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A Genetic Analysis of Taoyuan Pig and Its Phylogenetic Relationship to Eurasian Pig Breeds

Kuan-Yi Li^a, Kuang-Ti Li^{1,a}, Chun-Chun Cheng², Chia-Hsuan Chen³, Chien-Yi Hung, and Yu-Ten Ju*

Department of Animal Science and Technology, National Taiwan University, Taipei 10673, Taiwan

- Supplementary Data -

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Supplementary Table S1. Information from the 18 microsatellite markers used

Satellite	Chromosome	Length	Forward and reverse primers	Annealing temperature (°C)	Fluorescence [†]
SW24	17q	96-120	5'-CTTTGGGTGGAGTGCCTGC-3' 5'-ATCCAAATGCTGCAAGCG-3'	58	HEX
SW72	3p	42-162	5'-TGAGAGGTCAAGTTACAGAAGACC-3' 5'-GATCCTCCTCCAAATCCCAT-3'	58	HEX
SW122	6q	116-138	5'-TTGTCTTTTTATTTTGGCTTTTGG-3' 5'-CAAAAAGGCAAAAAGATTGACA-3'	58	HEX
SW951	10q	120-136	5'-TTTCACAACCTCVGGCACCAG-3' 5'-GATCCTGCCCAAATGGAC-3'	58	HEX
S0215	13q	138-170	5'-TAGGCTCAGACCCTGCTGCAT-3' 5'-TGGGAGGCTGAAGGATTGGGT-3'	55	HEX
SW857	14q	96-114	5'-AGAAATTAGTGCCCTCAAATTGG-3' 5'-AAACCATTAAGTCCCTAGCAAA-3'	58	FAM
S0155	1q	148-170	5'-TGTTCTCTGTTTCTCCTCTGTTTGG-3' 5'-AAAGTGAAAGAGTCAATGGCTAT-3'	55	FAM
SW911	9p	157-173	5'-CTCAGTTCTTTGGGACTGAACC-3' 5'-CATCTGTGGAAAAAAAAGCC-3'	58	FAM
S0386	11q	156-172	5'-TCCTGGGTCTTATTTTCTA-3' 5'-TTTTTATCTCCAACAGTAT-3'	48	FAM
S0218	x	158-188	5'-GTGTAGGCTGGCGGTTGT-3' 5'-CCCTGAAACCTAAAGCAAAG-3'	55	FAM
S0225	8q	170-194	5'-GCTAATGCCAGAGAAATGCAGA-3' 5'-CAGGTGAAAGAATGGAATGAA-3'	55	FAM
S0226	2q	176-214	5'-GCACTTTTAACCTTTCATGATACTCC-3' 5'-GGTTAAACTTTTNCCTCAATACA-3'	55	FAM
S0005	5q	206-278	5'-TCCTTCCCTCCTGGTAACTA-3' 5'-GCACTTCCTGATTCTGGGTA-3'	58	FAM
IGF1	5q	194-250	5'-GCTTGGATGGACCATGTTG-3' 5'-CATATTTTCTGCATAACTTGAACCT-3'	58	TAMRA
S0068	13q	190-262	5'-AGTGGTCTCTCTCCCTCTTGCT-3' 5'-CCTTCAACCTTTGCGCAAGAAC-3'	58	TAMRA
S0228	6q	221-243	5'-GGCATAGGCTGGCAGCAACA-3' 5'-AGCCACCTCATCTTATCTACACT-3'	58	TAMRA
S0227	4p	228-258	5'-GATCCATTTATAATTTTAGCACAAAGT-3' 5'-GCATGGTGTGATGCTATGTCAAGC-3'	58	TAMRA
S0355	15q	236-276	5'-TCTGGCTCCTACACTCCTTCTTGATG-3' 5'-TTGGGTGGGTGCTGAAAAATAGGA-3'	58	TAMRA

[†] FAM, 6-carboxyfluorescein; HEX, hexachlorofluorescein; TAMRA, carboxytetramethylrhodamine.



Supplementary Figure S1. A picture of a 5-month-old female Taoyuan pig.



Supplementary Figure S2. Maximum likelihood phylogenetic tree based on Taoyuan, Asian, and European pig control region sequences.