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LAMPIRAN

Lampiran Uji T dimensi tubuh pada Locus GH1 dan GH2 menggunakan software SPSS

Dimensi lingkar dada GH1 dan GH2

Group Statistics

	Genotype	N	Mean	Std. Deviation	Std. Error Mean
GH1	AA	17	28,8471	2,10717	,51106
	AB	22	28,0500	2,77845	,59237

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	T	df
GH1	Equal variances assumed	,328	,570	,983	37
	Equal variances not assumed			1,019	36,995

Independent Samples Test

		t-test for Equality of Means			
		Sig. (2-tailed)	Mean Difference	Std. Error Difference	95% Confidence Interval of the Difference Lower
GH1	Equal variances assumed	,332	,79706	,81063	-,84542
	Equal variances not assumed	,315	,79706	,78236	-,78816

Independent Samples Test

		t-test for Equality of Means: 95% Confidence Interval of the Difference: Upper
GH1	Equal variances assumed	2,43954
	Equal variances not assumed	2,38227

Group Statistics

	Genotype	N	Mean	Std. Deviation	Std. Error Mean
GH1	AA	17	28,8471	2,10717	,51106
	BB	23	29,7691	1,75419	,36577

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	t	df
GH1	Equal variances assumed	,264	,611	-1,509	38
	Equal variances not assumed			-1,467	30,727

Independent Samples Test

		t-test for Equality of Means			
		Sig. (2-tailed)	Mean Difference	Std. Error Difference	95% Confidence Interval of the Difference: Lower
GH1	Equal variances assumed	,140	-,92207	,61116	-2,15929
	Equal variances not assumed	,152	-,92207	,62847	-2,20431

Independent Samples Test

		t-test for Equality of Means
		95% Confidence Interval of the Difference
		Upper
GH1	Equal variances assumed	,31515
	Equal variances not assumed	,36017

Group Statistics

	Genotype	N	Mean	Std. Deviation	Std. Error Mean
GH1	AB	22	28,0500	2,77845	,59237
	BB	23	29,7691	1,75419	,36577

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	T	df
GH1	Equal variances assumed	1,197	,280	-2,494	43
	Equal variances not assumed			-2,469	35,184

Independent Samples Test

		t-test for Equality of Means			
		Sig. (2-tailed)	Mean Difference	Std. Error Difference	95% Confidence Interval of the Difference Lower
GH1	Equal variances assumed	,017	-1,71913	,68942	-3,10948
	Equal variances not assumed	,019	-1,71913	,69620	-3,13222

Group Statistics

	Genotype	N	Mean	Std. Deviation	Std. Error Mean
GH2	CC	46	29,0998	2,46376	,36326
	CD	9	28,7889	1,89766	,63255

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	T	df
GH2	Equal variances assumed	,337	,564	,357	53
	Equal variances not assumed			,426	13,879

Independent Samples Test

		t-test for Equality of Means			
		Sig. (2-tailed)	Mean Difference	Std. Error Difference	95% Confidence Interval of the Difference Lower
GH2	Equal variances assumed	,722	,31089	,87000	-1,43411
	Equal variances not assumed	,676	,31089	,72944	-1,25489

Independent Samples Test

		t-test for Equality of Means
		95% Confidence Interval of the Difference Upper
GH2	Equal variances assumed	2,05590
	Equal variances not assumed	1,87667

Group Statistics

	Genotype	N	Mean	Std. Deviation	Std. Error Mean
GH2	CC	46	29,0998	2,46376	,36326
	DD	3	28,6333	,49329	,28480

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	t	df
GH2	Equal variances assumed	1,915	,173	,324	47
	Equal variances not assumed			1,011	12,349

Independent Samples Test

		t-test for Equality of Means			
		Sig. (2-tailed)	Mean Difference	Std. Error Difference	95% Confidence Interval of the Difference Lower
GH2	Equal variances assumed	,747	,46645	1,43781	-2,42605
	Equal variances not assumed	,332	,46645	,46160	-,53614

