

## V. SIMPULAN DAN SARAN

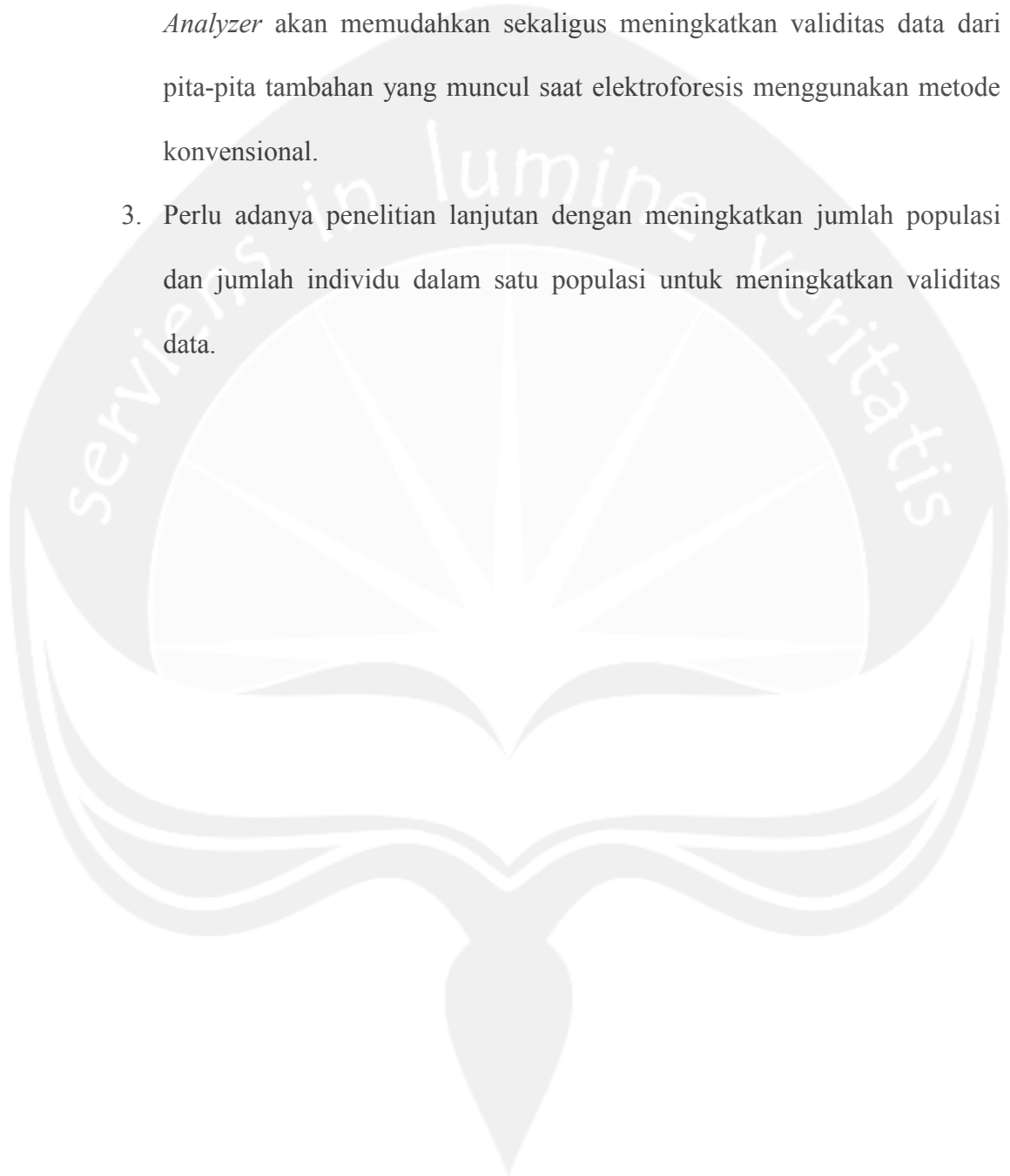
### A. Simpulan

1. Nilai keragaman genetik populasi burung walet sarang putih di Riau tergolong tinggi, yaitu sebesar 0,855. Demikian juga nilai keragaman genetik populasi burung walet sarang putih di Airmolek sebesar 0,855 dan nilai keragaman genetik populasi burung walet sarang putih di Belilas sebesar 0,875.
2. Hasil perhitungan Amova menunjukkan variasi genetik diantara populasi burung walet sarang putih di Airmolek dengan di Belilas sangat kecil, yaitu 2,772 %. Variasi antar individu dalam suatu populasi cukup tinggi, yaitu 22,268 %. Variasi dalam setiap individunya dapat dikatakan tinggi, yaitu 74,960 %.
3. Populasi burung walet sarang putih di Airmolek dan Belilas masih dalam satu populasi dan belum terjadi isolasi antara dua populasi tersebut ( $F_{st} = 2,8\%$ ).

### B. Saran

1. Pita – pita tambahan (*extra band* atau *stutter band*) yang muncul pada hasil elektroforesis dapat merupakan hasil PCR yang kurang optimal. Perlu adanya optimalisasi dengan metode touchdown PCR untuk mengurangi munculnya pita – pita tambahan (*extra band* atau *stutter band*).

2. Pembacaan hasil elektroforesis cukup membingungkan jika mengandalkan gel documentation. Penggunaan alat *genotyping* seperti *ABI 3500 Genetic Analyzer* akan memudahkan sekaligus meningkatkan validitas data dari pita-pita tambahan yang muncul saat elektroforesis menggunakan metode konvensional.
3. Perlu adanya penelitian lanjutan dengan meningkatkan jumlah populasi dan jumlah individu dalam satu populasi untuk meningkatkan validitas data.



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## LAMPIRAN

### I. Hasil perhitungan menggunakan *software Arlequin*

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#### ANALYSES AT THE INTRA-GROUP LEVEL

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Sample : Group1

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#### Standard diversity indices : (Group1)

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No. of gene copies : 20  
 No. of loci : 3  
 No. of usable loci : 3 loci with less than 5.00 % missing data  
