

ACKNOWLEDGMENT

We are grateful to Yamanashi Pegintron Ribavirin Study Group and Ochanomizu Liver Conference Group for their cooperation and advices. Especially, we thank Asuka Kanayama and Takako Ohmori for their technical assistance, and Takatoshi Kitamura and Shunichi Okada for their cooperation and advices.

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65

REFERENCES

1. Ghany MG, Strader DB, Thomas DL, Seeff LB. Diagnosis, management, and treatment of hepatitis C: an update. *Hepatology*2009 Apr;49(4):1335-74.
2. Di Bisceglie AM, Martin P, Kassianides C, Lisker-Melman M, Murray L, Waggoner J, Goodman Z, Banks SM, Hoofnagle JH. Recombinant interferon alfa therapy for chronic hepatitis C. A randomized, double-blind, placebo-controlled trial. *N Engl J Med*1989 Nov 30;321(22):1506-10.
3. Haydon GH, Jarvis LM, Blair CS, Simmonds P, Harrison DJ, Simpson KJ, Hayes PC. Clinical significance of intrahepatic hepatitis C virus levels in patients with chronic HCV infection. *Gut*1998 Apr;42(4):570-5.
4. Simmonds P. Clinical relevance of hepatitis C virus genotypes. *Gut*1997 Mar;40(3):291-3.
5. Hadziyannis SJ, Sette H, Jr., Morgan TR, Balan V, Diago M, Marcellin P, Ramadori G, Bodenheimer H, Jr., Bernstein D, Rizzetto M, Zeuzem S, Pockros PJ, Lin A, Ackrill AM. Peginterferon-alpha2a and ribavirin combination therapy in chronic hepatitis C: a randomized study of treatment duration and ribavirin dose. *Ann Intern Med*2004 Mar 2;140(5):346-55.
6. Manns MP, McHutchison JG, Gordon SC, Rustgi VK, Shiffman M, Reindollar R, Goodman ZD, Koury K, Ling M, Albrecht JK. Peginterferon alfa-2b plus ribavirin compared with interferon alfa-2b plus ribavirin for initial treatment of chronic hepatitis C: a randomised trial. *Lancet*2001 Sep 22;358(9286):958-65.
7. Dalgard O, Bjoro K, Hellum KB, Myrvang B, Ritland S, Skaug K, Raknerud N, Bell H. Treatment with pegylated interferon and ribavirin in HCV infection with genotype 2 or 3 for 14 weeks: a pilot study. *Hepatology*2004 Dec;40(6):1260-5.
8. Mangia A, Santoro R, Minerva N, Ricci GL, Carretta V, Persico M, Vinelli F, Scotto G, Bacca D, Annese M, Romano M, Zechini F, Sogari F, Spirito F, Andriulli A. Peginterferon alfa-2b and ribavirin for 12 vs. 24 weeks in HCV genotype 2 or 3. *N Engl J Med*2005 Jun

1
2 23:352(25):2609-17.
3

4 9. Enomoto N, Sakuma I, Asahina Y, Kurosaki M, Murakami T, Yamamoto C, Ogura
5 Y, Izumi N, Marumo F, Sato C. Mutations in the nonstructural protein 5A gene and response
6 to interferon in patients with chronic hepatitis C virus 1b infection. *N Engl J Med*1996 Jan
7 11:334(2):77-81.
8

9
10
11
12 10. El-Shamy A, Nagano-Fujii M, Sasase N, Imoto S, Kim SR, Hotta H. Sequence
13 variation in hepatitis C virus nonstructural protein 5A predicts clinical outcome of pegylated
14 interferon/ribavirin combination therapy. *Hepatology*2008 Jul;48(1):38-47.
15

16
17
18 11. Hamano K, Sakamoto N, Enomoto N, Izumi N, Asahina Y, Kurosaki M, Ueda E,
19 Tanabe Y, Maekawa S, Itakura J, Watanabe H, Kakinuma S, Watanabe M. Mutations in the
20 NS5B region of the hepatitis C virus genome correlate with clinical outcomes of
21 interferon-alpha plus ribavirin combination therapy. *J Gastroenterol Hepatol*2005
22 Sep;20(9):1401-9.
23

24
25
26 12. Chayama K, Suzuki F, Tsubota A, Kobayashi M, Arase Y, Saitoh S, Suzuki Y,
27 Murashima N, Ikeda K, Takahashi N, Kinoshita M, Kumada H. Association of amino acid
28 sequence in the PKR-eIF2 phosphorylation homology domain and response to interferon
29 therapy. *Hepatology*2000 Nov;32(5):1138-44.
30

31
32
33 13. Akuta N, Suzuki F, Sezaki H, Suzuki Y, Hosaka T, Someya T, Kobayashi M, Saitoh
34 S, Watahiki S, Sato J, Matsuda M, Arase Y, Ikeda K, Kumada H. Association of amino acid
35 substitution pattern in core protein of hepatitis C virus genotype 1b high viral load and
36 non-virological response to interferon-ribavirin combination therapy. *Intervirology*2005
37 Nov-Dec;48(6):372-80.
38

39
40
41 14. Toyoda H, Kumada T, Tada T, Arakawa T, Hayashi K, Honda T, Katano Y, Goto H.
42 Association between HCV amino acid substitutions and outcome of peginterferon and
43 ribavirin combination therapy in HCV genotype 1b and high viral load. *J Gastroenterol*
44 Hepatol2010 Jun;25(6):1072-8.
45

46
47
48 15. Donlin MJ, Cannon NA, Aurora R, Li J, Wahed AS, Di Bisceglie AM, Tavis JE.
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65