Independent Samples Test

		t-test for Equality of Means
		95% Confidence Interval of the Difference Upper
GH2	Equal variances assumed	3,35895
	Equal variances not assumed	1,46904

Group Statistics

	Genotype	N	Mean	Std. Deviation	Std. Error Mean
GH2	CD	9	28,7889	1,89766	,63255
	DD	3	28,6333	,49329	,28480

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	t	df
GH2	Equal variances assumed	2,183	,170	,136	10
	Equal variances not assumed			,224	9,939

Independent Samples Test

		t-test for Equality of Means			
		Sig. (2-tailed)	Mean Difference	Std. Error Difference	95% Confidence Interval of the Difference Lower
GH2	Equal variances assumed	,894	,15556	1,14106	-2,38689
	Equal variances not assumed	,827	,15556	,69371	-1,39142

Independent Samples Test

		t-test for Equality of Means
		95% Confidence Interval of the Difference Upper
GH2	Equal variances assumed	2,69800
	Equal variances not assumed	1,70254

Dimensi bobot badan GH1 dan GH2

Group Statistics

	Genotype	N	Mean	Std. Deviation	Std. Error Mean
GH1	AA	17	1,4476	,16475	,03996
	AB	22	1,3973	,15489	,03302

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	t	df
GH1	Equal variances assumed	,653	,424	,980	37
	Equal variances not assumed			,972	33,436

Independent Samples Test

		t-test for Equality of Means			
		Sig. (2-tailed)	Mean Difference	Std. Error Difference	95% Confidence Interval of the Difference Lower
GH1	Equal variances assumed	,334	,05037	,05142	-,05381
	Equal variances not assumed	,338	,05037	,05184	-,05504

Independent Samples Test

t-test for Equality of Means
95% Confidence Interval of the Difference
Upper

GH1	Equal variances assumed	,15456
	Equal variances not assumed	,15579

Group Statistics

	Genotype	N	Mean	Std. Deviation	Std. Error Mean
GH1	AA	17	1,4476	,16475	,03996
	BB	23	1,5700	,22863	,04767

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	t	df
GH1	Equal variances assumed	3,103	,086	-1,873	38
	Equal variances not assumed			-1,967	37,989

Independent Samples Test

		t-test for Equality of Means			
		Sig. (2-tailed)	Mean Difference	Std. Error Difference	95% Confidence Interval of the Difference Lower
GH1	Equal variances assumed	,069	-,12235	,06531	-,25456
	Equal variances not assumed	,057	-,12235	,06220	-,24828

Independent Samples Test

		t-test for Equality of Means
		95% Confidence Interval of the Difference
		Upper
GH1	Equal variances assumed	,00986
	Equal variances not assumed	,00358

Group Statistics

	Genotype	N	Mean	Std. Deviation	Std. Error Mean
GH1	AB	22	1,3973	,15489	,03302
	BB	23	1,5700	,22863	,04767

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	t	df
GH1	Equal variances assumed	6,466	,015	-2,953	43
	Equal variances not assumed			-2,978	38,816

Independent Samples Test

		t-test for Equality of Means			
		Sig. (2-tailed)	Mean Difference	Std. Error Difference	95% Confidence Interval of the Difference Lower
GH1	Equal variances assumed	,005	-,17273	,05848	-,29067
	Equal variances not assumed	,005	-,17273	,05799	-,29005

Independent Samples Test

		t-test for Equality of Means
		95% Confidence Interval of the Difference
		Upper
GH1	Equal variances assumed	-,05478
	Equal variances not assumed	-,05541

Group Statistics

	Genotype	N	Mean	Std. Deviation	Std. Error Mean
GH2	CC	46	1,4954	,20289	,02991
	CD	9	1,3789	,21239	,07080