 No. of polymorphic loci : 3

Results are only shown for polymorphic loci

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Locus#	Num. gene copies	Num. alleles	Obs. Het.	Exp. Het	Allelic range	G-W stat.
1	20	6	0.50000	0.82632	40	0.14634
2	20	8	1.00000	0.90000	61	0.12903
3	20	7	0.50000	0.81053	37	0.18421
Mean	20.000	7.000	0.66667	0.84561	46.000	0.15319
s.d.	0.000	1.000	0.28868	0.04776	13.077	0.02822

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#### Molecular diversity indices : (Group1)

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Sample size : 20.00000  
 No. of haplotypes : 20  
 Allowed level of missing data : 5.00000 %  
 Number of usable loci : 3  
 Distance method : No. of different alleles  
 Average gene diversity over loci : 0.845614 +/- 0.529841  
 (Standard deviations are for both the sampling and the stochastic processes)

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**Pairwise linkage disequilibrium : (Group1)**


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**Test of linkage disequilibrium for all pairs of loci:**

Permutation test using the EM algorithm

Number of permutations : 10000

Number of initial conditions for EM : 2

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Pair	LnLHood LD	LnLHood LE	Exact P	Chi-square test value
(0, 1)	-46.91475	-62.69600	0.46198 ± 0.00612 (10100 permutations done) (P = 0.63483, 35 d.f.)	31.56249
(0, 2)	-45.35855	-60.27676	0.20812 ± 0.00423 (10100 permutations done) (P = 0.47406, 30 d.f.)	29.83640
(1, 2)	-46.91475	-63.31747	0.60436 ± 0.00527 (10100 permutations done) (P = 0.84453, 42 d.f.)	32.80544

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**Histogram of the number of linked loci per locus**


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Locus:	0	1	2
	0	0	0

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**Table of significant linkage disequilibrium (significance level=0.0500):**


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Locus #	0	1	2
0	*	-	-
1	-	*	-
2	-	-	*

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**Hardy-Weinberg equilibrium : (Group1)**


