Table S1. All primer information for this study.

Primers ID	Primers equences(5'→3')	Product size	GenBank ID	Annealing temperature
CYP11A1-CDS	F:GCCCAGGATTCAGGGATAAGAG R:ACAGAGCAAATCAGAGGCGAAG	1723 bp	NM_001001756.2	58.5℃
CYP11A1-qPCR	F:GCCACCTCAACACCAAGACA R:TGCAGAGTCATGGAAGTCGTG	241 bp	NM_001001756.2	59℃
GAPDH-qPCR	F:ATCTTCCAGGAGCGTGACC R:CACGATGCATTGCTGACAA	230 bp	NM_204305.2	59℃
CYP11A1-OE	F:ctcgagATGCTCTCCAGGGCTGCACCCATAG R:aagcttCTCCTGGCGCTGGAGGGGCCGGAGT	1524 bp	NM_001001756.2	66℃
BMP15-qPCR	F:CTGTCACCTCACCCCTTGTC R:CGTTGGTACAGCTCCAGCAT	241 bp	NM_001006589.3	61.5℃
FSHR-qPCR	F:CTGAGTTACACCGTGAGGTCT R:TGGTGAGGACAAATCTCAGTTC	242 bp	NM_205079.2	61.5℃
CYP17A1-qPCR	F:CTGGGTGCTGCAGAGATTCA R:ACCCACCCCATTCCACCTAT	182 bp	NM_001001901.3	61.5℃
HSD3B1-qPCR	F:GCCAAAGAGGAGCAAACCAGAG R:TCCAGCAGTAAGCGAACGATCC	223 bp	NM_205118.2	60℃
STAR-qPCR	F:TGCCATCTCCTACCAACA R:CATCTCCATCTCGCTGAAG	190 bp	NM_204686.3	61.5℃
CYP19A1-qPCR	F:ATGTTCCATCACGCTATTT R:GATTCTTGTTTGGGCTTCT	240 bp	NM_001001761.4	61.5℃
PCNA-qPCR	F:AGCACCAAATCAGGAAAAG R:GCACAGGAGATGACAACAG	177 bp	NM_204170.3	60℃
AKT1-qPCR	F:TGATGGCACATTCATTGGCTAC R:TGTTTGGTTTAGGTCGTTCTGTCT	122 bp	NM_001396387.1	60℃
mTOR-qPCR	F:GCACAAACCTCTGCGACAT R:CGTGAGCAAGCGAGAACAA	250 bp	XM_040689168.2	62℃

Table S2. Bioinformatics analysis tools.

Name of online website or software	Website	Usage
NCBI	https://www.ncbi.nlm.nih.gov/datasets/genome/#!/overview/	Genome Annotation File
ORF Finder	https://www.ncbi.nlm.nih.gov/orffinder/	CDS Sequence Identification
Gene Structure Display Server	https://gsds.gao-lab.org/	Transcriptional Region Structure
MEME Suite	https://meme-suite.org/meme/	Protein Motif Structure
Conserved Domains	https://www.ncbi.nlm.nih.gov/Structure/bwrpsb/bwrpsb.cgi	Protein Conserved Domain
ProtParam	https://web.expasy.org/protparam/	Protein Physicochemical Properties
PSORT	https://www.genscript.com/psort.html	Subcellular Localization Prediction
Prabi	https://prabi.ibcp.fr/htm/site/web/app.php/	Protein Secondary Structure
SOPMA	http://npsa-pbil.ibcp.fr/	Protein Tertiary Structure
String	https://cn.string-db.org/	Protein Interaction Network
MegAlign		Protein Sequence Identity
MEGA 12		Phylogenetic Tree Construction
TBtools		Graphing

Table S3. *CYP11A1* interference primer information.

Sequence name	Sequence	Purpose
si-243	S:GGGAGAAGUUGGGUGUCUA A:UAGACACCCAACUUCUCCC	Gene interference
si-885	S:GCCUCCUUGUGCAGGACAA A:UUGUCCUGCACAAGGAGGC	Gene interference
NC	S:UUCUCCGAACGUGUCACGUTT A:ACGUGACACGUUCGGAGAATT	Gene interference

Table S4. Structural information of the *CYP11A1* transcription region in galliform and non-galliform species.