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	T	df
GH2	Equal variances assumed	,029	,865	1,565	53
	Equal variances not assumed			1,516	11,049

Independent Samples Test

		t-test for Equality of Means			
		Sig. (2-tailed)	Mean Difference	Std. Error Difference	95% Confidence Interval of the Difference Lower
GH2	Equal variances assumed	,124	,11655	,07448	-,03285
	Equal variances not assumed	,158	,11655	,07686	-,05253

Independent Samples Test

		t-test for Equality of Means
		95% Confidence Interval of the Difference Upper
GH2	Equal variances assumed	,26594
	Equal variances not assumed	,28562

Group Statistics

	Genotype	N	Mean	Std. Deviation	Std. Error Mean
GH2	CD	9	1,3789	,21239	,07080
	DD	3	1,3500	,14799	,08544

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	t	df
GH2	Equal variances assumed	,279	,609	,215	10
	Equal variances not assumed			,260	5,090

Independent Samples Test

		t-test for Equality of Means			
		Sig. (2-tailed)	Mean Difference	Std. Error Difference	95% Confidence Interval of the Difference Lower
GH2	Equal variances assumed	,834	,02889	,13411	-,26993
	Equal variances not assumed	,805	,02889	,11096	-,25484

Independent Samples Test

		t-test for Equality of Means
		95% Confidence Interval of the Difference Upper
GH2	Equal variances assumed	,32771
	Equal variances not assumed	,31262

Group Statistics

	Genotype	N	Mean	Std. Deviation	Std. Error Mean
GH2	CC	46	1,4954	,20289	,02991
	DD	3	1,3500	,14799	,08544

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	t	df
GH2	Equal variances assumed	,532	,470	1,215	47
	Equal variances not assumed			1,607	2,519

Independent Samples Test

		t-test for Equality of Means			
		Sig. (2-tailed)	Mean Difference	Std. Error Difference	95% Confidence Interval of the Difference Lower
GH2	Equal variances assumed	,230	,14543	,11969	-,09534
	Equal variances not assumed	,223	,14543	,09053	-,17645

Independent Samples Test

		t-test for Equality of Means 95% Confidence Interval of the Difference Upper
GH2	Equal variances assumed	,38621
	Equal variances not assumed	,46732

Dimensi Sayap GH1 dan GH2

Group Statistics

	Genotype	N	Mean	Std. Deviation	Std. Error Mean
GH1	AA	17	19,7894	1,71949	,41704
	AB	22	19,5045	2,82615	,60254

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	t	df
GH1	Equal variances assumed	2,088	,157	,366	37
	Equal variances not assumed			,389	35,305

Independent Samples Test

		t-test for Equality of Means			
		Sig. (2-tailed)	Mean Difference	Std. Error Difference	95% Confidence Interval of the Difference Lower
GH1	Equal variances assumed	,717	,28487	,77849	-1,29250
	Equal variances not assumed	,700	,28487	,73278	-1,20230

Group Statistics

	Genotype	N	Mean	Std. Deviation	Std. Error Mean
GH1	AB	22	19,5045	2,82615	,60254
	BB	23	20,2957	2,07265	,43218

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	t	df
GH1	Equal variances assumed	1,369	,248	-1,074	43
	Equal variances not assumed			-1,067	38,451

Independent Samples Test

		t-test for Equality of Means			
		Sig. (2-tailed)	Mean Difference	Std. Error Difference	95% Confidence Interval of the Difference Lower
GH1	Equal variances assumed	,289	-,79111	,73645	-2,27631
	Equal variances not assumed	,293	-,79111	,74150	-2,29163

Independent Samples Test

		t-test for Equality of Means 95% Confidence Interval of the Difference Upper
GH1	Equal variances assumed	,69409
	Equal variances not assumed	,70941

Group Statistics

	Genotype	N	Mean	Std. Deviation	Std. Error Mean
GH1	AA	17	19,7894	1,71949	,41704
	BB	23	20,2957	2,07265	,43218

