, however, they were most probably Tocharian speakers, as were the Wu-sun and also the K'ang-chü, who first occupied the region around Tashkent and then moved south into Sogdia (Pulleyblank, 1966). Recently H. W. Bailey (1981) has claimed that the Hsiung-nu may have spoken an Iranian language, but his argument, which is based on possible Iranian etymologies for some Hsiung-nu words transcribed in Chinese, is not very convincing. The cultural affinities between the Hsiung-nu as described by Ssu-ma Ch'ien and the Scythians as described by Herodotus are probably to be explained by the rapid spread of full-scale nomadism and the associated technique of cavalry warfare from west to east across the Eurasian steppes during the first millennium b.c.e. The language of the Hsiung-nu is not known with certainty, but there are some grounds for thinking it may have been related to that of the present day Ket in Siberia (Ligeti, 1950; Pulleyblank, 1962).

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(Edwin G. Pulleyblank)

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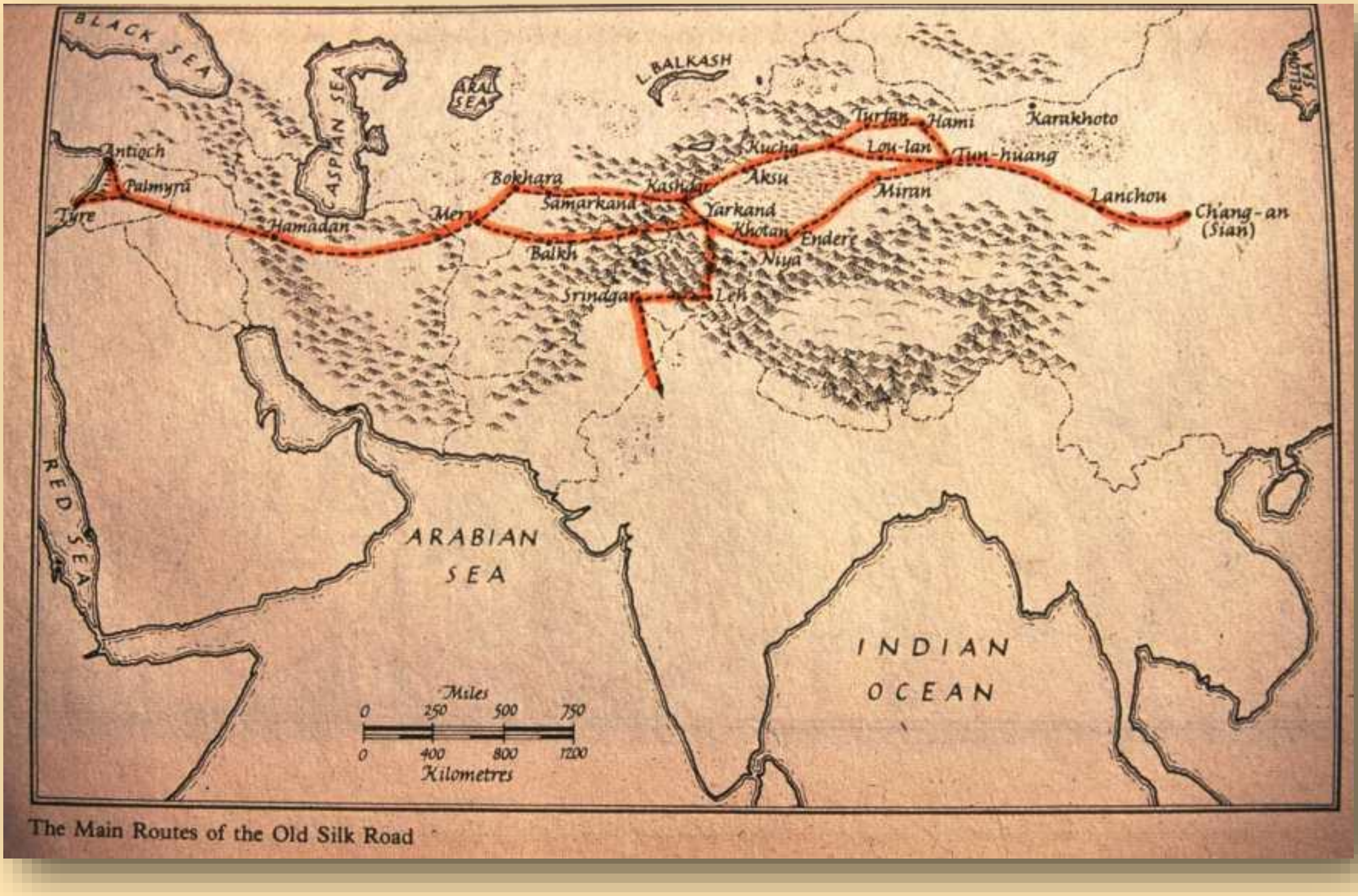


The Main Routes of the Old Silk Road

The Silk Road was a network of trade routes connecting China and the Far East with the Middle East and Europe. Established when the Han Dynasty in China officially opened trade with the West in 130 B.C., the Silk Road routes remained in use until 1453 A.D., when the Ottoman Empire boycotted trade with China and closed them. Although it's been nearly 600 years since the Silk Road has been used for international trade, the routes had a lasting impact on commerce, culture and history that resonates even today.

Qushabee's gifts Treasured Always

Gayle Marks - Wisconsin

Melik Boorchin O'rod

Melik Boorchin Parveneh

MBISS GCHS TAMARISK DIWAN JOVIAL NAIRANG E SKYE TKN (Jovie)

Multiple group
placing
SBIS x 4
2018 #8 saluki
2019 #6 saluki

NATIONAL SPECIALTY AWARD OF MERIT
Thank you judge Deric Aube

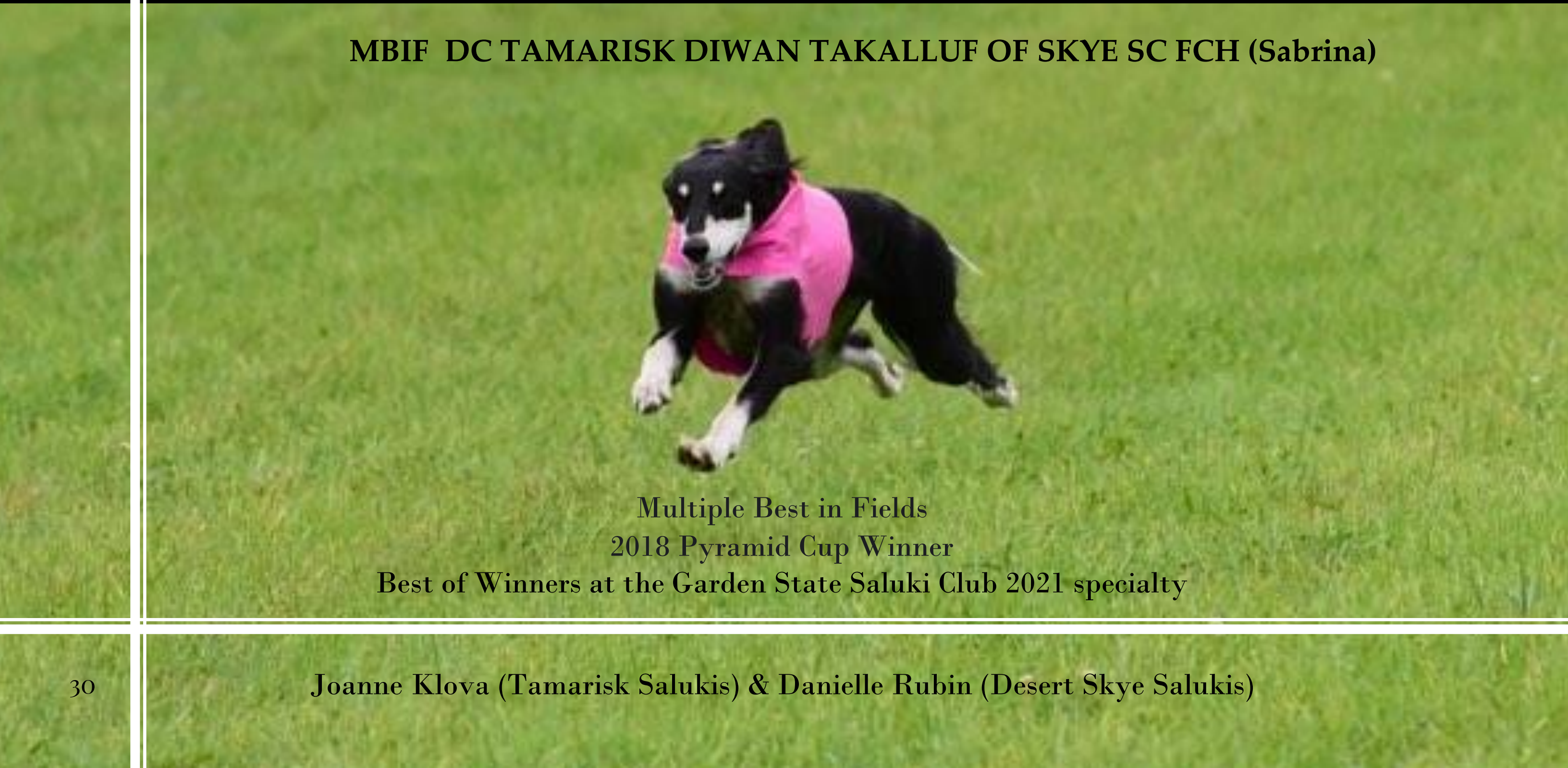
BEST IN TOP 20 (2020 Qualifying year-judged virtually)
Thank you judges Dee Laurie Beaumont, Melissa Williams, & Cheryl Paterson

RESERVE BEST IN TOP 20 & PEOPLE'S CHOICE
(2019 Qualifying year)
Thank you judges Lex Robertson, Anne Midgarden, & Debbie Feliciano and audience.

BISS AT LIBERTY SALUKI CLUB'S 1st
Independent Specialty
Thank you judge Starr White

4th Generation and Beyond!!

MBIF DC TAMARISK DIWAN TAKALLUF OF SKYE SC FCH (Sabrina)



Multiple Best in Fields
2018 Pyramid Cup Winner
Best of Winners at the Garden State Saluki Club 2021 specialty

Joanne Klova (Tamarisk Salukis) & Danielle Rubin (Desert Skye Salukis)

Achievements:

Trick Dog Novice

UKC Champion

Senior Courser

ASFA
Field Champion

◆

Notable:

AKC Best in Field
Chickasha,OK

MBIF Rataki Yalda De Valle Compel SC,TKN,FCh

Melik Nadin Jenn CC,CM x Rataki Valle Voo

Generation 3

Priah!!!!!

Marissa Jo Wagenaar -Topeka, Kansas

*Nazee, FCh, VFCh

Import, Iran

12/09/2004 – 04/23/2021

© Big Paw Prints 2009

The End of an Era

*Nazee's love of the lure earned her:

- The Bill Henry Cup in the 2010 ASFA International Invitational.
- The ASFA Pyramid Cup at the Saluki Club of America's National Specialty, first in 2010 to finish her Field Championship, and again in 2012 as a veteran.

In addition to being a great ambassador for the breed and for desert breds, *Nazee ran our house with the same intensity she brought to lure coursing.

ASH-SHI'RA **BILL AND SUSAN SCHR**

On the road of life

The Beginning of New One

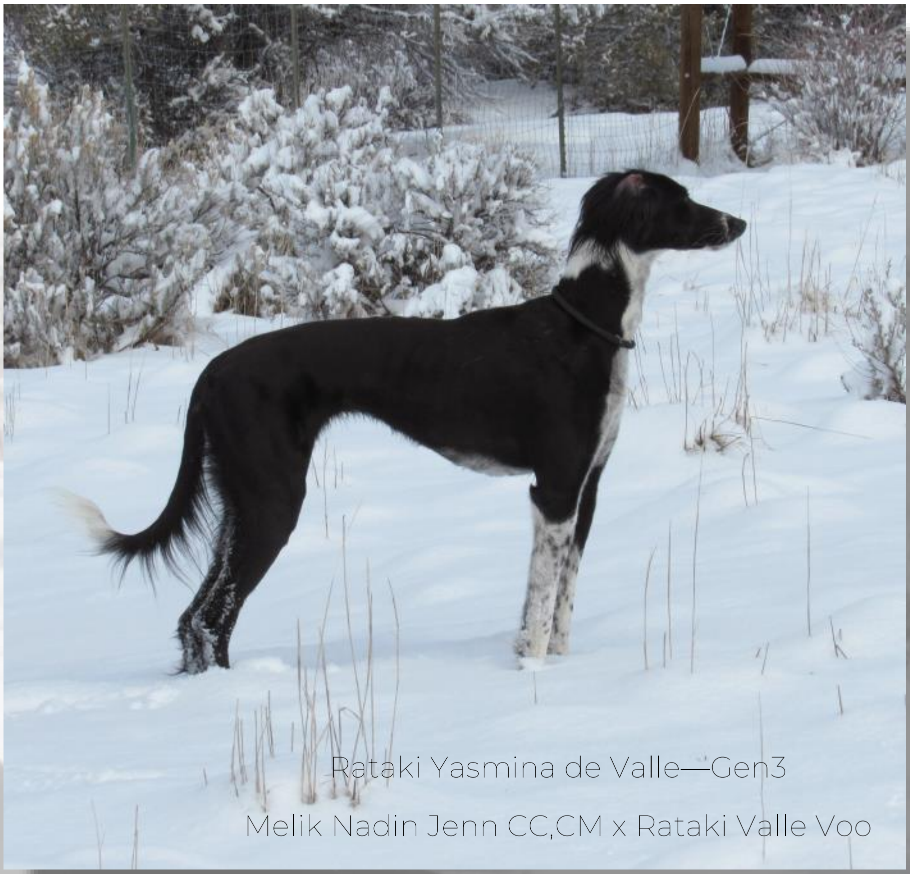
Yaar-Jan made his lure coursing debut in 2021, running in six trials, earning four Best of Breeds with competition including winning the ASFA Region 5 Invitational AmunRa Cup, and two 2nd placements – both to his sister Priah. He has 62 points towards his Field Championship and tied for #10 in the 2021 ASFA 20 Salukis. We are looking forward to seeing what the coming years hold for him.