Species	Number of Exon	Number of Intron	Length/bp											
			5'UTR	E1	E2	E3	E4	E5	E6	E7	E8	E9	3'UTR	CDS
Gallus gallus NM_001001756.2	9	8	84	245	156	200	204	161	167	79	192	123	183	1527
Coturnix japonica XM_015872775.1	9	8	73	245	156	200	204	161	167	79	192	123	182	1527
Meleagris gallopavo XM_010717201.2	9	8	58	245	156	200	204	161	167	79	192	123	178	1527
Phasianus colchicus XM_031616309.1	9	8	449	245	156	200	204	161	167	79	192	123	192	1527
Centrocercus urophasianus XM_042824559.1	9	8	154	245	156	200	204	161	167	79	192	123	-	1527
Tympanuchus pallidicinctus XM_052671691.1	9	8	73	245	156	200	204	161	167	79	192	123	166	1527
Lagopus muta XM_048956035.1	9	8	74	245	156	200	204	161	167	79	192	123	180	1527
Lagopus leucura XM_042885784.1	9	8	16	245	156	200	204	161	167	79	192	123	186	1527
Numida meleagris XM_021407406.1	9	8	233	245	156	200	204	161	167	79	192	123	-	1527
Mute swan XM_040570580.1	9	8	219	275	156	200	204	161	167	79	192	123	243	1557
Anas platyrhynchos XM_027466310.2	9	8	54	275	156	200	204	161	167	79	192	123	174	1557
Mus musculus NM_019779.4	9	8	87	260	156	200	204	158	167	79	198	159	179	1581
Mus musculus NM_001346787.1	7	6	1495	151	204	158	167	79	198	159	-	-	179	1116
Homo sapiens NM_000781.3	9	8	61	269	156	200	204	161	167	79	198	132	210	1566
Homo sapiens NM_001099773.2	7	6	684	151	204	161	167	79	198	132	-	-	210	1092

Table S5. Basic physicochemical properties of CYP11A1 protein.

Physical and chemical properties	1	2	3	4	5
Number of amino acids	508	508	508	508	508
Isoelectric Point	9.24	9.24	9.23	9.25	9.32
Molecular weight	58201.57	58201.43	58207.47	58193.49	58155.5
Strongly Acidic(-) Amino Acids	55	55	54	55	54
Strongly Basic(+) Amino Acids	65	65	64	66	66
Hydrophobic Amino Acids	191	191	188	189	189
Polar Amino Acids	107	107	108	108	108
Grand average of hydropathicity (GRAVY)	-0.236	-0.236	-0.246	-0.247	-0.247
Aliphatic index	90.02	90.02	89.43	89.63	89.25

1 Wuding chicken; 2 Chicken; 3 Japanese quail; 4 Turkey; 5 Ring-necked pheasant.

Table S6. Amino acids forming the secondary structure of CYP11A1 protein in various species.

Species	Alpha helix	Beta turn	Random coil	Extended strand
Wuding chicken_CYP11A1	46.46%	2.95%	40.55%	10.04%
Gallus gallus NP_001001756.2	46.46%	2.95%	40.55%	10.04%
Coturnix japonica XP_015728261.1	49.02%	3.94%	38.39%	8.66%
Meleagris gallopavo XP_010715503.1	48.43%	3.15%	39.76%	8.66%
Phasianus colchicus XP_031472169.1	49.61%	3.74%	37.60%	9.06%

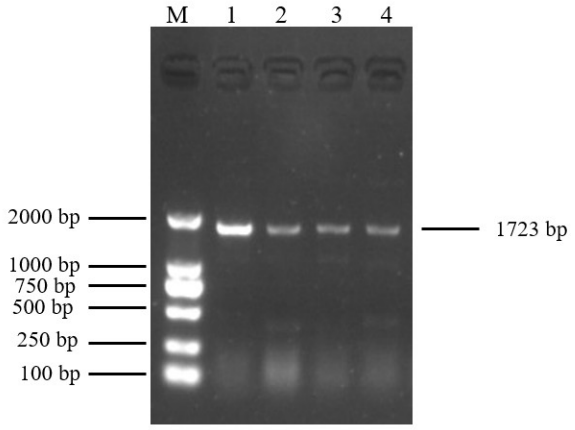


Figure S1. The PCR results for the Wuding chicken CYP11A1 coding region. M,DL2000 DNA Marker;1-4,PCR product of Wuding chicken *CYP11A1* coding region.