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	t	df
GH1	Equal variances assumed	,147	,704	-,819	38
	Equal variances not assumed			-,843	37,426

Independent Samples Test

		t-test for Equality of Means			
		Sig. (2-tailed)	Mean Difference	Std. Error Difference	95% Confidence Interval of the Difference Lower
GH1	Equal variances assumed	,418	-,50624	,61789	-1,75710
	Equal variances not assumed	,405	-,50624	,60058	-1,72267

Independent Samples Test

		t-test for Equality of Means
		95% Confidence Interval of the Difference Upper
GH1	Equal variances assumed	,74462
	Equal variances not assumed	,71019

Dimensi Panjang Dada GH1 dan GH2

Group Statistics

	Genotype	N	Mean	Std. Deviation	Std. Error Mean
GH1	AA	17	10,9941	,77255	,18737
	AB	22	11,7082	1,70242	,36296

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	t	df
GH1	Equal variances assumed	2,907	,097	-1,603	37
	Equal variances not assumed			-1,748	30,812

Independent Samples Test

		t-test for Equality of Means			
		Sig. (2-tailed)	Mean Difference	Std. Error Difference	95% Confidence Interval of the Difference Lower
GH1	Equal variances assumed	,117	-,71406	,44547	-1,61668
	Equal variances not assumed	,090	-,71406	,40847	-1,54735

Independent Samples Test

		t-test for Equality of Means
		95% Confidence Interval of the Difference
		Upper
GH1	Equal variances assumed	,18855
	Equal variances not assumed	,11922

Group Statistics

	Genotype	N	Mean	Std. Deviation	Std. Error Mean
GH1	AA	17	10,9941	,77255	,18737
	BB	23	11,7435	1,21012	,25233

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	t	df
GH1	Equal variances assumed	1,177	,285	-2,235	38
	Equal variances not assumed			-2,384	37,340

Independent Samples Test

		t-test for Equality of Means			
		Sig. (2-tailed)	Mean Difference	Std. Error Difference	95% Confidence Interval of the Difference Lower
GH1	Equal variances assumed	,031	-,74936	,33532	-1,42818
	Equal variances not assumed	,022	-,74936	,31429	-1,38597

Independent Samples Test

		t-test for Equality of Means
		95% Confidence Interval of the Difference
		Upper
GH1	Equal variances assumed	-,07054
	Equal variances not assumed	-,11275

Group Statistics

	Genotype	N	Mean	Std. Deviation	Std. Error Mean
GH1	AB	22	11,7082	1,70242	,36296
	BB	23	11,7435	1,21012	,25233

Independent Samples Test

		Levene's Test for Equality of Variances		t-test for Equality of Means	
		F	Sig.	t	df
GH1	Equal variances assumed	,898	,349	-,080	43
	Equal variances not assumed			-,080	37,780

Independent Samples Test

		t-test for Equality of Means			
		Sig. (2-tailed)	Mean Difference	Std. Error Difference	95% Confidence Interval of the Difference Lower
GH1	Equal variances assumed	,936	-,03530	,43876	-,92013
	Equal variances not assumed	,937	-,03530	,44205	-,93035

Independent Samples Test

		t-test for Equality of Means
		95% Confidence Interval of the Difference Upper
GH1	Equal variances assumed	,84954
	Equal variances not assumed	,85976