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Exact test using a Markov chain (for all Loci):

Forecasted chain length :1000000

Dememorization steps :100000

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Locus #	Genot	Obs.Het.	Exp.Het.	P-value	s.d.	Steps done
1	10	0.50000	0.82632	0.00663	0.00008	1001000
2	10	1.00000	0.90000	0.89452	0.00027	1001000
3	10	0.50000	0.81053	0.00491	0.00006	1001000

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Sample : Group2

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Standard diversity indices : (Group2)

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No. of gene copies : 18  
 No. of loci : 3  
 No. of usable loci : 3 loci with less than 5.00 % missing data  
 No. of polymorphic loci : 3  
 Results are only shown for polymorphic loci

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Locus#	Num. gene copies	Num. alleles	Obs. Het.	Exp. Het	Allelic range	G-W stat.
1	18	6	0.44444	0.83007	50	0.11765
2	18	9	0.77778	0.86928	61	0.14516
3	18	8	0.77778	0.88889	44	0.17778
Mean	18.000	7.667	0.66667	0.86275	51.667	0.14686
s.d.	0.000	1.528	0.19245	0.02995	8.622	0.03010

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Molecular diversity indices : (Group2)

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Sample size : 18.00000  
 No. of haplotypes : 18

Allowed level of missing data : 5.00000 %  
 Number of usable loci : 3

Distance method : No. of different alleles  
 Average gene diversity over loci : 0.862745 +/- 0.541873  
 (Standard deviations are for both the sampling and the stochastic processes)

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**Pairwise linkage disequilibrium : (Group2)**


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Test of linkage disequilibrium for all pairs of loci:

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 Permutation test using the EM algorithm

Number of permutations : 10000

Number of initial conditions for EM : 2

Pair	LnLHood LD	LnLHood LE	Exact P	Chi-square test value
(0, 1)	-40.41309	-57.24562	0.13248 ± 0.00352 (10100 permutations done) (P = 0.74981, 40 d.f.)	33.66507
(0, 2)	-40.93634	-56.90582	0.24723 ± 0.00447 (10100 permutations done) (P = 0.61666, 35 d.f.)	31.93897
(1, 2)	-43.01578	-60.37156	0.86525 ± 0.00346 (10100 permutations done) (P = 0.98866, 56 d.f.)	34.71156

Histogram of the number of linked loci per locus

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 Locus: 0 1 2

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 0 0 0  
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Table of significant linkage disequilibrium (significance level=0.0500):

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 Locus # | 0 | 1 | 2 |

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 0 | \* - -  
 1 | - \* -  
 2 | - - \*  
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Hardy-Weinberg equilibrium : (Group2)

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Exact test using a Markov chain (for all Loci):

Forecasted chain length :1000000

Dememorization steps :100000

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Locus	#Genot	Obs.Het.	Exp.Het.	P-value	s.d.	Steps done
1	9	0.44444	0.83007	0.00895	0.00009	1001000
2	9	0.77778	0.86928	0.08791	0.00017	1001000
3	9	0.77778	0.88889	0.21445	0.00036	1001000

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Summary of computations done within groups

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Basic properties

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Statistics	Group1	Group2	Mean	s.d.
No. of gene copies	20	18	19.000	1.414
No. of loci	3	3	3.000	0.000
No. of usable loci	3	3	3.000	0.000
No. of polym. loci	3	3	3.000	0.000

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Expected heterozygosity <sumExpHeterozygosity samp="heteroz" time="17/10/13 at 19:01:04">

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Locus#	Group1	Group2	Mean	s.d.	Tot. Het.
1	0.82632	0.83007	0.82819	0.00265	0.85633
2	0.90000	0.86928	0.88464	0.02172	0.91465
3	0.81053	0.88889	0.84971	0.05541	0.84495
Mean	0.84561	0.86275	0.85418	0.01211	0.87198
s.d.	0.04776	0.02995	0.03885	0.01259	0.03739

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Theta(H) under the stepwise mutation model</data> <sumThetaH samp="thetaH" time="17/10/13 at 19:01:04">