Most importantly, Yaar-Jan has sense of fun and love of cuddles that are unrivalled.

Rataki Yaar-Jan at Ash-Shi'ra

(Melik Nadin Jenn x Rataki Valle Voo)

06/28/2019



Rataki Yasmina de Valle—Gen3

Melik Nadin Jenn CC,CM x Rataki Valle Voo

Rataki Salukis Can't stop running!

Rataki Xyla has 3 Best of Breeds in NOFCA AND she finished in the top ten in Salukis in ASFA.

Rataki Yasmina de Valle is now placed and pointed in NOFCA in her first year with limited competing.

ZOOM ZOOM!

Rataki Xyla—Gen1

Melik Khaliis x *Aram de Diba of Boorchin

Rataki Salukis

Lorraine Trenholm

rataki2@capecod.net

Running Off Lead - A Free Coursing Primer

By Paul Domski

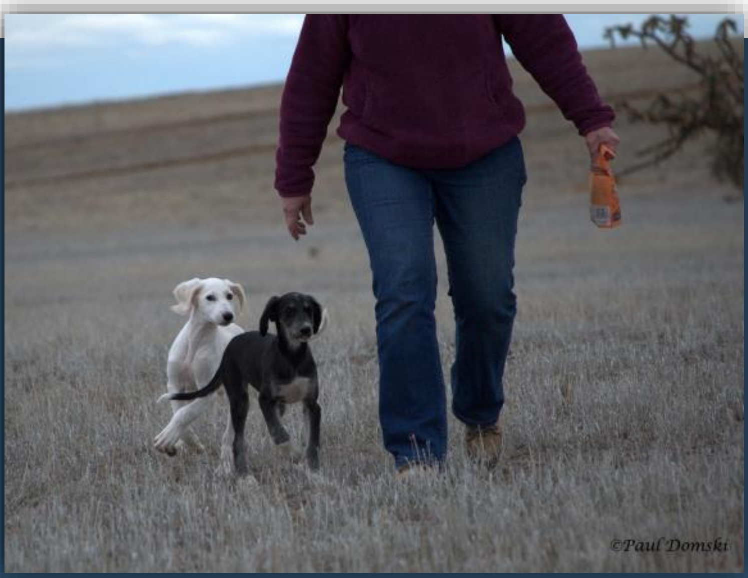
Over the years I've met many saluki owners who would love to let their salukis run free but have a great fear of doing so. Most are afraid that once their treasured companion realizes they are no longer confined to an 4' lead they'll take off never to return, or maybe they'll chase a deer or some other creature and become lost, or they'll run to the nearest road and put themselves in grave danger. Those are all legitimate concerns and risks that need to be minimized when making the decision to run off lead.

My wife and I have been free coursing our salukis since we got into the breed nearly 20 years ago. In the beginning we didn't give it much thought; we have access to large tracts of New Mexico prairie where we would regularly go to practice falconry. Naturally, the dogs were always with us so it evolved organically. As the years passed and we acquired more salukis we learned many more things and we really started focusing our attention on the dogs and free coursing jack rabbits. We are lucky to live where we can and do have the opportunity for these activities, but even if you live in the steamy south, or the forested hills of the New England you can still give your saluki the opportunity to run free while you enjoy their beauty doing what they've been bred through the eons for – running. There exists no happier and more content (and tired!) saluki than one that gets to run unleashed, full speed through the countryside.

Location, Location, Location

For running off lead you'll want to find a location that's as remote, as far away from roads and other people as possible, a place where you have permission to walk and preferably a location that offers some large open fields. I use an app called onXMaps (onxmaps.com) which uses satellite imagery and superimposes property boundaries, for public, private, and tribal lands, and provides ownership

Exploring a new world.



©Paul Domski

Don't forget the treats!

information. I find this app to be indispensable when it comes to identifying potential new areas to run my dogs, it works both on my phone and on my home computer so I can research new areas on the big screen. Here in New Mexico, I like to explore NM State Trust lands and federal lands, mostly Bureau of Land Management (BLM) properties and national forest lands. In states where public lands are uncommon, you'll need at to look at private land and knock on some doors for permission.

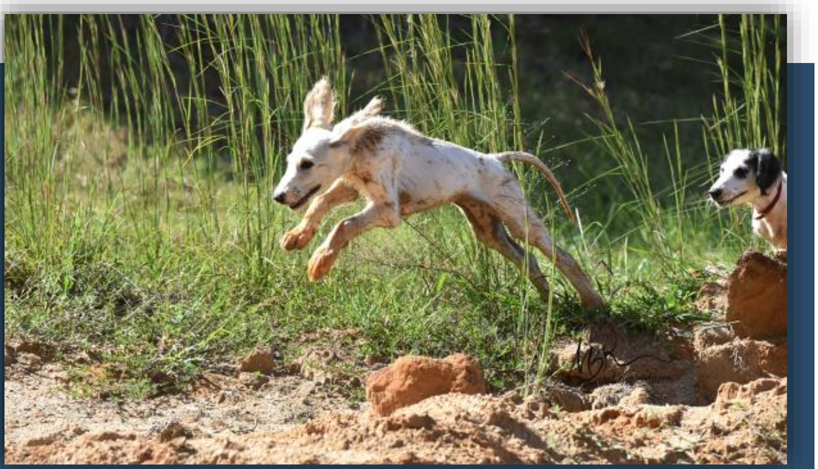
In terms of terrain, salukis are highly adaptable to nearly all situations and can differentiate and adjust their behavior depending on the type of country you are in. For example, in the forest they'll tend to stay closer and check in more frequently compared to when you're walking in the prairie where the sightlines are much longer and visual contact is maintained. This quality makes it possible to run your saluki off leash pretty much anywhere there is adequate space.

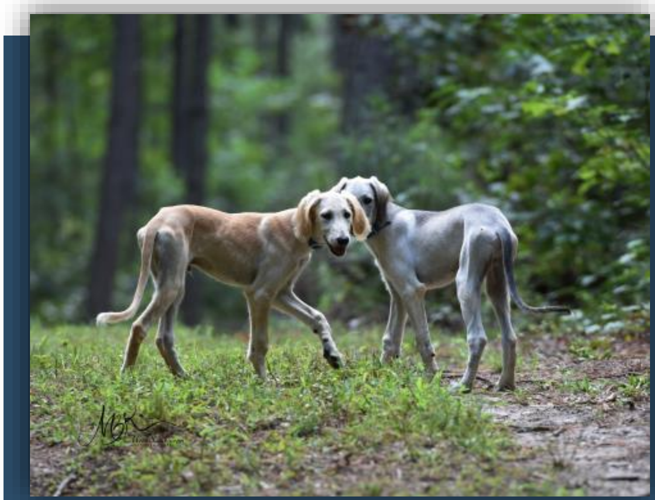
Start Them Young

Your best insurance to keep your saluki safe in the field is to start them young, not to say you cannot run your older dogs off leash too. I'll talk about starting both young and older salukis on off-leash adventures. We typically pick up our pups when they're around twelve weeks old and field training starts immediately. Up until they're around 6-8 months saluki puppies won't stray far from you, so it's the perfect time to get them accustomed to the many things they need to learn in the field. Work with them at home and figure out their favorite treat, and then in the field every time the pup returns, we load on the praise and reward them with a small treat. This early recall work pays off as they grow up.

During this early developmental period, before they can run really fast, they learn "field craft", for example, how to negotiate fences (more on this in a minute), which plants are not fun to step on (we have a lot of cactus here in NM), how to move and control

I can FLY!!!




Not lost in the woods.

their bodies in the natural world, and most importantly the basics of homing.

Salukis seem to have the innate ability to home; they can run far out of our sight range and return to the point where they started. I believe that this is an instinctual behavior, and I also believe that it is improved if it's cultivated from a young age. Play a game of hide and seek in the field with your youngster, when they run out 50 – 100 yards, you lay down or hide behind a bush and wait, then when they find you give them a treat and praise them, it goes a long way to developing their homing instinct. I've brought dogs to fields where they've never run before and they'll chase a hare far out of sight, and then like a miracle you spot them on the horizon through your binos coming towards you, still a half mile out and you realize they are following their track that they took out when they were chasing the hare to return to you.

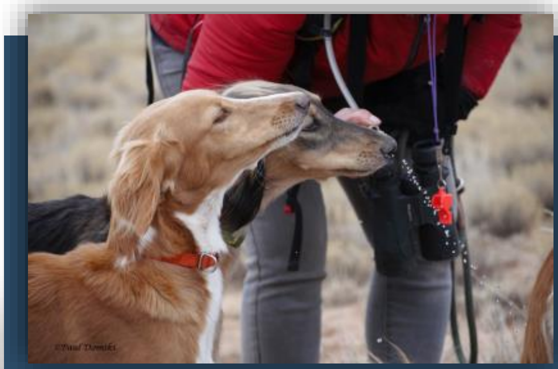
Now, a word about tracking collars, they are worth their weight in gold and can eliminate a lot of the worry that goes along with running your saluki off lead. It's important to remember that they are not a substitute for training your dog. Do not wait until your dog is lost to learn how to use your collar. Practice using the collar before you go to the field with your dog. Find a friend and play a game where they walk, or ride a bike. Give them a half hour lead time, and then go and track them down. The time to learn how to use a tracking collar is NOT when your dog may be lost.

If you plan to run your dogs in areas with barbed wire fences, or stone hedge rows with barbed wire, your dog will need to learn how to navigate through them. Barbed wire fences are ubiquitous in the western landscape and it's crucial for the dog's safety to learn how to go through them at full speed. There's no better time to learn about fences than as a puppy. We train ours by walking along a fence line, with a supply of treats, and as the puppy naturally will be running and playing, we'll toss treats to the other side of the fence and the pup will cross over and back effortlessly. Maintaining this game as the puppy grows teaches them how to go under a fence and avoid the barbs. Once they're full grown and chasing a hare at full speed, they know to slow down and go through unscathed. Accidents do happen, we've had plenty of cuts and scratches and the occasional bad laceration, but those are rare. Salukis are smart and tough-skinned and will slow down to go through fences, and unlike their faster thinner-skinned cousins, the greyhound, they rarely get badly hurt.


Tracking collar fashion model.

The Older Saluki

While there are many advantages to starting your off-



Drinking in the field can be tricky!

leash adventures with your saluki as a youngster, it doesn't mean that can't let your older saluki run off lead. To get started I would recommend walking your older saluki on leash for the first few visits in the area where you intend go off leash. This has a few advantages, first you get to learn the lay of the land of the animals that inhabit the area, and secondly, your dog also learns the lay of the land and lays down a scent trail that later can aid them if you become separated. Once off-lead you may find your older saluki will tend stay closer to you because that's all they've known all their lives. After they get accustomed to their newfound freedom they'll begin to explore and takes romps and return to you with that unforgettable saluki smile.

Essential items for your backpack

- ♦ Water
- ♦ Treats
- ♦ Spare leash
- ♦ Hemostats
- ♦ Vet Wrap
- ♦ Elastikon tape
- ♦ Medical scissors
- ♦ Styptic

Wildlife

As you get to know an area, whether from field training your young saluki, or getting an older dog familiar with a new area, you'll start to figure out the natural rhythm of the animals that live there. Pay attention to the times of the day when different species are active and where they can be found. This information will inform you on the best time and place to let your saluki run free. It's the larger species of mammals, deer, pronghorns, coyotes, etc. that you'll need to be cognizant of because they can run for long distances and lead your dog astray. Small animals like rabbits and squirrels offer recreational opportunities and usually don't have to run very far to find safe haven. The exception being the jack rabbit, but I'll assume that if you're in area with jacks that you are already familiar with chasing them with your saluki. Also, familiarize yourself with hunting seasons and avoid those times and places where there may be active hunting.

Learning from your elders!

Conclusions

Nothing that we do in this life is free of risk, from getting out of bed in the morning to the commute on the interstate, we are constantly putting ourselves and the ones we love in danger. The same holds true when we choose to let our salukis run off leash; there's always that possibility they'll sustain an injury, or much worse. The best we can do is make ourselves aware of the risks and make all attempts to mitigate and minimize them. By finding some good country and preparing yourself and your saluki, you can allow them the freedom run uninhibited, allowing them to truly be themselves. There is no happier saluki than one that gets to run free on a regular basis.

Let's run naked!

RESEARCH ARTICLE

True Colors: Commercially-acquired morphological genotypes reveal hidden allele variation among dog breeds, informing both trait ancestry and breed potential

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Abstract

Direct-to-consumer canine genetic testing is becoming increasingly popular among dog owners. The data collected therein provides intriguing insight into the current status of morphological variation present within purebred populations. Mars WISDOM PANELTM data from 11,790 anonymized dogs, representing 212 breeds and 4 wild canine species, were evaluated at genes associated with 7 coat color traits and 5 physical characteristics. Frequencies for all tested alleles at these 12 genes were determined by breed and by phylogenetic grouping. A sub-set of the data, consisting of 30 breeds, was divided into separate same-breed populations based on country of collection, body size, coat variation, or line-ages selected for working or conformation traits. Significantly different ($p \leq 0.00167$) allele frequencies were observed between populations for at least one of the tested genes in 26 of the 30 breeds. Next, standard breed descriptions from major American and international registries were used to determine colors and tail lengths (e.g. genetic bobtail) accepted within each breed. Alleles capable of producing traits incongruous with breed descriptions were observed in 143 breeds, such that random mating within breeds has probabilities of between $4.9e^{-7}$and 0.25 of creating undesirable phenotypes. Finally, the presence of rare alleles within breeds, such as those for the recessive black coloration and natural bobtail, was combined with previously published identity-by-decent haplotype sharing levels to propose pathways by which the alleles may have spread throughout dog breeds. Taken together, this work demonstrates that: 1) the occurrence of low frequency alleles within breeds can reveal the influence of regional or functional selection practices; 2) it is possible to visualize the potential historic connections between breeds that share rare alleles; and 3) the necessity of addressing conflicting ideals in breed descriptions relative to actual genetic potential is crucial.

