凱馨烏骨雞之微衛星遺傳標記多態性分析

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前　言

凱馨錦達雞選育族群係凱馨實業股份有限公司於2008年進駐行政院農業委員會畜產試驗所創新育成中心，進行「有色雞種育種及飼養模式之建立」育成案，針對種原固定、雛白痢篩檢、膚色及產蛋性能進行選育所育成之烏骨雞群。微衛型遺傳標記提供大量多態性及幾近中性的遺傳訊息，除被應用於基因定位與標記輔助選拔，以及探討物種族群分化程度與保育遺傳學的研究外，也被應用於親子鑑定與法醫學的鑑識中，是一種強力的分子遺傳指紋的技術。試本試驗應用24組微衛星型遺傳標記來評估此選育族群的遺傳多態性。

材料與方法

以含EDTAK_3抗凝劑的採血器採集64隻凱馨錦達雞選育族群第G3世代種雞個體之翼靜脈血樣，再使用核酸萃取試劑組(EasyPure Genomic DNA Extraction Kit, Taiwan)萃取血樣DNA。應用FAO(2010)建議使用的24組雞微衛星標記組(MCW0295、MCW0014、LEI0192、MCW0111、MCW0216、MCW0183、MCW0206、ADL0112、MCW0069、ADL0268、MCW0067、MCW0098、ADL0278、MCW0248、MCW0103、MCW0330、MCW0037、MCW0222、MCW0081、MCW0034、MCW0016、MCW0078、LEI0234與LEI0258)微衛星標記組進行聚合酶連瑣反應後，使用ABI 3730核酸定序儀進行微衛星遺傳標記分析，以Excel Microsatellite Toolkit 套裝軟體進行多態性分析。

結　果

使用的24組雞微衛星標記組分析64隻凱馨錦達雞選育族群第G3世代種雞個體DNA。其中除MCW0103微衛星標記所檢測的基因型在所有檢測個體皆為單型外，其它23組微衛星標記皆有檢出多態型的基因型。共檢測到98個對偶基因，平均每個基因座具有4.1個對偶基因(0~7個)；期望異質度介於0到0.798，平均為0.548；觀測異質度介於0到0.641，平均為0.400，而多態性訊息含量平均為0.491 (表1)。

結　論

選用的24組微衛星標記組中有13 組呈現高度多態性資訊(PIC ≥ 0.5)，有9組呈現中度多態性資訊(0.5> PIC ≥ 0.25)，2組呈現低度多態性資訊(PIC < 0.25)。本結果提供此選育族群遺傳多態性之基本分子資訊。

表 1. 凱馨錦達雞選育族群之微衛星型遺傳標記分析

Markers	chromo-some	Fragment (bp)	Number of alleles	Expected heterozygosity	Observed heterozygosity	PIC
MCW0295	4	87~99	5	0.627	0.641	0.552
MCW0014	6	167~181	3	0.508	0.078	0.416
LEI0192	6	254~302	6	0.769	0.359	0.728
MCW0111	1	98~104	4	0.576	0.469	0.505
MCW0216	13	142~146	3	0.574	0.438	0.506
MCW0183	7	293~317	4	0.176	0.094	0.168
MCW0206	2	221~229	4	0.711	0.547	0.652
ADL0112	10	122~128	3	0.625	0.594	0.541
MCW0069	E60C04W23	157~173	4	0.339	0.250	0.315
ADL0268	1	100~112	4	0.730	0.547	0.673
MCW0067	10	177~183	3	0.447	0.359	0.401
MCW0098	4	255~257	2	0.502	0.375	0.374
ADL0278	8	109-127	7	0.771	0.547	0.734
MCW0248	W29	215~233	3	0.465	0.344	0.398
MCW0103	3	268	1	0	0	0
MCW0330	17	254~284	4	0.660	0.547	0.594
MCW0037	3	153~157	3	0.553	0.547	0.447
MCW0222	3	220~224	3	0.412	0.375	0.331
MCW0081	5	109~133	4	0.435	0.266	0.400
MCW0034	2	223~237	7	0.630	0.531	0.592
MCW0016	3	137~147	5	0.758	0.531	0.707
MCW0078	5	133~143	5	0.415	0.141	0.383
LEI0234	2	217~311	4	0.674	0.484	0.608
LEI0258	16	206~384	7	0.798	0.531	0.760
Mean ± SD			4.1±1.5	0.55±0.19	0.40±0.18	0.49±0.19

Polymorphism analysis of Kai Shing silkie chicken by microsatellite markers

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In order to evaluate genetic variation of Kai Shing silkie chicken flock. we use a set of 24 microsatellite markers recommended by FAO to analyze 64 candidate bred chickens from this flock. Except MCW0103, all the microsatellites were polymorphic with average allelic number 4.1, ranged from 0 to 7 per locus. The expected heterozygosity ranged from 0 to 0.798, and the average expected heterozygosity was 0.548. The observed heterozygosity of the population ranged from 0 to 0.641, and the average observed heterozygosity was 0.400. The estimated average polymorphic information content (PIC) was 0.491. In 24 markers, 13 markers were highly informative with polymorphism information content (PIC ≥ 0.50), nine markers were reasonably informative(0.5 > PIC ≥ 0.25) and the other two markers were slightly informative (PIC < 0.25). These results could be provided basic molecular information for the research on the germplasm characteristics of the population.