Locus#	Group1	Group2	Mean	s.d.
1	16.07484	16.81435	16.44459	0.52291
2	49.50000	28.76125	39.13063	14.66451
3	13.42747	40.00000	26.71373	18.78962

Theta from  
Mean H 3.32992 3.72240 3.52616 0.27753

Number of alleles</data> <sumNumAlleles samp="numAlleles" time="17/10/13 at 19:01:04">

Locus#	Group1	Group2	Mean	s.d.	Tot. number
1	6	6	6.000	0.000	8
2	8	9	8.500	0.707	11
3	7	8	7.500	0.707	9
Mean	7.000	7.667	7.333	0.471	9.333
s.d.	1.000	1.528	1.264	0.373	1.528

Allelic size range</data> <sumAllelicSizeRange samp="range" time="17/10/13 at 19:01:04">

Locus#	Group1	Group2	Mean	s.d.	Tot. range
1	40	50	45.000	7.071	59
2	61	61	61.000	0.000	61
3	37	44	40.500	4.950	49
Mean	46.000	51.667	48.833	4.007	56.333
s.d.	13.077	8.622	10.849	3.150	6.429

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 Garza-Williamson index</data> <sumGWIndex samp="GWIndex"  
 time="17/10/13 at 19:01:04">  
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Locus#	Group1	Group2	Mean	s.d.
1	0.14634	0.11765	0.13199	0.02029
2	0.12903	0.14516	0.13710	0.01140
3	0.18421	0.17778	0.18099	0.00455
Mean	0.15319	0.14686	0.15003	0.00448
s.d.	0.02822	0.03010	0.02916	0.00133

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 Garza-Williamson modified index</data> <sumModGWIndex  
 samp="modGWIndex" time="17/10/13 at 19:01:04">  
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Locus#	Group1	Group2	Mean	s.d.
1	0.10000	0.10000	0.10000	0.00000
2	0.12903	0.14516	0.13710	0.01140
3	0.14000	0.16000	0.15000	0.01414
Mean	0.12301	0.13505	0.12903	0.00852
s.d.	0.02067	0.03125	0.02596	0.00748

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### GENETIC STRUCTURE ANALYSIS

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Number of usable loci for distance computation : 3  
 Allowed level of missing data : 0.05000

List of usable loci :

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 1 2 3

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### Comparisons of pairs of population samples

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List of labels for population samples used below:

</data> <pairDistPopLabels time="17/10/13 at 19:01:04">

Label Population name

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1: Group1

2: Group2

</pairDistPopLabels> <data>

Population pairwise FSTs

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</data> <PairFstMat time="17/10/13 at 19:01:04">

Distance method: No. of different alleles (FST)

	1	2
1	0.00000	
2	0.04012	0.00000

</PairFstMat> <data>

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FST P values

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Number of permutations : 110

</data> <PairFstPvalMat time="17/10/13 at 19:01:04">

	1	2
1	*	
2	0.11712+-0.0360	*

</PairFstPvalMat> <data>

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Matrix of significant Fst P values

Significance Level=0.0500

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Number of permutations : 110

	1	2
1	-	
2	-	

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 Population average pairwise differences  
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Above diagonal : Average number of pairwise differences between populations  
 ( $P_{iXY}$ )

Diagonal elements : Average number of pairwise differences within population  
 ( $P_{iX}$ )

Below diagonal : Corrected average pairwise difference  $(P_{iXY} - (P_{iX} + P_{iY})/2)$

Distance method: No. of different alleles (FST)

</data> <pairwiseDifferenceMatrix time="17/10/13 at 19:01:04">

	1	2
1	2.53684	2.66944
2	0.10691	2.58824

</pairwiseDifferenceMatrix> <data>

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 PXY P value  
 -----

	1
2	0.10000

-----  
 Corrected PXY P value  
 -----

	1
2	0.11818

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 Matrix of coancestry coefficients as  $t/M = -\ln(1-F_{ST})$   
 ( $M=N$  for haploid data,  $M=2N$  for diploid data)  
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	1	2
1	-0.00000	
2	0.04095	-0.00000