Introduction

Guided by human selection, the domestic dog (*Canis lupus familiaris*) has become one of the most physically diverse species, with hundreds of recognized breeds, differentiated from each other by specific morphological and behavioral characteristics [1]. One of the most readily accessible and easily visualized defining characteristics of dog breeds is in their presentation of pigmentation and color patterns. The nomenclature used currently to refer to dog pigmentation genetics was outlined by Little in 1957 [2]. Scientific advancement since that time has allowed for the validation of many of his postulated loci and the identification of causal genetic variants for many of the common coat colors in the species. These coat color and trait variants are increasingly included in commercially-available genetic test panels, the emergence of which has contributed greatly to the acceptance and implementation of genetic screening of purebred dogs by owners, breeders, and veterinarians. In addition to providing valuable information regarding the genetic status of potential breeding dogs in terms of disease state and morphological traits, the combined genotype databases collected by these commercial entities provide a valuable resource for monitoring the diversity of selected alleles, such as those driving coat color, within breeds.

"The entirety of coat color patterns in mammals consist of spatial and temporal production of phaeomelanin, yellow- to red-based pigment, and eumelanin, black- to brown-based pigment, controlled by the interaction of multiple genes."

The entirety of coat color patterns in mammals consist of spatial and temporal production of phaeomelanin, yellow- to red-based pigment, and eumelanin, black- to brown-based pigment, controlled by the interaction of multiple genes. In dogs, variation at the Agouti Signaling Protein (ASIP) gene determines the distribution of eumelanin and phaeomelanin across the body of the dog and along the individual hair shafts, as dictated by a four-allele dominance hierarchy: a^y (fawn) > a^w (wolf sable) > a^t (tan points) > a (recessive black) [3–5]. However, regardless of the accompanying *ASIP* genotype, the *Melanocortin 1 Receptor (MC1R)* gene determines the ability of a melanocyte to produce eumelanin at all, presenting its own dominance hierarchy of four alleles: E^M (melanistic mask) > E^G (grizzle/domino) > E (wild type) > e (recessive red) [6–8]. While the E^M, E^G, and E alleles all allow for the production of both eumelanin and phaeomelanin, dependent on the pattern dictated by *ASIP*, homozygous inheritance of e prevents eumelanin production, resulting in a completely phaeomelanin color [6–8]. Further, the dominant derived K^B allele of *Canine Beta-Defensin 103 (CBD103)* prevents the production of patterning by *ASIP*, resulting in a solid eumelanin phenotype when combined with a dominant *MC1R* genotype, or a solid phaeomelanin phenotype when combined with a *MC1R* genotype of e/e [9]. In this way, inheritance of homozygous e at *MC1R* or dominant K^B at *CBD103* are epistatic to any of the *ASIP* phenotypes [8,9]. In addition to the dominant K^B and recessive k^y alleles of *CBD103*, an intermediate allele, k^{br}, produces the brindle coat color pattern with alternating stripes of eumelanin and phaeomelanin [10]. However, due to the complex structural nature of the k^{br} allele, which has never been reliably defined and remains unpublished, it was not possible to distinguish between it and K^B for the purposes of this paper.

"An intermediate allele, k^{br}, produces the brindle coat color pattern with alternating stripes of eumelanin and phaeomelanin."

The base phaeomelanin and eumelanin pigments can be altered by a number of modifier genes, of which *Tyrosinase Related Protein 1 (TYRP1), Proteosome Subunit Beta 7 (PSMB7), Microophthalmia-associated Transcription Factor (MITF),* and *RALY heterogeneous nuclear ribonucleoprotein (RALY)* are explored further in the scope of this paper. *TYRP1* alters all eumelanin in hair and skin evenly from black to brown, and presents as a compound heterozygote with at least four alternate recessive alleles: b^s, b^c, b^d, and a variant that has thus far only been described in the Australian Shepherd [11–13]. *PSMB7* expression produces the harlequin pattern of white, dilute, and deeply pigmented patches only when inherited along with the merle phenotype of *Premelanosome 17* (*PMEL17*, not tested in the present study) [14–16]. The *harlequin* variant is homozygous lethal, so the pigmentation phenotype is only expressed when inherited heterozygously [14]. *MITF* expression produces white spotting on top of a regularly pigmented background and, depending on the breed background involved, is inherited as a co-dominant or recessive phenotype [17,18]. Expression of *RALY*, in combination with other yet-unknown genetic modifiers, alters a tan point background pattern, produced by the at allele of *ASIP*, such that the tan points, normally restricted to the paws, muzzle, eyebrows, and chest, extend up the extremities, forming a eumelanin "saddle-shaped" pattern on the dog's dorsal surface [19]. Expanding beyond pigmentation patterns, other phenotypic traits that are controlled by a relatively small number of genes and can be easily visualized include hair length and texture, tail length, muzzle length, and ear shape. Three genes, *Fibroblast Growth Factor 5 (FGF5), R-spondin 2 (RSPO2*, not tested in the present study), and *Keratin 71 (KRT71)*, define much of the coat type variation between dog breeds [20–24]. Specifically, expression of recessive *FGF5* variants produce a long coat, a dominant *RSPO2* variant produces longer hair specifically on the muzzle and eyebrows, and at least two variants in *KRT71*, one of which was tested in this study, produce a curly coat [20–24]. The tailless trait, whereby a dog is born with a truncated or absent tail, is caused in some breeds by a variant in the *T brachyury transcription factor (T)* gene [25,26]. Like harlequin, taillessness is homozygous lethal, so will be expressed viably only in heterozygotes [25,26]. Ear set and muzzle length are traits that are very likely impacted by numerous genetic variants, however a marker on canine chromosome 10 is known to segregate in some cases for erect versus drop ears [27,28], and the *Bone Morphogenic Protein 3 (BMP3)* gene is associated with foreshortening of the face [29]. A variant in *SMOC2* has also been shown to contribute to muzzle length, though it is not included in the present study [30].

> *"The base phaeomelanin and eumelanin pigments can be altered by a number of modifier genes."*

Epistatic effects are prevalent within coat color and morphological variation in the dog. We have previously mentioned epistasis between a homozygous non-functional genotype at *MC1R* or a dominant variation at *CBD103* with the ability to express *ASIP*-driven phenotypes. However, canine coat color also presents scenarios whereby a specific allelic background is required for expression of a modifier. This is exemplified in the requirement of the merle phenotype of *PMEL17* in order to express the harlequin pattern of *PSMB7*, the necessity for an a^t tan point base pattern at *ASIP* to display the *MC1R* grizzle or *RALY* saddle tan phenotypes, and a moderate to long hair length to produce a *KRT71* curly coated phenotype. On an incompatible background, presence of some gene variants may remain unexpressed for generations or, as many breeds are fixed for only a small number of phenotype options, may remain completely unobserved. As national and international breed organizations are charged with defining their breed's characteristics, which are then regulated by registering bodies such as the American Kennel Club (AKC), United Kennel Club (UKC), The Kennel Club (KC) in the United Kingdom, or Fe´de´ration Cynologique Internationale (FCI), failure of breed standards to account for rare—though naturally occurring—variation can lead to frustration or confusion when unexpected traits are expressed. That same existence of rare variants within breeds–which, due to epistasis and genetic back-ground, may never express the associated phenotypes—can provide intriguing information regarding the development of, or relationships between, breeds throughout history.

"Our primary objective for this study was to evaluate:
1) the breed-type distribution of morphologic variants;
2) the implications of founder effects and/or selection preferences between geographically or behaviorally independent populations of the same breed;
3) the breed-specific carrier status of variants disallowed within breed standard descriptions; and
4) the ancestral connections between breeds that share rare trait-causing variants."

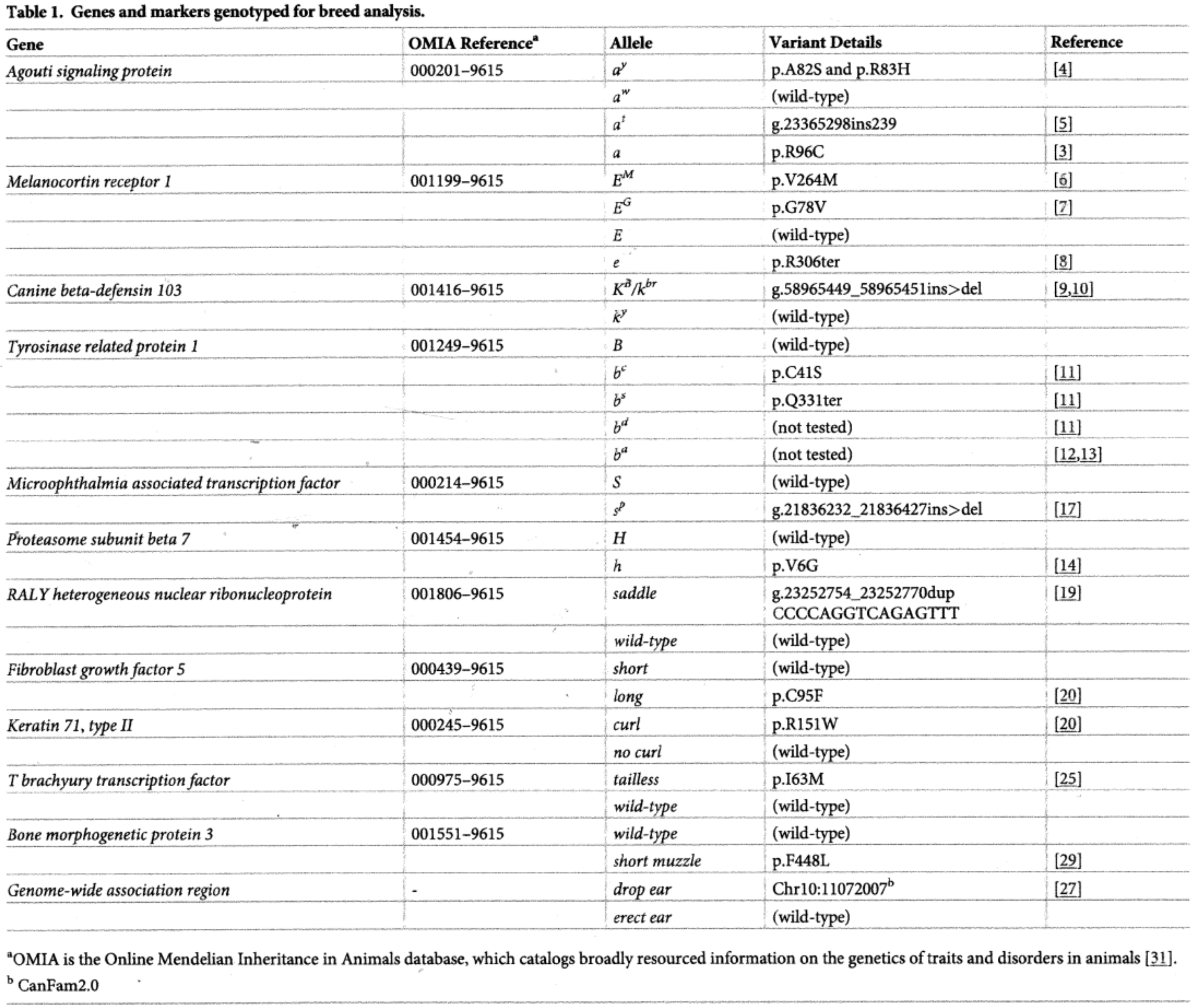

Table 1. Genes and markers genotyped for breed analysis.

Gene	OMIA Reference[a]	Allele	Variant Details	Reference
Agouti signaling protein	000201–9615	a^y	p.A82S and p.R83H	[4]
		a^w	(wild-type)	
		a^t	g.23365298ins239	[5]
		a	p.R96C	[3]
Melanocortin receptor 1	001199–9615	E^M	p.V264M	[6]
		E^G	p.G78V	[7]
		E	(wild-type)	
		e	p.R306ter	[8]
Canine beta-defensin 103	001416–9615	K^B/k^{br}	g.58965449_58965451ins>del	[9,10]
		k^y	(wild-type)	
Tyrosinase related protein 1	001249–9615	*B*	(wild-type)	
		b^c	p.C41S	[11]
		b^s	p.Q331ter	[11]
		b^d	(not tested)	[11]
		b^a	(not tested)	[12,13]
Microophthalmia associated transcription factor	000214–9615	*S*	(wild-type)	
		s^P	g.21836232_21836427ins>del	[17]
Proteasome subunit beta 7	001454–9615	*H*	(wild-type)	
		h	p.V6G	[14]
RALY heterogeneous nuclear ribonucleoprotein	001806–9615	*saddle*	g.23252754_23252770dup CCCCAGGTCAGAGTTT	[19]
		wild-type	(wild-type)	
Fibroblast growth factor 5	000439–9615	*short*	(wild-type)	
		long	p.C95F	[20]
Keratin 71, type II	000245–9615	*curl*	p.R151W	[20]
		no curl	(wild-type)	
T brachyury transcription factor	000975–9615	*tailless*	p.I63M	[25]
		wild-type	(wild-type)	
Bone morphogenetic protein 3	001551–9615	*wild-type*	(wild-type)	
		short muzzle	p.F448L	[29]
Genome-wide association region	-	*drop ear*	Chr10:11072007[b]	[27]
		erect ear	(wild-type)	

[a] OMIA is the Online Mendelian Inheritance in Animals database, which catalogs broadly resourced information on the genetics of traits and disorders in animals [31].

[b] CanFam2.0

We utilized custom genotyping array data from Mars Wisdom Health for 11,790 canids, representing 212 pure breeds and 4 wild canine populations (S1 Table), genotyped for seven coat color and five physical characteristic genes, as curated by OMIA [31] (Table 1). For each of these genes, we determined the frequency of each allele within each breed. Note that for one gene (*TYRP1*) not all alleles could be tested, these are indicated in Table 1. Our primary objective for this study was to evaluate: 1) the breed-type distribution of morphologic variants; 2) the implications of founder effects and/or selection preferences between geographically or behaviorally independent populations of the same breed; 3) the breed-specific carrier status of variants disallowed within breed standard descriptions; and 4) the ancestral connections between breeds that share rare trait-causing variants.