1	ATG CTC TCC AGG GCT GCA CCC ATA GCG GGC AGC TTT CAG GCA TGC CGC TGT GCC GGA GGG ATC CCA GCC CTC GCG GGG GTC CAC TAC CCA	90
1	M L S R A A P I A G S F Q A C R C A G G I P A L A G V H Y P	30
91	TTG CCC AGC TCC TCG GGA GCT CGG CCT TTC GAC CAG GTG CCG GGT GAA TGG AGA GCG GGT TGG CTC AAC CTG TAC CAC TTC TGG AAG GAG	180
31	L P S S S G A R P F D Q V P G E W R A G W L N L Y H F W K E	60
181	GGA GGC TTC CAC AAC GTG CAC AAC ATC ATG GCC AGC AAG TTC CAG CGC TTT GGG CCC ATC TAC AGG GAG AAG TTG GGT GTC TAC GAG AGC	270
61	G G F H N V H N I M A S K F Q R F G P I Y R E K L G V Y E S	90
271	GTG AAT ATC ATC AGC CCC CGC GAT GCG GCC ATG CTC TTC AAG TCA GAG GGG ATG CTG CCC GAG CGC TTC AGC GTG CCC CCA TGG GTG GCA	360
91	V N I I S P R D A A M L F K S E G M L P E R F S V P P W V A	120
361	TAC CGT GAC TAC CGC AAC AAG CCC TAC GGT GTG CTC CTC AAG ACA GGG GAG GCC TGG CGC TCG GAC CGC CTG ACC CTG AAC AAG GAG GTG	450
121	Y R D Y R N K P Y G V L L K T G E A W R S D R L T L N K E V	150
451	CTG TCG CCG CAG GTG GTG GAC AGC TTC GTG CCC CTG CTG GAC CAG GTG AGC CAG GAC TTT GTG CGG CGG GCA CGG GCG CAG GTC CAG CAG	540
151	L S P Q V V D S F V P L L D Q V S Q D F V R R A R A Q V Q Q	180
541	AGC GGC CGG GAG CGC TGG ACG GCC GAC TTC AGC CAC GAG CTC TTC CGC TTT GCC TTG GAG TCT GTA TGC CAC GTG CTG TAT GGG GAA CGC	630
181	S G R E R W T A D F S H E L F R F A L E S V C H V L Y G E R	210
631	CTG GGG CTG CTG CAG GAC TTT GTG GAC CCA GAG GCA CAG CAG TTC ATC GAC GCC GTC ACC CTC ATG TTC CAC ACC ACC TCC CCC ATG CTC	720
211	L G L L Q D F V D P E A Q Q F I D A V T L M F H T T S P M L	240
721	TAC GTG CCA CCC GCC CTG CTC CGC CAC CTC AAC ACC AAG ACA TGG CGT GAC CAC GTG CAT GCT TGG GAT GCC ATC TTC ACA CAG GCT GAC	810
241	Y V P P A L L R H L N T K T W R D H V H A W D A I F T Q A D	270
811	AAA TGT ATC CAA AAC GTT TAC CGG GAC ATC CGG CTG CAA CGC AAG AGC ACC GAG GAG CAC ACG GGC ATC CTC TTC AGC CTC CTT GTG CAG	900
271	K C I Q N V Y R D I R L Q R K S T E E H T G I L F S L L V Q	300
901	GAC AAG CTG CCC CTG GAT GAC ATC AAG GCC AGC GTC ACC GAG ATG ATG GCG GGC GGC GTG GAC ACG ACT TCC ATG ACT CTG CAA TGG GCC	990
301	D K L P L D D I K A S V T E M M A G G V D T T S M T L Q W A	330
991	ATG CTG GAG CTG GCA CGA TCC CCG GGC ATC CAG GAG CGG CTG CGG GCG GAG GTG CTG GCA GCC AAG CAG GAG GCA CAG GGG GAC AGG GTG	1080
331	M L E L A R S P G I Q E R L R A E V L A A K Q E A Q G D R V	360
1081	AAG ATG CTG AAG AGC ATC CGA CTG CTC AAA GCC GCC ATC AAG GAG ACT CTC AGG CTG CAC CCG GTG GCG GTG ACG CTG CAG AGG TAC ACC	1170
361	K M L K S I R L L K A A I K E T L R L H P V A V T L Q R Y T	390
1171	ACA CAG GAG GTC ATC CTG CAG GAC TAC CGC ATC CCC CCC AAG ACG CTG GTG CAG GTT GGT CTC TAC GCC ATG GGA CGA GAC CCT GAG GTC	1260
391	T Q E V I L Q D Y R I P P K T L V Q V G L Y A M G R D P E V	420
1261	TTC CCC AAG CCG GAG CAG TTC AAC CCT GAG CGC TGG CTG GTG ATG GGC TCC AAG CAC TTC AAG GGG CTG AGC TTT GGG CCA CGG	1350
421	F P K P E Q F N P E R W L V M G S K H F K G L S F G F G P R	450
1351	CAG TGT CTG GGT CGT CGC ATC GCC GAG CTG GAG ATG CAG CTC TTC CTC ATG CAC ATC CTG GAG AAC TTT AAG ATC GAA ACC AAG CGG GCG	1440
451	Q C L G R R I A E L E M Q L F L M H I L E N F K I E T K R A	480
1441	GTG GAA GTT GGG ACC AAG TTC GAC CTC ATC CTT GTC CCT GAC AAA CCC ATC TAC CTG ACA CTC CGG CCC CTC CAG CGC CAG GAG TGA	1527
481	V E V G T K F D L I L V P D K P I Y L T L R P L Q R Q E *	508