</coancestryCoefficients> <data>

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Locus by locus AMOVA:

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Distance method for locus-by-locus analysis: No. of different alleles (FST)

List of loci with only one allele:

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AMOVA Results for polymorphic loci only:

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Among populations:

Locus	SSD	d.f.	Va	% variation
1	0.93655	1	0.01712	3.87784
2	0.98216	1	0.02874	6.09949
3	0.37602	1	-0.00889	-2.11023

Among Individuals:

Locus	SSD	d.f.	Vb	% variation
1	10.40556	17	0.18762	42.48834
2	7.43889	17	-0.00489	-1.03845
3	9.25556	17	0.11433	27.14147

Within Individuals:

Locus	SSD	d.f.	Vc	% variation
1	4.50000	19	0.23684	53.63382
2	8.50000	19	0.44737	94.93896
3	6.00000	19	0.31579	74.96876

Fixation indices:

Locus	FIS	P-value	FST	P-value	FIT	P-value
1	0.44202	0.00000	0.03878	0.42229	0.46366	0.00000
2	-0.01106	0.70088	0.06099	0.08407	0.05061	0.51515
3	0.26581	0.00978	-0.02110	0.99609	0.25031	0.01955



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**Global AMOVA results as a weighted average over loci**


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 AMOVA design and results (average over 3 loci):  
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Source of variation	Sum of squares	Variance components	Percentage variation
Among populations	2.295	0.03698	2.77182
Among individuals within populations	27.100	0.29706	22.26768
Within individuals	19.000	1.00000	74.96050
Total	48.395	1.33404	

Average F-Statistics over all loci

Fixation Indices

FIS : 0.22902

FST : 0.02772

FIT : 0.25040

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 Significance tests (1023 permutations)  
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Vb and FIS : P(rand. value > obs. value) = 0.00000

P(rand. value = obs. value) = 0.00000

P-value = 0.00000

Va and FST : P(rand. value > obs. value) = 0.55327

P(rand. value = obs. value) = 0.00000

P-value = 0.55327

Vc and FIT : P(rand. value < obs. value) = 0.00000

P(rand. value = obs. value) = 0.00000

P-value = 0.00000

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 Population specific FIS indices per polymorphic locus (absolute values)  
 -----

Locus	Average FIS	Group1	Group2
1	0.44202	0.40789	0.47967
2	-0.01106	-0.11801	0.11111
3	0.26581	0.39597	0.13178

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 Population specific FIS indices per polymorphic locus (relative values (%)  
 compared to average FIS)  
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Locus	Average FIS	Group1	Group2
1	0.44202	-7.721	8.518
2	-0.01106	967.110	-1104.706
3	0.26581	48.971	-50.421

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 == Exact Test of Sample Differentiation Based on Genotype Frequencies  
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List of labels for population samples used below:  
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Label	Population name
1	Group1
2	Group2

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 Global test of differentiation among sample:  
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Non-differentiation: Exact P value = 1.00000 +- 0.00000 (30000 Markov steps done)

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 Differentiation test between all pairs of samples:  
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Markov chain length : 100000 steps)

Non-differentiation exact P values :

1	
2	1.00000+-0.0000

-----  
 Table of significant differences (significance level=0.0500):  
 -----

	1	2
1	-	
2	-	

-----  
 Histogram of the number of significant different populations (significance level=0.0500):  
 -----

	1	2
	0	0

-----

## II. Hasil perhitungan menggunakan *software* FSTAT

### Populasi Airmolek

\*\*\*\*\*  
 The following results were generated the 10/17/2013 at 5:40:58 AM with Fstat  
 for windows, V2.9.3 2 (Feb. 2002) from file A1-A10-FSTAT.dat.  
 \*\*\*\*\*

	pop1	All_W	All_UW
Locus: Aef 27			
N	10		
p: 222	0.150	0.150	0.150
p: 228	0.100	0.100	0.100
p: 234	0.100	0.100	0.100
p: 242	0.350	0.350	0.350
p: 253	0.100	0.100	0.100
p: 262	0.200	0.200	0.200