Results

Unexpectedly broad distribution of trait-causing alleles across breeds

Marker genotypes were combined to interpret the actual biallelic genotypes for each of the queried genes for every dog in the dataset. Individuals of the same breed were combined to calculate breed allele frequencies and are reported in S2 Table. Breeds were assigned to phylogenetic clades as previously reported [32,33] (S1 Table). Breeds not included in the earlier phylogenetic studies were assigned to defined clades based on known breed history, phenotypic commonalities, and geographic region of origin (indicated by parentheses in S1 Table).

Over all combined breeds, the ancestral allele (Table 1) predominates at all genes, except for *ASIP* and *MC1R*, where derived alleles account for 82% and 57% of alleles, respectively. The derived alleles at lowest frequency across all 11,790 canids are E^G (grizzle/domino) of *MC1R* and *tailless* of *T*, each representing ~1% of all alleles detected within their respective genes. E^G, which produces the grizzle or domino pattern when combined with a^t tan points at *ASIP*, is present in 28 breeds, with highest frequencies recorded in Borzois (56%), Polish Greyhounds (43%), and Salukis (31%). Cladistic representation of the E^G allele is heavily weighted to those breeds in the Mediterranean and UK Rural clades (Fig 1), with 60% and 31% of all E^G alleles in our dataset arising from those clades, respectively.

> *"The derived alleles at lowest frequency*
> *across all 11,790 canids are*
> *E^G (grizzle/domino) of MC1R*
> *and tailless of T,*
> *each representing ~1% of all alleles detected*
> *within their respective genes."*

Assignment of biallelic genotypes for the *ASIP* gene based on genotype tests for a^y, a^t, and a, and a genotype of a^w by exclusion of the other three alleles, revealed the presence of unusual triple-allele combinations in a few dogs. In these cases, dogs would appear to genotype as a^y/a^t, plus an additional third allele. This genotyping outcome reflects a scenario where the a^y point mutations and the a^t SINE insertion occur on the same chromosome. The resultant combinatorial allele, termed a^{yt}, was identified in 14 domestic breeds across 10 clades, and the Dingo (S2 Table). Phenotype descriptions of the evaluated dogs were not available, so the effect of the a^{yt} allele on phenotype is presently unknown. The breed with the highest frequency of a^{yt} is the Dogo Argentino (33%), a predominantly white mastiff breed.

The *tailless* allele was detected in 48 breeds, with greatest frequencies in the Tenterfield Terrier (30%), Swedish Vallhund (18%), Spanish Water Dog (14%) and Australian Shepherd(13%). The remaining 44 breeds carry the *tailless* allele at <10%.

The recessive *a* allele of *ASIP* has previously been reported in six breeds (German Shepherd Dog, Belgian Shepherd, Schipperke, Australian Shepherd, Shetland Sheepdog, and Eurasier)[3–5]. We identified the allele in 89 breeds, documenting for the first time the presence of the allele in an additional 83 breeds (S2 Table). The *RALY* duplication required for the *saddle* modification of the tan point phenotype was detected in 203 breeds (S2 Table). The E^M "melanistic mask" allele of *MC1R* has previously been identified in only 11 breeds [3,7]. We identified E^M as present in 164 breeds, 153 not previously documented (S2 Table). In many breeds, the mask phenotype is not observable due to epistatic interactions with non-compatible genotypes, such as solid eumelanin or solid white.

> *"We identified E^M (black mask) as present in 164 breeds, 153 not previously documented"*

Four populations of wild canines were included in the analyses, although they are not counted as "breeds" in the analyses presented here. The wild canine populations had high levels of wild-type fixation across all genes evaluated (S2 Table). Eastern coyotes (n = 29) show a 2% frequency of the *MC1R* E^G allele and a 2% frequency of the *TYRP1* b^s allele. The Western coyotes (n = 19) have a 21% frequency of the *FGF5 long* allele. The Dingo samples (n = 12) show an 8% frequency of the *TYRP1* b^s allele. The marker for ear shape, and the causal variants in *RALY*, *MITF*, and *ASIP* are moderately variable across all four wild populations.

Cladistic patterns of allele distribution

Allele frequencies of *ASIP*, *MC1R*, and *CBD103* are graphically represented in Fig 1, relative to the phylogenetic groupings of the breeds. Association of allele frequency with cladistic assignment highlights multiple key tendencies in regards to color preference within breed-type groups. The cladistic distribution of *CBD103* alleles reflects a tendency toward fixation of a single allele within related breeds. The Hungarian, Pointer/Setter, Poodle, and Retriever clades contain breeds nearing fixation for the K^B/k^{br} variant, presumably primarily K^B due to the predominantly solid-colored phenotypes of breeds in these clades. Conversely, the Asian/Arctic, Mediterranean, New World, Scent Hound, and Terrier clades consist of breeds nearing fixation for k^y. Since the K^B allele produces a solid colored animal and is epistatic to alleles of *ASIP* and all *MC1R alleles* except for *e,* variation of *MC1R* and *ASIP* alleles is relatively uncontrolled

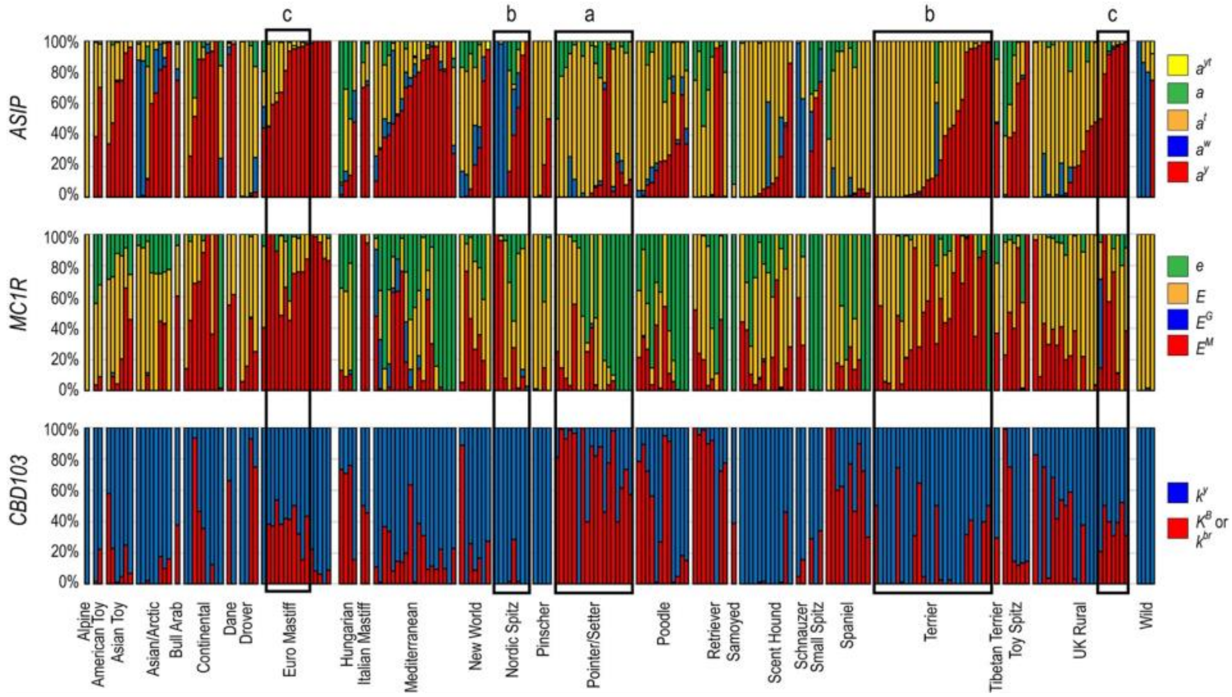

Fig 1. Allele frequencies for ASIP, MC1R, and CBD103 by phylogenetic breed relationship. Breeds are grouped by phylogenetic clade, as described, and sorted within clade by frequency of e and then ay to demonstrate patterns of phenotype expression across interacting genes. Thick black boxes highlight examples of color preference influencing interacting genes: a) Pointer/Setter breeds are commonly seen in solid colors, caused by the KB allele of CBD103 or the e/e genotype of MC1R. Since the solid-color genotypes are epistatic to the dominant alleles of MC1R and all alleles of ASIP, variation at those genes does not follow a trend for color preference. b) Related breeds with high frequency of the ky allele of CBD103 have a more structured pattern of ASIP allele preference. c) Breeds with a preference for the brindle pattern show heterogeneity for KB/kbr (reflective of a kbr phenotype) and high frequency of ay, required for the expression of brindle across

in breeds with a high frequency of K^B. Comparatively, clades with high frequency of the k^y allele show greater degrees of preference for the patterning alleles of *ASIP,* specifically a^y, a^w, *and* a^t. Clades with strong heterogeneity of *CBD103,* represented as multiple breeds within a clade with K^B frequency of 40–50% (e.g. Euro Mastiff, portions of UK Rural), are also those that consist of breeds presenting the brindle coloration. This is an accurate reflection of the present inability to distinguish between the brindle k^{br} and dominant black K^B alleles due to the complex genetic structure of the variants. Comparatively, clades with multiple breeds that show a 40–50% frequency of K^B likewise have a high frequency of a^y, the *ASIP* background that is necessary to produce brindling across the entire body of the dog.

The wild-type a^w allele of *ASIP,* while predominant in three of the four wild canine populations, is at greatest frequency in the spitz clades (Asian/Arctic, Nordic Spitz, Schnauzer). For *MC1R*, the *e* allele was identified in 24 of the 28 clades represented in this data, but it is seen at highest frequencies in hunting breeds (Pointer/Setter, Poodle, Retriever, Spaniel clades), continental sighthounds and flock guardians (Hungarian, Mediterranean clades), and white spitz breeds (Samoyed, Small Spitz clades). The melanistic mask allele, E^M, was likewise widespread, observed here in 164 breeds across 24 clades. Finally, the E^G allele is most prevalent in the Mediterranean clade, represented only sporadically in 11 other clades.

Allele frequencies for the nine remaining genes tested, sorted relative to phylogenetic breed relationships, are presented in S1 Fig. With the exception of the harlequin mutation, detected only in Great Dane and Yorkshire Terrier, all remaining gene variants were present broadly across all clades. There is no apparent excess of specific *TYRP1* brown alleles in any given clade or breed, despite, or perhaps due to, the identical phenotype produced by both alleles. Breeds fixed for the *MITF* SINE insertion, associated with piebald white spotting, are most abundant in the Pointer/Setter and Terrier clades, but are still widely distributed. Similarly, the *saddle* variant of *RALY* is seen in numerous clades, but is most abundant in the Euro Mastiff, Mediterranean, Scent Hound, and Terrier clades. Only eight breeds (AIRT, BEDT, IWSP, KOMO, LAKE, PULI, WELT, WFOX), in the Hungarian, Retriever, and Terrier clades are entirely fixed for the hair *curl* variant of *KRT71*. The *long* haired variant of *FGF5* is at the highest levels in the American Toy, Asian Toy, Continental, Hungarian, Poodle, Retriever, Small Spitz, and Spaniel clades. Conversely, the highest representation of the short haired wild-type genotype is in the Euro Mastiff clade. Toy breeds, Mastiffs, and Terriers represent the highest frequencies of the *BMP3 short muzzle* genotype. Finally, the only clades with breeds that are fixed for the *drop* ear marker are the Pointer/Setter, Retriever, Scent Hound, and Spaniel clades.

> *”the only clades with breeds that are fixed for the drop ear marker are the Pointer/Setter, Retriever, Scent Hound, and Spaniel clades.”*

Allele frequency is influenced by within-breed selection and geographic separation

Thirty breeds were divided into two or more distinct populations based on geographic region (27 breeds), body size (Dachshund and Poodle), coat type (Dachshund), and lineage or application, such as those selected for working applications (i.e. field, racing) or conformational traits (i.e. show) (6 breeds). All such populations were genetically distinguishable via principle components analysis (PCA). For the present study, allele distributions of the 12 tested genes between same-breed populations were evaluated for significance using either Pearson c^2 or Fisher’s Exact test (the latter was used when any allele grouping presented at <5 individuals). Distributions were deemed statistically significantly different at $p \leq 0.00167$, after correction for multiple testing. Nine breeds (BASS, BULM, DALM, KEES, MANT, POM, SCWT, WEIM, WELT) showed no significant difference between populations in allele distribution at any evaluated gene. The remaining 21 breeds had significant allele distribution differences between populations for at least one gene (Fig 2, S2 Fig). The gene with the greatest number of breeds displaying differences in allele distribution by population is *MC1R*, which was statistically different in 11 breeds (Fig 2). The *T* gene, responsible for the *tailless* phenotype, is not statistically different between populations of any breed (S2 Fig).