Analisa Keragaman Gen Aplikasi Popgene 3.21 pada Locus GH1

```
   ********************************************************************************
   **                                                                            **
   **                  Multi-populations Descriptive Statistics                  **
   **                                                                            **
   ********************************************************************************



* Overall @ Locus : AA        *
============================================================
Genotypes    Obs. (O)   Exp. (E)   (O-E)²/E     2*O*Ln(O/E)
============================================================
(A, A)           16     11.8264       1.4728    9.6720
(B, A)           22     30.3471       2.2959  -14.1530
(B, B)           23     18.8264       0.9252    9.2107
============================================================


Chi-square test for Hardy-Weinberg equilibrium :

    Chi-square :              4.693974
    Degree of freedom :       1
    Probability :             0.030269


Likelihood ratio test for Hardy-Weinberg equilibrium :

    G-square :                4.729685
    Degree of freedom :       1
    Probability :             0.029646

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~


Overall Allele Frequency :
==============================
Allele \ Locus      AA
==============================
Allele A            0.4426
Allele B            0.5574
==============================


Overall Summary Statistics:


   ********************************************************************************
   **                                                                            **
   **             Summary of Heterozygosity Statistics for All Loci              **
   **                                                                            **
   ********************************************************************************


================================================================================
Locus     Sample Size  Obs Hom   Obs Het   Exp Hom*  Exp Het*  Nei**     Ave Het
================================================================================
 AA              122    0.6393    0.3607    0.5025    0.4975    0.4934    0.4934

Mean             122    0.6393    0.3607    0.5025    0.4975    0.4934    0.4934
St. Dev                 0.0000    0.0000    0.0000    0.0000    0.0000    0.0000
================================================================================
*  Expected homozygosty and heterozygosity were computed using Levene (1949)
** Nei's (1973) expected heterozygosity


The number of polymorphic loci is :      1
The percentage of polymorphic loci is :  100.00 %
```

Analisa Keragaman Gen Aplikasi Popgene 1.32 pada Locus GH2

```
* Overall @ Locus : CC        *
============================================================
Genotypes     Obs. (O)    Exp. (E)    (O-E)²/E      2*O*Ln(O/E)
============================================================
(A, A)               0      0.0000      0.0000     0.0000
(B, A)               0      0.0000      0.0000     0.0000
(B, B)               0      0.0000      0.0000     0.0000
(C, A)               0      0.0000      0.0000     0.0000
(C, B)               0      0.0000      0.0000     0.0000
(C, C)              48     47.3982      0.0076     1.2111
(D, A)               0      0.0000      0.0000     0.0000
(D, B)               0      0.0000      0.0000     0.0000
(D, C)               8      9.2035      0.1574    -2.2423
(D, D)               1      0.3982      0.9093     1.8415
============================================================


Chi-square test for Hardy-Weinberg equilibrium :

    Chi-square :              1.074367
    Degree of freedom :       1
    Probability :             0.299961


Likelihood ratio test for Hardy-Weinberg equilibrium :

    G-square :                0.810252
    Degree of freedom :       1
    Probability :             0.368046

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
```

```
==============================
Allele \ Locus      CC
==============================
Allele A
Allele B
Allele C            0.9123
Allele D            0.0877
==============================


Overall Summary Statistics:


   ********************************************************************************************
   **                                                                                        **
   **              Summary of Heterozygosity Statistics for All Loci                         **
   **                                                                                        **
   ********************************************************************************************


=============================================================================
Locus     Sample Size  Obs Hom   Obs Het   Exp Hom*  Exp Het*  Nei**     Ave Het
=============================================================================
 CC              114    0.8596    0.1404    0.8385    0.1615    0.1600    0.1600

Mean             114    0.8596    0.1404    0.8385    0.1615    0.1600    0.1600
St. Dev                 0.0000    0.0000    0.0000    0.0000    0.0000    0.0000
=============================================================================
*  Expected homozygosty and heterozygosity were computed using Levene (1949)
** Nei's (1973) expected heterozygosity



The number of polymorphic loci is :      1
The percentage of polymorphic loci is :  100.00 %
```

Dokumentasi Kegiatan (Keterangan)

Keterangan : Membuat gel agarose untuk analisa PCR-RFLP

Keterangan : Menimbang bahan

Keterangan : Menuang cairan pelarut gel

Keterangan : Memasukkan sampel ke dalam gel

Keterangan : Melakukan analisa sampel pada gen GH1 dan GH2