	pop1	All_W	All_UW
Locus: Aef 10			
N	10		
p: 172	0.150	0.150	0.150
p: 176	0.150	0.150	0.150
p: 185	0.100	0.100	0.100
p: 192	0.150	0.150	0.150
p: 202	0.200	0.200	0.200
p: 215	0.150	0.150	0.150
p: 220	0.050	0.050	0.050
p: 233	0.050	0.050	0.050

	pop1	All_W	All_UW
Locus: Aef 13			
N	10		
p: 193	0.050	0.050	0.050
p: 198	0.150	0.150	0.150
p: 201	0.100	0.100	0.100
p: 209	0.400	0.400	0.400
p: 215	0.100	0.100	0.100
p: 223	0.050	0.050	0.050
p: 230	0.150	0.150	0.150

\*\*\*\*\*

Gene diversity per locus and population :

Aef 27 0.844

Aef 10 0.894

Aef 13 0.828

\*\*\*\*\*

number of alleles sampled :

Aef 27 6 6

Aef 10 8 8

Aef 13 7 7

\*\*\*\*\*

Allelic Richness per locus and population

based on min. sample size of: 10 diploid individuals.

Aef 27 6.000 6.000

Aef 10 8.000 8.000

Aef 13 7.000 7.000

\*\*\*\*\*

Fis Per population :

Aef 27 0.408

Aef 10 -0.118

Aef 13 0.396

All 0.221

\*\*\*\*\*

P-value for Fis within samples.

based on : 60 randomisations.

Indicative adjusted nominal level (5%) for one table is : 0.01667

Proportion of randomisations that gave a LARGER Fis than the observed:

Aef 27 0.0167

Aef 10 1.0000

Aef 13 0.0333

All 0.0333

Proportion of randomisations that gave a SMALLER Fis than the observed:

Aef 27 1.0000

Aef 10 0.3500

Aef 13 1.0000

All 1.0000

\*\*\*\*\*

P-value for genotypic disequilibrium

based on 60 permutations.

Adjusted P-value for 5% nominal level is : 0.016667

All  
Aef 27 X Aef 10 1.00000  
Aef 27 X Aef 13 1.00000  
Aef 10 X Aef 13 0.10000

**Populasi Belilas**

\*\*\*\*\*

The following results were generated the 10/17/2013 at 5:06:05 AM with Fstat for windows, V2.9.3 2 (Feb. 2002) from file B1-B9-FSTAT.dat.

\*\*\*\*\*

	pop1	All_W	All_UW
Locus: Aef 27			
N	9		
p: 203	0.167	0.167	0.167
p: 212	0.111	0.111	0.111
p: 222	0.333	0.333	0.333
p: 228	0.056	0.056	0.056
p: 242	0.111	0.111	0.111
p: 253	0.222	0.222	0.222

Locus: Aef 10			
N	9		
p: 172	0.056	0.056	0.056
p: 182	0.333	0.333	0.333
p: 185	0.111	0.111	0.111
p: 192	0.056	0.056	0.056
p: 197	0.167	0.167	0.167
p: 202	0.056	0.056	0.056
p: 208	0.056	0.056	0.056
p: 215	0.111	0.111	0.111
p: 233	0.056	0.056	0.056

Locus: Aef 13			
N	9		
p: 198	0.222	0.222	0.222
p: 201	0.056	0.056	0.056
p: 203	0.111	0.111	0.111
p: 209	0.222	0.222	0.222
p: 215	0.111	0.111	0.111
p: 223	0.167	0.167	0.167
p: 230	0.056	0.056	0.056
p: 242	0.056	0.056	0.056

\*\*\*\*\*

Gene diversity per locus and population :

Aef 27 0.854

Aef 10 0.875

Aef 13 0.896

\*\*\*\*\*

number of alleles sampled :

Aef 27	6	6
Aef 10	9	9
Aef 13	8	8

\*\*\*\*\*

Allelic Richness per locus and population  
based on min. sample size of: 9 diploid individuals.