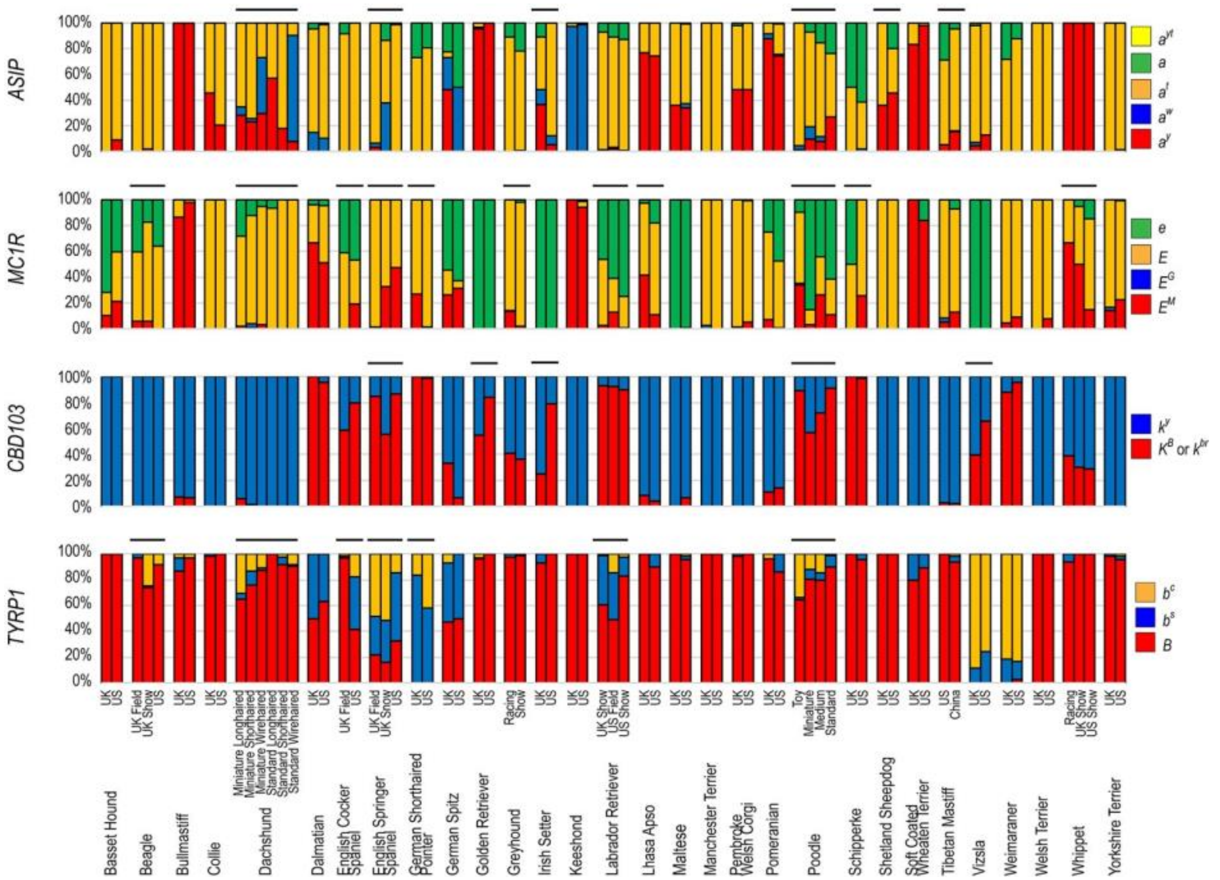

Fig 2. Allele frequencies for*MC1R*, *ASIP*, *TYRP1*, and *CBD103* across same-breed populations. Horizontal black bars indicate within-breed allele distributions that are significantly different ($p \leq 0.00167$).

The effect of same-breed population divergence is readily observable in the system of coat color gene interactions and epistasis. Five breeds (ESSP, GOLD, ISET, POOD, VIZS) have significantly different *CBD103* allele distributions between same-breed sample populations (Fig 2). Of these five breeds, three are uniformly fixed for an *MC1R* genotype of *e/e* (GOLD, ISET, VIZS), effectively preventing the expression of the phenotype variability that the different alleles of *CBD103* would otherwise produce. Conversely, regional phenotype preference can be seen in breeds such as the Labrador Retriever (Fig 2). The breed shows significantly different allele distributions by population for *MC1R* and *TYRP1*, indicating that US conformation show lines prefer yellow (*MC1R e/e*) dogs with black noses (*TYRP1 B/_*), UK conformation show lines prefer black (*MC1R E/_, TYRP1 B/_*) dogs, and US field lines consist mainly of brown (*MC1R E/_,TYRP1 b/b*) or yellow dogs (*MC1R e/e*) ($p \leq 0.003$).

The natural probability of disallowed traits in pure breeds

The approved phenotypes for each breed were determined based on the written breed standards of the AKC, FCI, UKC, and KC (Britain). Of the 212 breeds evaluated, 143 were observed to carry at least one allele that would result in an unfavorable phenotype, termed "fault", relative to at least one of the four queried breed registries (S3 Table). The breeds with the highest number of fault-causing alleles are the Treeing Walker Coonhound and

> *"The approved phenotypes for each breed were determined based on the written breed standards of the AKC, FCI, UKC, and KC."(Britain).*

> *“At least one of the four registries describes the allowed phenotypes indistinctly. This consists of situations where the trait is preferred to a lesser extent than alternatives, is not described at all, or is worded in such a way as to lead to ambiguous interpretation.”*

Great Dane with 6 fault alleles present in each, and the Yorkshire Terrier and Rottweiler with 5 fault alleles present in each. Seventy-eight percent of the total number of fault allele occurrences produce phenotypes disallowed by all queried registries that recognize the breed. For 8.9% of fault allele observations, one or more of the queried breed registries allow the phenotype produced without bias, with the remaining registries disallowing it entirely or imparting a preference bias. In 15.1% of the fault allele observations, at least one of the four registries describes the allowed phenotypes indistinctly. This consists of situations where the trait is preferred to a lesser extent than alternatives, is not described at all, or is worded in such a way as to lead to ambiguous interpretation. The most frequently observed fault-causing alleles are the recessive brown alleles of *TYRP1*, representing 29.8% of all fault allele instances. Notably, 79.6% of all fault alleles are recessively inherited.

The probability of producing the disallowed phenotype associated with each fault allele was calculated assuming a random breeding same-breed population, and taking into consideration the inheritance patterns and gene interactions required for the phenotype expression. The fault-producing probabilities range from 4.9e^{-7}(any non-solid color in the Black Russian Terrier) to 0.25 (red in the UK population of Schipperkes). Overall, the fault alleles were detected at low frequencies and, due to complex inheritance hierarchies and epistasis, have a <0.01 probability (<1% chance) of producing the fault phenotype in 58.9% of instances. Only 4.2%of fault alleles have a >0.10 probability (>10% chance) of producing the fault phenotype.

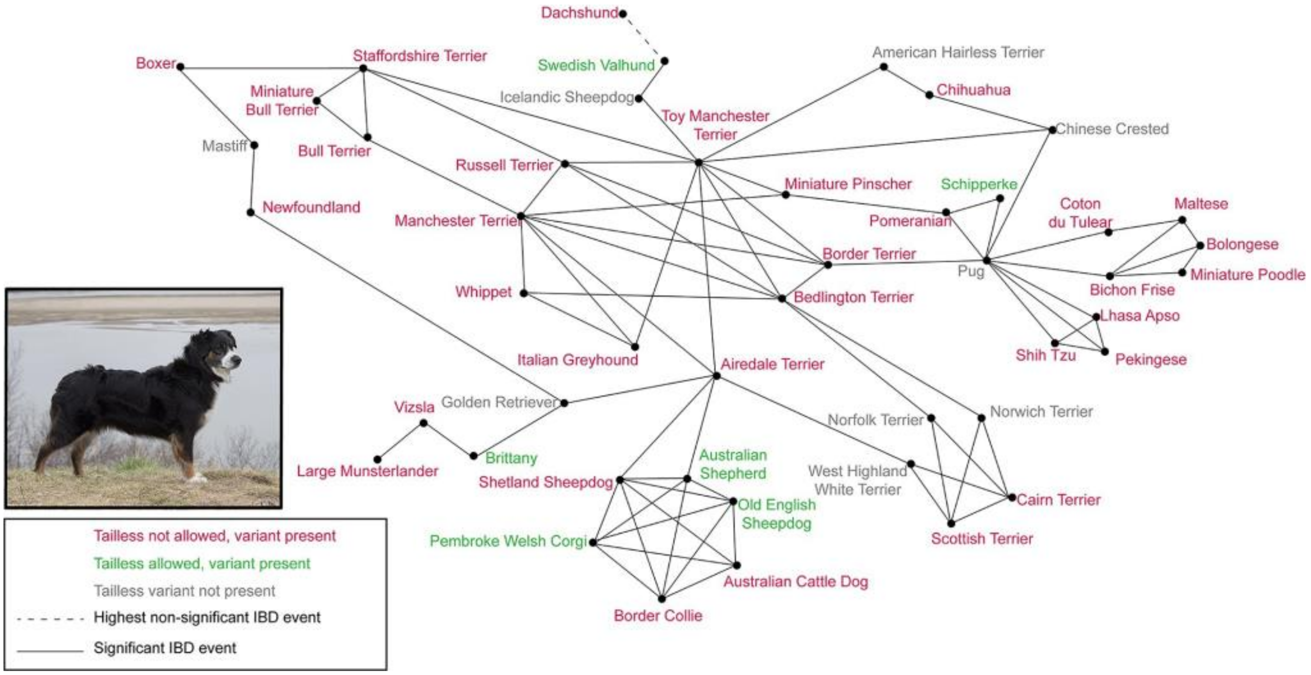

Fig 3. Identity-by-descent (IBD) haplotype sharing breed relationships connect breeds carrying the *T* allele for *tailless*. Solid black lines represent instances of significant haplotype sharing levels between breeds. The color of the breed names reflects the proposed carrier status of the tailless variant in the sampled members of those breeds, indicating not present (grey), present and permitted within the breed standard (green), and present and not permitted within the breed standard (red). The Dachshund breed shows no significant haplotype sharing with any other breed, however, its highest non-significant haplotype sharing value is with the Swedish Valhund (dashed line). Inset, the Australian Shepherd breed permits natural taillessness.

Ancestral routes of allele transmission

Previous research has demonstrated the ability of identity-by-descent (IBD) haplotype sharing to reveal shared ancestry events between modern dog breeds, accurate to approximately 150 years ago [32]. We used these previously identified significant breed relationships to successfully connect breeds genotyped to possess the rare phenotype alleles: *T tailless* (Fig 3) and *ASIP a* (Fig 4). Forty-eight breeds were identified as carrying the *tailless* allele of *T*, in many cases at very low frequencies, in the present study. Thirty-eight of these breeds were represented in previous research [32,33], allowing identification of IBD haplotype sharing relationships. By using these pre-determined breed relationships, each of the 38 breeds (Fig 3, represented by red or green text) can be connected into a single relationship matrix, providing a potential route of transmission of the *tailless* allele. Only nine non-carrier breeds (Fig 3, represented by grey text) were required to serve as potential transmitters of the *tailless* allele, reflecting populations that have successfully eliminated the allele from the breed, or have decreased the frequency enough so as to not be detected in our sampling. Likewise, 89 breeds were identified as carrying the *ASIP* a allele in the present study, 68 of which were also analyzed for IBD haplotype sharing previously [32,33]. Of these 68, all but three breeds (Tibetan Mastiff, Kuvasz, and Anatolian Shepherd) could be connected via significant IBD haplotype sharing events (Fig 4).

> *"Previous research has demonstrated the ability of identity-by-descent (IBD) haplotype sharing to reveal shared ancestry events between modern dog breeds, accurate to approximately 150 years ago."*

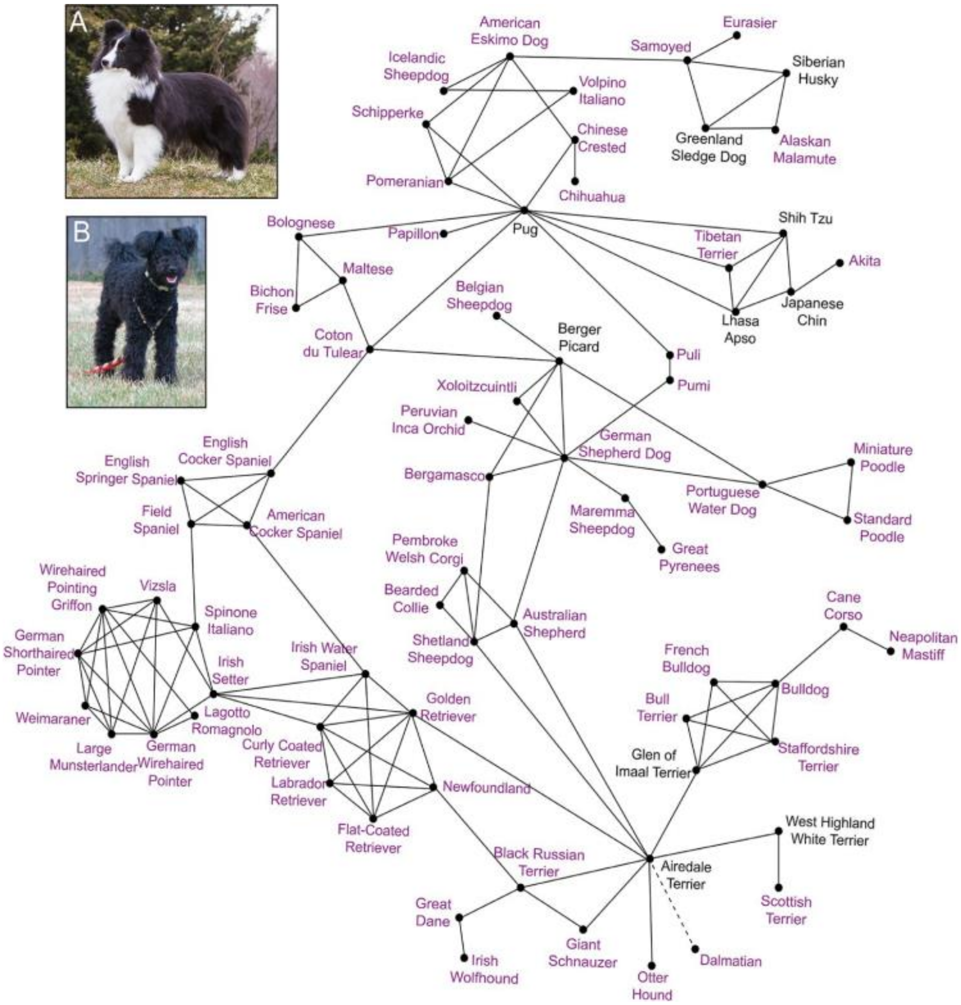

Fig 4. Identity-by-descent (IBD) haplotype sharing breed relationships connect breeds carrying the *a* allele of *ASIP*. Solid black lines indicate instances of significant haplotype sharing between breeds. Breed names in purple indicate observed frequency of the a allele within the breed in the present study. Breed names in black indicate that the *a* allele was not detected within the sampled individuals of that breed. The dashed line connecting the Dalmatian to the Airedale Terrier indicates that no significant haplotype sharing was detected with the Dalmatian, however the highest non-significant level of haplotype sharing was measured with the Airedale Terrier. Inset images show examples of dogs with the recessive black phenotype,

A) Shetland Sheepdog,

B) B) Pumi.