Figure S2. The Wuding_CYP11A1 Coding DNA Sequence obtained in this study and its encoded amino acid sequence. ATG is the start codon; * is the stop codon.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16		
1		100	96.5	97.2	96.7	97.4	96.9	97.6	97.6	95.1	85.8	86.6	52.1	53.2	50.9	53.1	1	Wuding chicken CYP11A1
2	0		96.5	97.2	96.7	97.4	96.9	97.6	97.6	95.1	85.8	86.6	52.2	53.4	51	53.2	2	*Gallus gallus* NP_001001756.2
3	3.6	3.6		97	96.5	97.4	96.9	97.6	97.6	94.9	85.6	86	52	53.1	50.4	52.4	3	*Coturnix japonica* XP_015728261.1
4	2.8	2.8	3		98.6	98.6	98	98.8	98.8	96.3	86.2	87	51.8	52.8	50.4	52.4	4	*Meleagris gallopavo* XP_010715503.1
5	3.4	3.4	3.6	1.4		98	97.4	98.2	98.2	96.5	86.4	86.8	51.8	52.8	50.2	52.4	5	*Phasianus colchicus* XP_031472169.1
6	2.6	2.6	2.6	1.4	2		99.4	99.8	99.8	96.5	86.4	87	51.8	52.8	50.4	52.4	6	*Centrocercus urophasianus* XP_042680493.1
7	3.2	3.2	3.2	2	2.6	0.6		99.2	99.2	95.9	85.8	86.4	51.4	52.2	50.4	52.4	7	*Tympanuchus pallidicinctus* XP_052527651.1
8	2.4	2.4	2.4	1.2	1.8	0.2	0.8		100	96.3	86.4	86.8	51.8	52.8	50.2	52.1	8	*Lagopus muta* XP_048811992.1
9	2.4	2.4	2.4	1.2	1.8	0.2	0.8	0		96.3	86.4	86.8	51.8	52.8	50.2	52.1	9	*Lagopus leucura* XP_042741718.1
10	5.1	5.1	5.3	3.8	3.6	3.6	4.3	3.8	3.8		86.8	87	51.8	53.4	50.4	52.7	10	*Numida meleagris* XP_021263081.1
11	15.8	15.8	16	15.3	15	15	15.8	15	15	14.5		96.5	51.9	53.9	50.5	53.5	11	*Cygnus olor* XP_040426514.1
12	14.8	14.8	15.5	14.3	14.5	14.3	15	14.5	14.5	14.3	3.6		52.4	54.5	51.3	54.1	12	*Anas platyrhynchos* XP_027322111.2
13	74.5	74.3	74.8	75.2	75.2	75.2	76.3	75.2	75.2	75.2	75	73.6		100	75.8	76	13	*Homo sapiens* NP_000772.2
14	71.7	71.3	72	72.7	72.7	72.7	74.1	72.7	72.7	71.3	70	68.7	0		76	76	14	*Homo sapiens* NP_001093243.1
15	77.5	77.2	78.8	78.8	79.3	78.8	78.8	79.3	79.3	78.8	78.6	76.5	29.2	29		100	15	*Mus musculus* NP_062753.3
16	72	71.7	73.7	73.7	73.7	73.7	73.7	74.4	74.4	73	71	69.6	29	29	0		16	*Mus musculus* NP_001333716.1
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16		

Figure S3. Consistency and divergence of CYP11A1 amino acid sequences between pheasant species and non-pheasant species. Values above the diagonal represent sequence identity,while values below the diagonal represent sequence divergence.

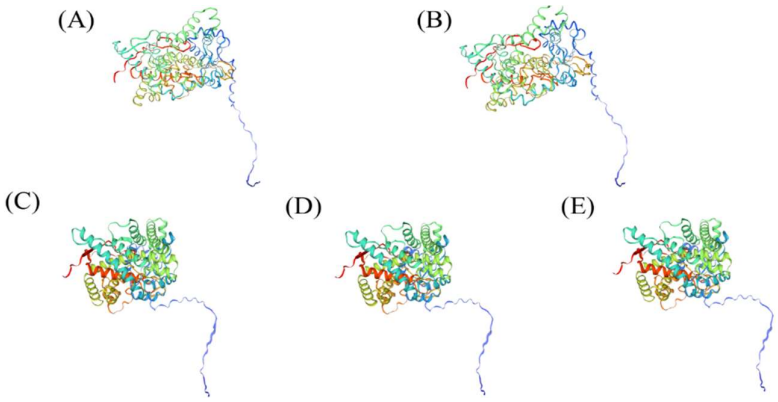


Figure S4. Predicted tertiary structure of CYP11A1 protein in Wuding chicken and other phasianidae species. (A) Wuding chicken; (B) Chicken; (C) Japanese quail; (D) Turkey; (E) Ring-necked pheasant; Prediction software is SOPMA.