Aef 27	6.000	6.000
Aef 10	9.000	9.000
Aef 13	8.000	8.000

\*\*\*\*\*

Fis Per population :

Aef 27	0.480
Aef 10	0.111
Aef 13	0.132
All	0.238

\*\*\*\*\*

P-value for Fis within samples.

based on : 60 randomisations.

Indicative adjusted nominal level (5%) for one table is : 0.01667

Proportion of randomisations that gave a LARGER Fis than the observed:

Aef 27	0.0333
Aef 10	0.3167
Aef 13	0.2667
All	0.0167

Proportion of randomisations that gave a SMALLER Fis than the observed:

Aef 27	1.0000
Aef 10	0.9667
Aef 13	0.9333
All	1.0000

\*\*\*\*\*

P-value for genotypic disequilibrium

based on 60 permutations.

Adjusted P-value for 5% nominal level is : 0.016667

All		
Aef 27 X Aef 10		1.00000
Aef 27 X Aef 13		1.00000
Aef 10 X Aef 13		1.00000

### Populasi Riau (Populasi Airmolek dan Populasi Belilas )

\*\*\*\*\*  
 The following results were generated the 10/28/2013 at 2:27:46 AM with  
 Fstat for windows, V2.9.3 2 (Feb. 2002) from file A1-B9-FSTAT.dat.  
 \*\*\*\*\*

	pop1	pop2	All_W	All_UW
Locus: Locus 27				
N	10	9		
p: 203	0.000	0.167	0.079	0.083
p: 212	0.000	0.111	0.053	0.056
p: 222	0.150	0.333	0.237	0.242
p: 228	0.100	0.056	0.079	0.078
p: 234	0.100	0.000	0.053	0.050
p: 242	0.350	0.111	0.237	0.231
p: 253	0.100	0.222	0.158	0.161
p: 262	0.200	0.000	0.105	0.100

	10	9		
Locus: Locus 104				
N	10	9		
p: 172	0.150	0.056	0.105	0.103
p: 176	0.150	0.000	0.079	0.075
p: 182	0.000	0.333	0.158	0.167
p: 185	0.100	0.111	0.105	0.106
p: 192	0.150	0.056	0.105	0.103
p: 197	0.000	0.167	0.079	0.083
p: 202	0.200	0.056	0.132	0.128
p: 208	0.000	0.056	0.026	0.028
p: 215	0.150	0.111	0.132	0.131
p: 220	0.050	0.000	0.026	0.025
p: 233	0.050	0.056	0.053	0.053

	10	9		
Locus: Locus 133				
N	10	9		
p: 193	0.050	0.000	0.026	0.025
p: 198	0.150	0.222	0.184	0.186
p: 201	0.100	0.056	0.079	0.078
p: 203	0.000	0.111	0.053	0.056
p: 209	0.400	0.222	0.316	0.311
p: 215	0.100	0.111	0.105	0.106
p: 223	0.050	0.167	0.105	0.108
p: 230	0.150	0.056	0.105	0.103
p: 242	0.000	0.056	0.026	0.028



\*\*\*\*\*

Gene diversity per locus and population :

Locus 27	0.844	0.854
Locus 104	0.894	0.875
Locus 133	0.828	0.896

\*\*\*\*\*

number of alleles sampled :

Locus 27	6	6	8
Locus 104	8	9	11
Locus 133	7	8	9

\*\*\*\*\*

Allelic Richness per locus and population

based on min. sample size of: 9 diploid individuals.

Locus 27	5.984	6.000	7.107
Locus 104	7.795	9.000	9.134
Locus 133	6.789	8.000	7.339

\*\*\*\*\*

Fis Per population :

Locus 27	0.408	0.480
Locus 104	-0.118	0.111
Locus 133	0.396	0.132

All	0.221	0.238
-----	-------	-------

\*\*\*\*\*

P-value for Fis within samples.

based on : 120 randomisations.