Discussion

Most publications to date that assess allele frequency within dog breeds have been conducted on a relatively small scale, limited to select sets of breeds and/or variants of known relevance to specific breeds [34–40]. A recent publication focused on a very large set of purebred and mixed-breed dogs and a panel of 152 disease markers [41], but did not evaluate morphological or pigmentation gene variants. Here, we have leveraged an expansive number of DNA samples, both in terms of dog numbers and breed representation for which 12 genes impacting coat color and morphological variation have been genotyped on a commercial genotyping platform (Table 1). In doing so, we have revealed patterns of allele frequency and distribution that inform our understanding of breed development and relationships, regional phenotypic preferences, and the impact of canine registering bodies on the prevalence of rare alleles.

"we have revealed patterns of allele frequency and distribution that inform our understanding of breed development and relationships, regional phenotypic preferences, and the impact of canine registering bodies on the prevalence of rare alleles."

Unexpected breed distribution of low frequency alleles

The majority of the alleles evaluated in the present study are broadly recognized across many modern dog breeds. However, a small number of the variants have only previously been recognized in select breeds. For example, the E^G allele of *MC1R* was initially detected in Salukis and Afghan Hounds [7]. We have here described 26 additional breeds in which the E^G allele has not previously been reported (S2 Table). Seven breeds (ANAT, CAAN, CASD, CAUC, KKLG,POLG, TAIG) carrying E^G are phylogenetically related to the Saluki and Afghan Hound, suggesting shared traits due to common ancestry, but E^G was also found in the Asian/Arctic, Hungarian, Nordic Spitz, Pointer/Setter, Poodle, and Scent Hound clades. The E^G allele requires an *ASIP* tan point phenotype in order to express as an observable pattern [7], the lack of which would allow the allele to persist within a breed undetected. This may be the case in breeds such as the Anatolian Shepherd, Black Russian Terrier, Maltese, Norwegian Buhund, Puli, and Toy Poodle, where the tan point phenotype is rare or absent.

"Seven breeds (ANAT, CAAN, CASD, CAUC, KKLG,POLG, TAIG) carrying E^G are phylogenetically related to the Saluki and Afghan Hound, suggesting shared traits due to common ancestry.......The E^G allele requires an ASIP tan point phenotype in order to express as an observable pattern, the lack of which would allow the allele to persist within a breed undetected. This may be the case in breeds such as the Anatolian Shepherd..."

The *tailless* allele of the *T* gene has previously been investigated in breeds known to have the natural tailless phenotype, confirming the cause of the trait in 18 breeds [25,26]. The frequency of the variant has not, however, been evaluated in breeds not necessarily expected to harbor the trait. We report the occurrence of the *tailless* allele in 38 new dog breeds (S2 Table, Fig 3). The tailless phenotype is variably expressed, ranging from complete anury to a truncated or kinked tail [25,26]. While absence of a tail in a breed expected to have a full length tail would be immediately noticeable, a mildly shortened or bent tail may be dismissed as inconsequential, thus allowing a low frequency of the allele to persist within some breeds. Likewise, surgical tail docking is still a common practice among certain breeds in some countries, rendering the natural length of the tail unknown beyond a neonatal age. Among the 38 newly reported carrier breeds of *tailless*: two allow a natural tailless phenotype (MCNB, OES); seven follow tail docking procedures in the US (AIRT, BOX, MPIN, MPOO, TENT, VIZS, WELT); eight have breed standards that describe a shorter than average ideal tail length (BORT, BULT, CAIR, MANT, MBLT, RWST, SCOT, TMNT); and nine have naturally curled tails (BICH, BOLO, COTO, GSPZ, LHAS, MALT, PEKE, POM, SHIH), which would mask small variations in length or structure. Indeed, anecdotal reports of abnormally short and/or kinked tails have been reported in at least eight of the newly reported *tailless* carrier breeds (BEDT, BULT, DACH, LHAS, SSHP, STAF, SCOT, VIZS) [42–46] (personal communications with breeders). It is important to note that many of the breeds in which we have now detected the *tailless* allele show the allele as present at very low frequencies. This allows for the possibility that some of these calls may be false positive errors that have escaped our quality control efforts.

“The identification of an allele with the combined a^y and a^t variants in the ASIP gene poses a number of intriguing implications.”

The identification of an allele with the combined a^y and a^t variants in the *ASIP* gene poses a number of intriguing implications. The variant associated with the a^t allele is a SINE insertion located on CFA chr24:23,365,298–23,365,537, in the upstream regulatory region of *ASIP*, and has been attributed to dorsoventral and banded hair patterning [5]. The a^y variant consists of two adjacent amino acid substitutions in exon four of the *ASIP* gene (p.A82S R83H), located at CFA chr24:23,393,510–23,393,515 [4]. At approximately 28 kb apart, a canine recombination rate of 1.2 cM/Mb [47] would predict a 0.042% rate of crossover between the two variants. We observed the a^y and a^t variants on the same chromosome, briefly termed the a^{yt} allele, a total of 48 times within the 11,790 genotyped dogs, and within 14 seemingly unrelated breeds, and the Dingo. The phenotypes of individual genotyped dogs were not available, but relying on the accepted colorations with each breed, the remaining 11 breeds with a^{yt} all allow for the standard a^y fawn phenotype. Frequencies of a^{yt} varied within the fawn breeds from 1% to 8%, suggesting that any phenotypic difference caused by the allele combination would not be immediately recognized as outside the acceptable a^Y fawn coloration. Indeed, with the added a^t SINE insertion, preventing the production of banded hair patterning, a^{yt} may result in a fully phaeomelanin color, lacking the eumelanin tips on the hairs that are commonly present in a^y fawn dogs. The current method of determining the biallelic genotype of *ASIP* relies on assaying the a^y, a^t, and a variants, and assigning the presence of a^w in the absence of the other detectable markers. In this way, a genotype of a^{yt}/a^w and a^y/a^t would appear to be the same. Seven breeds (ANAT, DANE, GPYR, LAGO, MARM, TIBM, TIBS) in which the a^{yt} allele was detected also showed observable levels of the a^w allele, presenting situations where the true frequencies of a^w may be higher than reported here. An additional 63 breeds have the a^y, a^w, and a^t alleles, reflecting the opportunity for the a^{yt}/a^w genotype to be incorrectly recorded as a^y/a^t, which would also result in underestimate of a^w frequency. There is, of course, the possibility that either the a^y or a^t variants previously described are not causal variants, but rather very accurate markers. However, both variants have been successfully used to predict coat color

“the added a^t SINE insertion, preventing the production of banded hair patterning, a^{yt} may result in a fully phaeomelanin color, lacking the eumelanin tips on the hairs that are commonly present in a^y fawn dogs.”

genotypes in multiple studies without raising concern [7,19,48,49]. Further pursuit of the phenotypic impact of the a^{yt} allele, along with determining its inheritance pattern, is ongoing.

The RALY duplication associated with the saddle tan modification of the tan point phenotype was detected in 203 breeds (S2 Table), thirty-eight of which are either fixed or variable for the saddle tan phenotype, and 119 of which have epistatic variation at additional coat color genes that prevent the expression of *saddle tan*. However, both the saddle tan and tan point mutations were detected in 14 breeds for which only a tan point phenotype is permitted or expected. For instance, Bernese Mountain Dogs have a fixed phenotype of black, tan points, and white spotting; despite the 100% a^t allele frequency and the addition of an 18% *saddle tan* allele frequency, no readily identifiable dogs exist with the saddle tan phenotype. These instances reiterate the findings of the initial canine RALY research, suggesting at least one additional modifier gene that is required for the production of the saddle tan phenotype [19].

> *"both the saddle tan and tan point mutations were detected in 14 breeds for which only a tan point phenotype is permitted or expected...suggesting at least one additional modifier gene that is required for the production of the saddle tan phenotype."*

The *Harlequin* allele was identified, as expected, in the Great Dane population [14], but was also identified–unexpectedly–in the Yorkshire Terrier population, where it has not been previously described. Yorkshire Terriers are not known to possess the variant at *PMEL17* that produces the merle phenotype and is required for the expression of harlequin when combined with the *PSMB7* variant. Therefore, even with the *Harlequin* mutation, it would presently be impossible to produce a harlequin patterned Yorkshire Terrier. Despite this, there is no recent haplotype sharing between the Yorkshire Terrier and Great Dane breeds, which could have resulted in transfer of the allele [32]. The detected presence of the allele in our data set could be explained by a *de novo* mutation in the Yorkshire Terrier breed, inaccurate marker selection, or genotype quality in the SNP array. The latter is unlikely due to the accuracy of this test on the positive control population (Great Danes) and the negative control population (all other dog breeds). The *de novo* mutation theory is supported by the fact that *Harlequin* was only identified in the UK Yorkshire Terrier population (2 dogs with the *Harlequin* allele out of 24 UK Yorkshire Terriers) and not at all in the US Yorkshire Terrier population (n = 107 dogs); these two populations interbreed only rarely, suggesting the *de novo* mutation arose privately in the UK. Further investigation is required to draw definitive conclusions.

Given the expectation of ancestral alleles in wild canine species, the level of derived alleles detected in the wild canine populations was somewhat surprising. While 99% of *MC1R* alleles in the grey wolf, Eastern coyote, Western coyote, and Dingo were found to be wild-type *E*, only 72% of *ASIP* alleles from wild canines were wild-type a^w, with only the Western coyote fixed for a^w. The genotyped Dingos were predominantly (75%) a^y fawn, consistent with their usual phenotype. Somewhat unexpectedly, however, the a^t tan point allele of *ASIP* was detected at levels of 20% in Eastern coyotes and 14% in grey wolves. Likewise, derived coat color alleles at *TYRP1* and *MITF*, and the morphologic variants associated with long hair, and drop ears, were detected at within-species levels between 2–46% (b^s in Eastern coyotes and drop ear in Grey wolves, respectively). The derived alleles at *ASIP*, *MC1R*, *CBD103* have previously been detected at low frequency in various populations of coyotes and wolves, most of which have been postulated to occur due to introgression with domestic dogs [49–52]. Such introgression between grey wolves and domestic dogs has been documented to occur at low levels across Eurasia, but detailed studies of domestic dog introgression with wolves and other species (coyotes, dingoes) in other geographic areas are sparse [53,54]. This is the first report of the tan point

(*ASIP*), and long hair (*FGF5*) variants in wild canine populations. A recent paper verified the CFA10 ear shape locus, and demonstrated that, while definitively a contributing locus, it does not perfectly account for ear phenotype [28]. Thus, the higher frequency of ear shape and hair length variant alleles in wild populations is perhaps not surprising, as these phenotypes are known to be driven by more than one locus [20,27,52].

Intended working application influences phenotypic variation

"White spotting, resultant of variation at the MITF gene, is broadly present across all clades."

Phylogenetic analysis of dog breeds is conducted in the absence of phenotypic data and provides intriguing insight into the history of breed formation. Reversing that scenario by assessing phenotypic association relative to phylogenetic relationships begins to unravel the individual characteristics that define cladistic groupings. The comparison of allele frequencies of the interacting coat color genes *ASIP, MC1R,* and *CBD103* (Fig 1) reveal preferred clade-specific colorations. *ASIP*-driven patterns are widely preferred in the Scent Hound, Spitz, and Terrier clades; conversely, single-pigment patterns, characterized by high frequencies of *CBD103* K^B or *MC1R e* alleles, are prevalent in the clades with a history of hunting applications, namely those of the Pointer/Setter, Poodle, Retriever, and Spaniel clades. Similarly, the hunting-related clades also generally display a higher incidence of brown pigment production, though they do not show preference for a specific recessive *TYRP1* allele (S1 Fig).

Historically, white has been selected for in breeds to improve their visibility. A human's ability to visually locate their dog, aided by bright white patterning, is important for hunting and terrier breeds that traditionally work in dense vegetation to locate, subdue, or retrieve quarry [55–59]. Conversely, when a dog is meant to remain camouflaged and not startle game, as with retriever breeds, a bland or solid color that will blend into the surrounding foliage is desired [55,58]. White spotting, resultant of variation at the *MITF* gene [17], is broadly present across all clades. However, reflecting the applicable purpose of the color pattern, the presence of breeds fixed for white markings appears to be greatest in the Pointer/Setter, Spaniel, and Terrier clades (S1 Fig).

Geography and lineage influence allele distribution among same-breed populations

Dog breeds, while standardized and often interchangeable around the world, have previously been shown to differ in their genetic composition based on geographic locale [32,60–63]. We detected significant ($p \leq 0.00167$) allele distribution differences based on geographic site of sample collection in 17 of the 26 breeds for which genomic sub-populations could be identified based on geography. Similarly, six breeds (BEAG, ESSP, ECKR, GREY, LAB, WHIP) encompassed multiple lineages differentiated by the application of the dogs to hunting, racing, or conformation competitions. In each case, at least one of the genes queried showed significant allele distribution differences between lineages. These disparate allele frequencies can represent either regional differences in preference or influence of prominent ancestor bias.

" disparate allele frequencies can represent either regional differences in preference or influence of prominent ancestor bias."

TYRP1 is a representative example. The various recessive alleles of *TYRP1* all ultimately produce the same pigmentation shade (brown instead of black), regardless of the specific alleles present. Therefore, significant variation between *TYRP1* recessive allele frequencies relative to population may indicate a founder genotype or the effect of an influential ancestor. The frequency of the b^c allele is significantly higher in US Field Beagles ($p \leq 0.003$) and UK English Springer Spaniels ($p \leq 0.003$), compared to conformation lineage Beagles and US English Springer Spaniels which each have higher frequencies of b^s (S2 Fig). As the specific *TYRP1* allele cannot be purposefully selected for through phenotype observation alone, these differences between populations may reflect divergent selection of the lineages. There is no apparent pattern to the distribution of the b^s and b^c alleles relative to clade distinctions (S1 Fig). This would imply that these two *b* alleles are substantially old enough so as to have propagated throughout dog types prior to the development of closed-breed populations.

Traditionally, many dog breeds have had their tails surgically docked to a shorter length, predominantly for the purposes of preventing injury to the tail while the dog carries out its defined function. With the changing use of dogs over time, the necessity for tail docking has recently become a source of discussion among canine enthusiasts and the veterinary community. Between 1987 and 2018, 35 countries have banned or restricted tail docking or the ability to exhibit dogs with docked tails in regulated kennel club events [64–68]. There are currently no restrictions placed on docking in the US, while the UK has banned tail docking since 2006 [64]. Dog breeders in countries with docking bans wanting to uphold the traditional appearance of a dock-tailed breed could therefore select for the *tailless* variant of the *T* gene to produce naturally shortened tails in their dogs. However, none of the breeds from the US and the UK that were genotyped in the present study show significant differences in the *tailless* variant frequencies. Eleven breeds collected in both locations traditionally have docked tails, while only four of these breeds (PEMB, SKIP, VIZS, WELT) had any measurable level of the *tailless* variant present. While the level of *tailless* is numerically higher in the UK populations of the Pembroke Welsh Corgi, Schipperke, and Vizsla compared to US populations, the differences were not significantly different ($p \leq 0.00167$). This lack of disparity likely reflects the age of the samples used in this dataset, which were collected between 2005 and 2016. It is probable that insufficient time has passed to accurately reflect the efforts of selection for natural taillessness resulting from the procedural ban, and the *T* allele frequencies are expected to increase in select breeds over time in those countries banning surgical docking.

It is worth noting that, while overall numbers for most breeds were quite high, once split into geographic or lineage groups, the cohort size in some cases became smaller. These small numbers may ultimately influence the accuracy of allele frequency estimates in these subpopulations, and larger sample sizes in future studies would solidify true differences between such populations.

" A breed standard is a written description of a given breed, as determined by a committee of educated breeders, that details how a typical dog of that breed should look and behave."

The natural probability of disallowed traits in pure breeds

A breed standard is a written description of a given breed, as determined by a committee of educated breeders, that details how a typical dog of that breed should look and behave. Historically, the standards functioned as a framework for breeders to aim at when producing dogs of that breed. Breed standards outline traits that are disallowed, so that breeders can opt to breed away from or minimize their occurrence. Each canine registering organization, usually specific to country or region, employs its own set of breed standards and, for the most part, these standards are concordant breed-to-breed across registries. However, there are instances where the wording between standards is not precisely mirrored, such that variations in color, size, or morphology are more or less tolerated from registry to registry.

> *“there are instances where the wording between standards is not precisely mirrored, such that variations in color, size, or morphology are more or less tolerated from registry to registry.”*

Our analyses detected genetic variants that would cause disallowed phenotypes in 67.5% of breeds tested (S3 Table). The majority of these, 58.9%, have a <1% probability of producing that undesirable phenotype given random breeding. These values represent multi-generational efforts to eliminate unfavorable phenotypes within breeds, however they also highlight that conformity to breed standard is certainly not yet universal or complete. They also illustrate the difficulty in selecting against alleles that are masked not just by dominance, but also epistasis, even in a highly-visible trait such as coat color. In general, these findings exemplify three separate scenarios: 1) traits broadly disallowed but carried at low frequencies, 2) traits allowed under some registries but not others, and 3) single traits that persist due to breed-specific allowances for particular trait combinations (Fig 5). For example, regardless of breed registry (AKC, UKC, KC, and FCI), the Bull Terrier is described as always having a black colored nose, and never showing brown hair pigmentation. However, we detected the b^c and b^s alleles of *TYRP1* at a frequency of 3% each in our population of pure bred Bull Terriers. This results in a probability of 0.0036 in producing a brown colored purebred Bull Terrier, present as brown pigmented skin and/or coat, assuming random breeding (Fig 5; S3 Table). Conversely, Shetland Sheepdog breed standards differ in that the AKC disallows piebald spotting in the breed, the FCI and KC tolerate, but do not prefer, excessive white spotting, and the UKC allows any variation from no white to fully piebald. We detected the *MITF* variant for white spotting, known to cause the piebald phenotype in this particular breed [18], at a frequency of 16% in the UK population of the breed and 6% in the US population (Fig 5; S2 and S3 Tables). Finally, the Great Dane breed standard is relatively cohesive across breed registries, but defines acceptable coat colors in terms of pattern combinations; for example, white spotting and the harlequin pattern are only allowed on a black base color. However, because black base color is dictated by *CBD103* on chromosome 16 with a breed frequency of 66%, white spotting is controlled by *MITF* on chromosome 20 with a breed frequency of 6%, and harlequin is caused

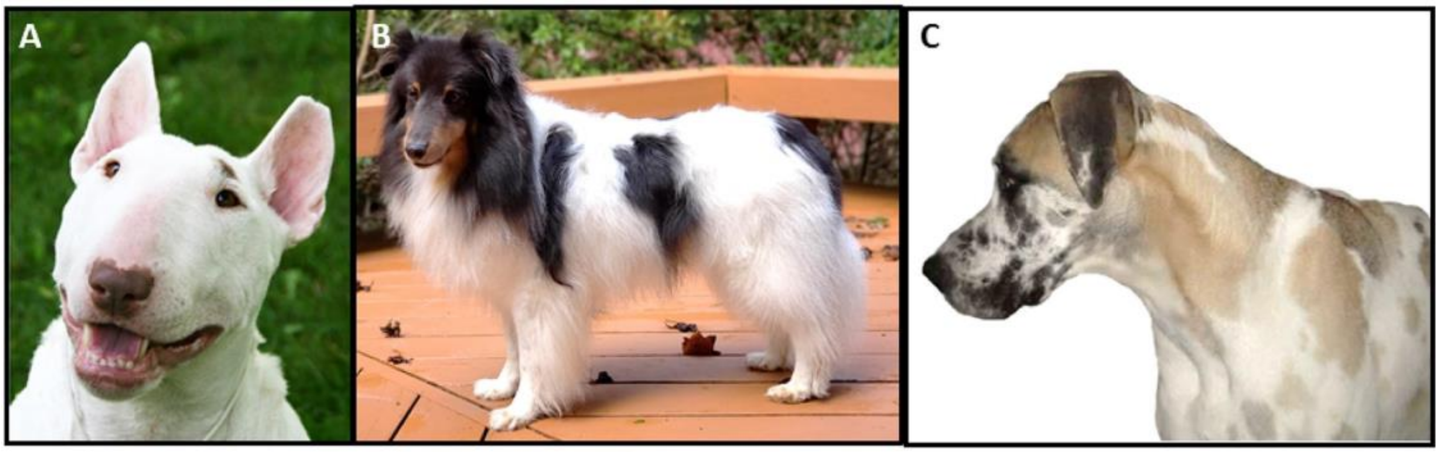

Fig 5. Purebred dogs exhibiting color traits deemed inappropriate by one or more breed registries. A) Bull Terrier with a brown nose and brown patch above its eye. B) Shetland Sheepdog with piebald white spotting. C) Great Dane with the harlequin pattern on a fawn base color.

by *PSMB7* on chromosome 9 with a breed frequency of 21%, the realistic potential to produce a fawn-based harlequin or a fawn and white spotted Great Dane is unavoidable (Fig 5, S2 Table). These values result in a 1.33% probability of producing a fawn and white Great Dane through random breeding of purebred dogs, or a 3.80% probability of producing a fawn Great Dane with one copy of the harlequin mutation. Since the frequency levels of the merle variant–required for production of the harlequin phenotype–are not known, the latter value does not necessarily reflect the number of fawn-based harlequin dogs produced.

The Schipperke breed, collected from populations in the US and the UK, presents a clear example of how regional acceptance of certain characteristics can drive the frequency of a variant within a population. The Schipperke breed standards for AKC, UKC, and FCI all state that the dog must be entirely black in color. However, the KC in the UK states that "any solid color" is permissible. As such, the allele frequencies for the *MC1R* recessive *e* allele, which produces a solid red color when homozygous, was observed at 50% among the dogs sampled in the UK (n = 6), and 0% among the dogs sampled in the US (n = 44) (Fig 2).

Much recent emphasis has been placed on the importance of genetic diversity within breeds [69–76]. With the conservation of diversity in mind, breeders and breed organizations must weigh the relative value of breed standard conformity with preservation of genetic diversity. The existence of unfavorable, though arguably benign pigmentation or morphological variations, has here been quantified and can be addressed by applied genetic screening to reduce the carrier frequency of breeding stock, or by reassessing breed standards to broaden the acceptance of preexisting variation. Likewise, though our analyses have indicated that production of disallowed phenotypes is generally quite low, the occurrence of an undesirable pigmentation trait should not necessarily exclude a dog from purebred status if that variant has been detected in the appropriate population. As a recent example, effective 1 January 2019, the Great Dane Club of America revised their breed standard to allow merle coloring on a black base. Canine genetic research has clarified that the presence of the merle allele is required for the Harlequin phenotype [14]; since this relationship was previously unclear, the breed had not allowed merle (without the Harlequin modifier) until this change. These revisions demonstrate the purebred dog community recognizing and willingly implementing the findings from canine genetic research. The present work will guide similar decision-making by breed clubs regarding definition of acceptable breed colors.

> *"we can assume that the presence of a given allele in two breeds may indicate shared ancestry between those breeds."*

Diverse breed representation of rare alleles informed by ancestral haplotype sharing

The unique structure of the dog genome dictates that, even across breeds, large regions of link-age disequilibrium can accompany trait-causing variants [77], as measured by IBD haplotype sharing. As such, we can assume that the presence of a given allele in two breeds may indicate shared ancestry between those breeds. For example, it has long been assumed that the recessive black allele of *ASIP* (*a*) is predominantly found in herding breeds [3–5]. However, among the 212 breeds analyzed here, the *a* allele was identified in 89 breeds, 83 of which are not previously reported as carrying the allele, representing 23 of the possible 28 clades assigned using IBD haplotype sharing in previous work [32,33]. While herding breeds, present in the Continental Shepherd, Hungarian, New World, Nordic Spitz, and UK Rural clades, comprise 14 of the *a* allele-possessing breeds–an expected result–the greatest breed representation was among the Pointer/Setter clade with 13 breeds possessing the *a* allele. The only clades without measured frequency of the *a* allele are the Alpine, American Terrier, Asian Toy, Pinscher, and Standard/Miniature Schnauzer clades.

IBD haplotype sharing can reflect a shared ancestry between populations, and the amount of haplotype sharing between breeds correlates significantly with the time point at which those breeds shared a common ancestry [32].

Using instances of significant levels of haplotype sharing between breeds, with reliably dating introgression events to as early as the late 1800's [32], 65 of the 89 breeds displaying carrier frequencies >0% for the *a* allele can be connected (Fig 4). While not necessarily reflecting the exact mode of allele sharing between breeds, the measured haplotype sharing instances successfully demonstrate a recent ancestral history between the breeds. There are 21 breeds with positive *a* allele frequencies that cannot be connected via haplotype sharing due to not being included in the previous haplotype sharing analyses [32], but are predicted to be in phylogenetic clades already represented among *a*-carrying breeds. Three breeds, the Anatolian Shepherd, Kuvasz, and Tibetan Mastiff, carry the *a* allele and are included in the haplotype sharing analyses, but do not show significant ancestry with other breeds. Therefore, while the extensive 65-breed relationship matrix supports the potential for the *a* allele to spread between breeds via recent introgression events, the presence of the allele in the Anatolian Shepherd, Kuvasz, and Tibetan Mastiff, for which no recent introgression events have been detected, suggests that the allele itself arose early in the history of the domestic dog, establishing a broad distribution well before the development of modern breeds in the late 1800's.

The tailless allele of the *T* gene was identified in 48 breeds, representing 14 clades. While 10 of these breeds have been previously identified as carriers of the *tailless* allele [25,26], 38 are reported here for the first time. Thirty-eight of the 48 *T*-carrying breeds are represented in the identity-by-descent dataset [32], all of which can be connected into a single relationship matrix (Fig 3). In some instances, such as with the Brittany and Newfoundland, which have *tailless* carrier frequencies of 0.04 and 0.01 respectively, there is no direct identity-by-descent relation-ship with a potential source breed of taillessness. However, both show ancestral relationships with the Golden Retriever, who then further shows ancestry with the Airedale Terrier, a carrier of *tailless* at a frequency of 0.02. It is possible that the Golden Retriever either carries *tailless* at a frequency not detected in our screening, or the trait previously existed within the breed and has since been selected against and eliminated. Other possible historic sources of *tailless* that have decreased or eliminated their current carrier frequency include the Icelandic Sheepdog, Keeshond, Mastiff, and Pug.

While the allele frequencies reported herein are intended to provide general information regarding the existence of particular alleles within breeds, they are not likely to be perfectly accurate estimates of actual breed-wide allele frequencies. For instance, while the German Shepherd Dog, Lagotto Romagnolo, and Australian Shepherd are represented by 162, 139, and 137 dogs, respectively, our dataset only includes eight Small Munsterlanders, and nine each of Redbone Coonhounds and Bergamascos. Despite these limitations, no other published genotype dataset matches the presently reported size and diversity of dog samples across a dozen pigmentation and morphologically relevant genes.

> *"The modern existence of domestic dogs is such that coat color is primarily a matter of aesthetics. …conservation of genetic diversity within breeds must be weighed."*

Conclusions

The broad adoption of commercial genotyping services yields an immense amount of genetic information. We have demonstrated how this data can be utilized to detail the current phenotypic diversity of 212 dog breeds, and the impact of population divergence due to geographic separation or selection practices. While most dog breeds have existed as closed breeding populations since the late 19th century, we have shown that rare trait-causing variants continue to persist within most breeds. Conflicting breed standard descriptions of multiple registering organizations may have facilitated the persistence of these traits within certain populations. In addition, epistatic masking effects have contributed to the continuance of various trait-causing alleles, due to the complicated multi-gene pathways whereby recessive alleles can remain unexpressed over multiple generations, and making selection for or against them challenging without the use of genotyping services.