Indicative adjusted nominal level (5%) for one table is : 0.00833

Proportion of randomisations that gave a LARGER Fis than the observed:

Locus 27	0.0167	0.0083
Locus 104	1.0000	0.2000
Locus 133	0.0083	0.2750

All	0.0333	0.0083
-----	--------	--------

Proportion of randomisations that gave a SMALLER Fis than the observed:

Locus 27	0.9917	1.0000
Locus 104	0.2667	0.9500
Locus 133	1.0000	0.9667

All	1.0000	1.0000
-----	--------	--------

\*\*\*\*\*

Nei's estimation of heterozygosity

LocName	Ho	Hs	Ht	Dst	Dst'	Ht'	Gst	Gst'	Gis
Locus 27	0.472	0.849	0.866	0.017	0.034	0.883	0.020	0.039	0.444
Locus 104	0.889	0.884	0.913	0.029	0.057	0.942	0.031	0.061	-0.005
Locus 133	0.639	0.862	0.853	-0.009	-0.018	0.844	-0.010	-0.021	0.259
Overall	0.667	0.865	0.878	0.012	0.025	0.890	0.014	0.028	0.229

\*\*\*\*\*

P-value for genotypic disequilibrium

based on 60 permutations.

Adjusted P-value for 5% nominal level is : 0.016667

All

Locus 27 X Locus 104	1.00000
Locus 27 X Locus 133	1.00000
Locus 104 X Locus 133	0.25000

\*\*\*\*\*

Weir & Cockerham (1984) estimation of Fit (CapF), Fst (theta) and Fis (smallF).

relat is Relatedness estimated following Queller & Goodnight (1989)

relatc is relatedness inbreeding corrected following Pamilo (1984, 1985)

sig\_a, sig\_b and sig\_w are the component of variance

among samples, among individuals within samples and within individuals respectively.

For locus : Locus 27

Allele	Capf	Theta	Smallf	Relat	Relatc	Sig_a	Sig_b	Sig_w
203	0.670	0.096	0.634	0.115				
212	1.000	0.012	1.000	0.012				
222	0.583	0.006	0.580	0.008				
228	0.640	-0.082	0.668	-0.100				
234	-0.005	0.048	-0.056	0.097				
242	0.325	0.085	0.262	0.129				
253	0.230	-0.011	0.239	-0.019				
262	0.495	0.126	0.422	0.169				
All	0.464	0.039	0.442	0.053	-1.584	0.034	0.375	0.474

For locus : Locus 104

Allele	Capf	Theta	Smallf	Relat	Relatc	Sig_a	Sig_b	Sig_w
172	-0.092	-0.002	-0.090	-0.004				
176	-0.008	0.102	-0.122	0.206				
182	0.673	0.288	0.541	0.344				
185	-0.117	-0.051	-0.063	-0.116				
192	-0.092	-0.002	-0.090	-0.004				
197	0.009	0.135	-0.146	0.268				
202	-0.101	0.045	-0.153	0.099				
208	0.003	0.006	-0.003	0.012				
215	-0.148	-0.043	-0.101	-0.101				
220	-0.003	-0.006	0.003	-0.011				
233	-0.056	-0.055	-0.000	-0.117				
All	0.051	0.061	-0.011	0.116	0.022	0.057	-0.010	0.895

For locus : Locus 133

Allele	Capf	Theta	Smallf	Relat	Relatc	Sig_a	Sig_b	Sig_w
193	-0.003	-0.006	0.003	-0.011				
198	-0.215	-0.027	-0.183	-0.069				
201	0.640	-0.082	0.668	-0.100				
203	1.000	0.012	1.000	0.012				
209	0.530	-0.011	0.535	-0.015				
215	-0.117	-0.051	-0.063	-0.116				
223	-0.079	0.024	-0.105	0.051				
230	0.454	-0.034	0.472	-0.047				
242	0.003	0.006	-0.003	0.012				
All	0.250	-0.021	0.266	-0.034	-0.724	-0.018	0.229	0.632

\*\*\*\*\*

Over all loci

Capf	Theta	Smallf	Relat	Relatc	Sig_a	Sig_b	Sig_w
0.250	0.028	0.229	0.044	-0.724	0.074	0.594	2.000

\*\*\*\*\*