The modern existence of domestic dogs is such that coat color is primarily a matter of aesthetics. Consideration should be given by breed associations to unifying breed standards across registering bodies, either with the intent of increasing selective pressure against truly undesirable characteristics, or expanding the standards to permit phenotypes for which the causal variants exist ancestrally within the breed. Simultaneously, conservation of genetic diversity within breeds must be weighed. The present study documents for the first time the frequencies of alleles at 12 coat color and morphological genes, across 11,790 dogs, representing 212 breeds, and demonstrates not only the anticipated genotypic variations within breeds, but also rare and unexpected alleles not previously reported.

Materials and methods

Sample collections

Genotype data from 11,790 canids, representing 212 pure dog breeds and 4 wild canine populations, was compiled during the development and implementation of the Mars WISDOM PANEL platform (Wisdom Health, Vancouver, WA, USA). DNA collections herein represent a subset of those initially reported in Donner, et al. [41]. Dog DNA samples were obtained by Wisdom Health (formerly Mars Veterinary) and Genoscoper Laboratories (Helsinki, Finland), between January 2005 and October 2016, as owner-submitted, noninvasive cheek swab collections. Dog owners provided consent for use of their dog's DNA in research. The dogs sampled predominantly originated from the US and UK, though samples were also obtained in smaller numbers from several other countries. Dogs were considered to be purebred if registered with a relevant all-breed registry, the predominant ones being: Fe´de´ration Cynologique Internationale, American Kennel Club, United Kennel Club, and UK Kennel Club, or an applicable single-breed registry for rare breeds. Breed and species classification was further verified through principal component analysis (PCA) and genotyping on the WISDOM PANEL platform (Wisdom Health), particularly for the minority newer/rarer breeds not currently (at the time, or even now) recognized by a national registry. PCA further revealed that 30 breeds formed sub-populations based on geography, body size, coat type, or function (e.g., show vs. field). Archived wild canine samples were used to represent: 1) the grey wolf (*Canis lupus lupus*, sampled primarily from Eastern North America, n = 12); 2) coyote (*Canis latrans*) collected from Eastern North America (Eastern coyote, n = 29) or British Columbia and Southwestern US (Western coyote, n = 19), populations segregated as determined by PCA cluster analysis; and 3) dingo (*Canis lupus dingo*) (n = 12) populations. All dog breeds were represented by ≥10 individuals, with the exception of the Small Munsterlander (n = 8), Bergamasco (n = 9), and Redbone Coonhound (n = 9).

Genotyping

Genotyping of seven coat color and five morphological trait variants (Table 1) was conducted on a custom-designed Illumina Infinium HD bead chip using manufacturer-recommended protocols ([78]; Illumina, San Diego, CA, USA). The validation and genotyping quality control measures for this platform were previously described in detail [41,78]. Trait variant assays specifically were validated through extensive correlation of genotypes with established breed phenotypes and owner-submitted pictures of individual dogs.

Allele frequencies and statistical analysis

Allele frequencies for each variant were determined for each breed and, when appropriate, breed subpopulations, and converted to binary genotypes for genes with multiple alleles. The total number of dog samples per breed are reported in S1 Table. Due to sporadic failure, the number of genotypes obtained per breed for each gene may vary from the total number of dogs per breed (S2 Table). For breeds with subpopulations (n = 30 breeds, delineated primarily by geography, but also body size, breeding line of conformation versus working, etc.), within-breed statistical significance of the differences in genotype distribution between the subpopulations was evaluated by Pearson's chi-square contingency tables, or Fisher's exact tests (when allele counts in any single cell fell below 5), for each gene. Calculations were conducted with the MASS package in R [79,80]. A p-value of < 0.00167 was chosen to indicate a significantly different allele distribution between the same-breed subpopulations; this is the Bonferroni correction for multiple testing of 30 breeds for each gene (i.e., 0.05/30). In the case of *FGF5*, no genotypes were available for the US population of German Spitz, thus significance was corrected instead for 29 breeds, to a p-value of ≤ 0.00142 for this gene. Further correction (e.g., for testing of 12 different genes) was not applied because a balanced approach was desired and the initial Bonferroni correction was deemed suitable. Further analysis was conducted for the six breeds sampled from > 2 subpopulations. When these breeds differed significantly at any gene using the initial analysis described above, they were subsequently evaluated for pairwise significance using Pearson's chi-square or Fisher's exact tests. Significance for each breed sub-population was determined by p-value = 0.05/n, where n = maximum number of subpopulations remaining in analysis. This number therefore varied for each gene, depending on remaining significant breeds. For example, if Poodles–divided into four subpopulations–remained, the correction was 0.05/4, resulting in a p-value cut-off of 0.0125; however if Dachshunds–divided into six subpopulations–remained, the correction was 0.05/6, resulting in a p-value cut-off of 0.0083. Specific statistical applications and n values are indicated in the appropriate figure, table legends or footnotes.

Probability of phenotype expression

When alleles that would produce an undesirable or disallowed phenotype were observed in a given breed, relative to AKC, UKC, KC (Britain), or FCI breed standard descriptions, the probability of producing that phenotype was calculated with the following equation:

$$\textit{Probability of phenotype } X = \quad p^2 + \sum_{q=a}^{c} 2pq \Big) * \quad r^2 + \sum_{s=d}^{f} 2rs \Big) * \quad t^2 + \sum_{s=g}^{i} 2tu \Big)$$

Such that:

P = the frequency of the fault-producing allele, *P*, of the gene causal for *X*

q = the frequency of any same-gene allele recessive to *P*, of which there can be up to 3 (*a* to *c*)

r = the frequency of the most dominant allele, *R*, at an interacting gene that is required for production of the fault phenotype

s = the frequency of any same-gene allele recessive to *R*, of which there can be up to 3 (*d* to *f*)

t = the frequency of the most dominant allele, *T*, at an interacting gene that is required for production of the fault phenotype

u = the frequency of any same-gene allele recessive to *T*, of which there can be up to 3 (g to i)

The traits for which genotypes were obtained present scenarios in which up to two known interacting genes can influence the expression of a phenotype. Namely, expression of an *ASIP* phenotype relies on corresponding *CBD103* and *MC1R* genotypes, the *MC1R* phenotypes caused by E^M and E^G require specific genotypes at *ASIP* as well as a homozygous wild-type *CBD103* genotype, and a recessive genotype at *CBD103* can result in multiple possible *ASIP* phenotypes, only some of which may be undesirable. Conversely, recessive homozygosity at *TYRP1* will result in brown pigment of the hair and keratinized skin, which may present as a coat fault if coupled with eumelanin-producing *MC1R* and *ASIP* genotypes, or a nose pigment fault regardless of hair pigmentation. Taillessness is only expressed in the heterozygous state, as it is embryonic lethal when homozygous, therefore, probability values were corrected to reflect outcomes among live births.

Supporting information (found at this link as a separate pdf download.)

S1 Fig. Allele distribution. Distribution of alleles for a) *TYRP1*, b) *MITF*, c) *PSMB7*, d) *RALY*, e) *KRT71*, f) *FGF5*, g) *T*, h) *BMP3*, i) chr10 ear set marker. Breeds are grouped by phylogenetic relationship.

S2 Fig. Allele frequencies in breeds with multiple populations. List of breeds, their abbreviations used throughout the paper, and the number of samples genotyped. Each breed was assigned to a phylogenetic clade based on previously published results [32,33]. Clade names in parenthesis indicate breeds not included previously [32,33], but for which a clade was assigned based on known breed history and phenotypes.

S2 Table. Allele frequencies for all breeds and genes tested. Allele frequencies for (a) coat color genes *ASIP* and *MC1R*, (b) the brown (*TYRP1*) and dominant black (*CBD103*) genes, (c) the white spotting (*MITF*), harlequin (*PSMB71*), and saddle tan (*RALY*) genes, (d) hair length (*FGF5*), hair curl (*KRT71*), and ear set, and (e) skull shape (*BMP3*) and natural taillessness (T). Breeds fixed for a single allele at any gene are indicated with bold text.

S3 Table. Unfavorable or "fault" phenotypes possible by breed and breed registry. Breeds genotyped to have alleles that would produce phenotypes considered as a "fault" by either the American Kennel Club (AKC), Fe´de´ration Cynologique Internationale (FCI), United Kennel Club (UKC), or The Kennel Club of the UK (KC). The level of tolerance within each breed registry is designated as either not allowed (N), not preferred (n.p.), allowed (Y), or ambiguously worded (amb.). A breed not recognized by a given organization is indicated with a dash (-). Inheritance of the fault-causing allele is designated as dominant (D), recessive (R), or com-pound heterozygote (CH). Breed name abbreviations are as listed in S1 Table. Probabilities for producing the non-standard phenotype were calculated assuming random mating within the breed, and account for multi-gene inheritance, expression, and epistatic effects.

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Editor's note: It needs to be said that the AKC Saluki Standard has a partial listing of accepted colors and no disqualifications. Opinions expressed by individual members of the Fancy do not have bearing on reality as stated by our Standard in the West or as the Saluki is selected and bred in his homelands.

In 1929, two years after the formation of the Saluki Parent Club, SCOA, the AKC published its first iteration of the Complete Dog Book. The Parent Clubs provided the background for each breed and their Standard.

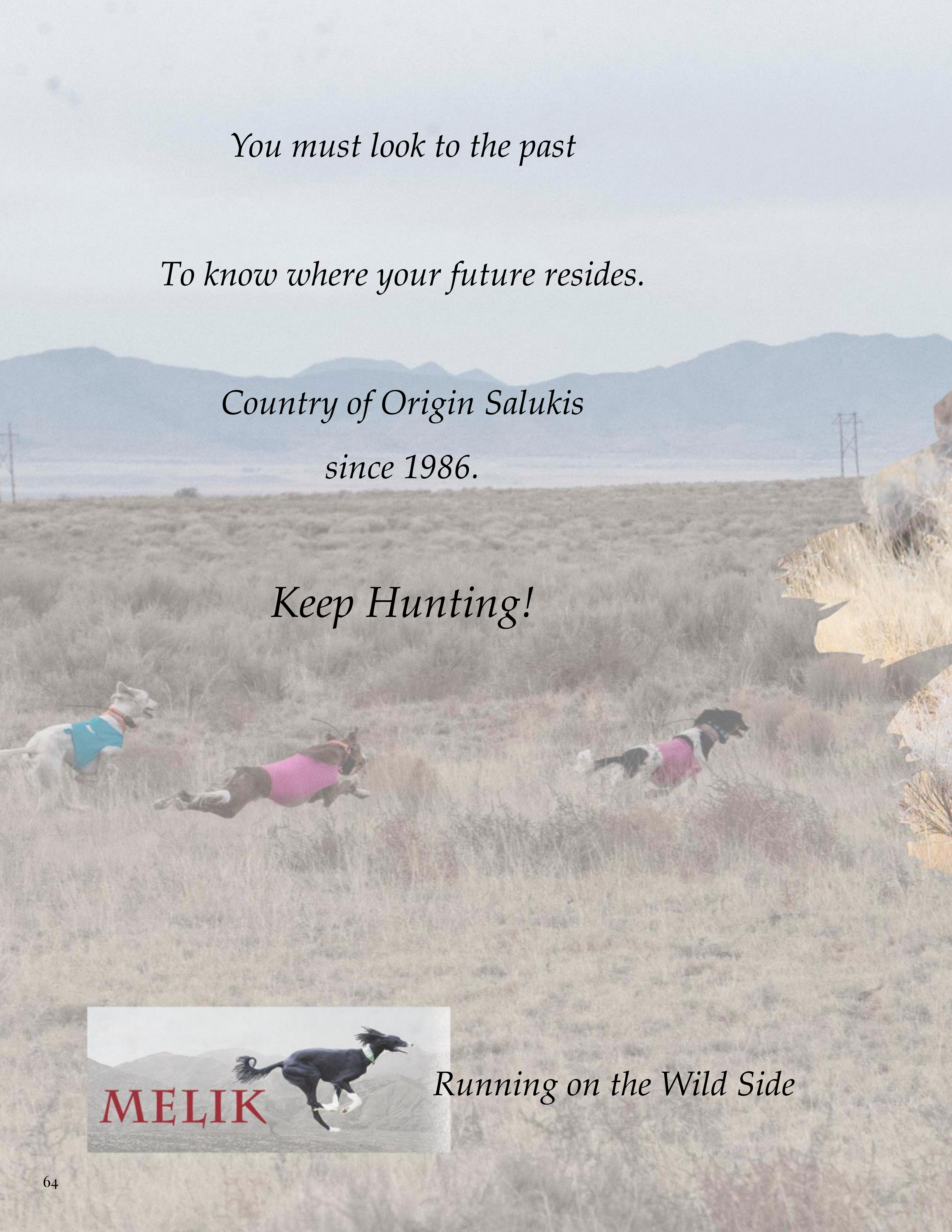
The original “History of the Saluki” was first published in the SCOA Yearbook of 1930, the year after the first printing of The Complete Dog. There is a clear statement on color.

“In colors the Saluki can meet the demands of the most fastidious, as while cream and fawn seem to predominate, there is red, grizzle and tan, white and chestnut, tricolor (black, white and tan), as well as solid black.”

In 1938 the “History of the Saluki” was printed as the preamble to our Standard in the AKC Complete Dog Book (second printing). It is clear SCOA did not intend the color list of *White, cream, fawn, golden, red, grizzle and tan, tricolor (white, black, and tan) and black and tan* to be the complete list of acceptable colors. By 1985 the wording had changed to state *“Salukis come in a wide variety of colors, including white, cream, fawn, golden, red, grizzle and tan, tri-color(white, black and tan), and black and tan.”* Today chocolate, red and white parti, grizzle parti, sabled red, and sabled fawn are all routinely seen in the AKC show ring, even though these colors and patterns are not specifically listed in the standard. We now see brindles and blacks, as well as the grey variants that come from black being modified by the Eg (grizzle) gene, as these colors have **again** been incorporated from the Saluki's countries of origin. Both brindle Salukis and black Salukis have gained their AKC Champion titles.

The Saluki's entire color palette remains accepted.

There are no disqualifications in the AKC Saluki Standard



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To know where your future resides.

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Desert Bred
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