- 1
2 Contribution of genome-wide HCV genetic differences to outcome of interferon-based
3 therapy in Caucasian American and African American patients. *PLoS One*2010;5(2):e9032.
4
5
6 16. Donlin MJ, Cannon NA, Yao E, Li J, Wahed A, Taylor MW, Belle SH, Di Bisceglie
7 AM, Aurora R, Tavis JE. Pretreatment sequence diversity differences in the full-length
8 hepatitis C virus open reading frame correlate with early response to therapy. *J Virol*2007
9 Aug;81(15):8211-24.
10
11 17. Murakami T, Enomoto N, Kurosaki M, Izumi N, Marumo F, Sato C. Mutations in
12 nonstructural protein 5A gene and response to interferon in hepatitis C virus genotype 2
13 infection. *Hepatology*1999 Oct;30(4):1045-53.
14
15 18. Hayashi K, Katano Y, Honda T, Ishigami M, Itoh A, Hirooka Y, Nakano I, Urano F,
16 Yoshioka K, Toyoda H, Kumada T, Goto H. Mutations in the interferon
17 sensitivity-determining region of hepatitis C virus genotype 2a correlate with response to
18 pegylated-interferon-alpha 2a monotherapy. *J Med Virol*2009 Mar;81(3):459-66.
19
20 19. Kobayashi M, Watanabe K, Ishigami M, Murase K, Ito H, Ukai K, Yano M, Takagi
21 K, Hattori M, Kakumu S, Yoshioka K. Amino acid substitutions in the nonstructural region
22 5A of hepatitis C virus genotypes 2a and 2b and its relation to viral load and response to
23 interferon. *Am J Gastroenterol*2002 Apr;97(4):988-98.
24
25 20. Akuta N, Suzuki F, Hirakawa M, Kawamura Y, Yatsuji H, Sezaki H, Suzuki Y,
26 Hosaka T, Kobayashi M, Saitoh S, Arase Y, Ikeda K, Kumada H. Association of Amino Acid
27 Substitution Pattern in Core Protein of Hepatitis C Virus Genotype 2a High Viral Load and
28 Virological Response to Interferon-Ribavirin Combination Therapy. *Intervirology*2009 May
29 5;52(6):301-9.
30
31 21. Saito T, Ito T, Ishiko H, Yonaha M, Morikawa K, Miyokawa A, Mitamura K.
32 Sequence analysis of PePHD within HCV E2 region and correlation with resistance of
33 interferon therapy in Japanese patients infected with HCV genotypes 2a and 2b. *Am J*
34 *Gastroenterol*2003 Jun;98(6):1377-83.
35
36 22. Watanabe H, Nagayama K, Enomoto N, Itakura J, Tanabe Y, Sato C, Izumi N,
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65

- 1
2 Watanabe M. Amino acid substitutions in PKR-eIF2 phosphorylation homology domain
3 (PePHD) of hepatitis C virus E2 protein in genotype 2a/2b and 1b in Japan and interferon
4 efficacy. *Hepatology* 2003 Aug;26(4):268-74.
5
6
7
8
9
10 23. Gale M, Jr., Blakely CM, Kwieciszewski B, Tan SL, Dossett M, Tang NM, Korth
11 MJ, Polyak SJ, Gretch DR, Katze MG. Control of PKR protein kinase by hepatitis C virus
12 nonstructural 5A protein: molecular mechanisms of kinase regulation. *Mol Cell Biol* 1998
13 Sep;18(9):5208-18.
14
15
16 24. Hiramatsu N, Oze T, Yakushijin T, Inoue Y, Igura T, Mochizuki K, Imanaka K,
17 Kaneko A, Oshita M, Hagiwara H, Mita E, Nagase T, Ito T, Inui Y, Hijioka T, Katayama K,
18 Tamura S, Yoshihara H, Imai Y, Kato M, Yoshida Y, Tatsumi T, Ohkawa K, Kiso S, Kanto T,
19 Kasahara A, Takehara T, Hayashi N. Ribavirin dose reduction raises relapse rate
20 dose-dependently in genotype 1 patients with hepatitis C responding to pegylated interferon
21 alpha-2b plus ribavirin. *J Viral Hepat* 2009 Aug;16(8):586-94.
22
23
24
25
26
27
28
29 25. Ge D, Fellay J, Thompson AJ, Simon JS, Shianna KV, Urban TJ, Heinzen EL, Qiu
30 P, Bertelsen AH, Muir AJ, Sulkowski M, McHutchison JG, Goldstein DB. Genetic variation
31 in IL28B predicts hepatitis C treatment-induced viral clearance. *Nature* 2009 Sep
32 17;461(7262):399-401.
33
34
35
36
37
38 26. Tanaka Y, Nishida N, Sugiyama M, Kurosaki M, Matsuura K, Sakamoto N,
39 Nakagawa M, Korenaga M, Hino K, Hige S, Ito Y, Mita E, Tanaka E, Mochida S, Murawaki
40 Y, Honda M, Sakai A, Hiasa Y, Nishiguchi S, Koike A, Sakaida I, Imamura M, Ito K, Yano K,
41 Masaki N, Sugauchi F, Izumi N, Tokunaga K, Mizokami M. Genome-wide association of
42 IL28B with response to pegylated interferon-alpha and ribavirin therapy for chronic
43 hepatitis C. *Nat Genet* 2009 Oct;41(10):1105-9.
44
45
46
47
48
49
50 27. Rauch A, Kutalik Z, Descombes P, Cai T, di Iulio J, Mueller T, Bochud M, Battegay
51 M, Bernasconi E, Borovicka J, Colombo S, Cerny A, Dufour JF, Furrer H, Gunthard HF,
52 Heim M, Hirschel B, Malinverni R, Moradpour D, Mullhaupt B, Witteck A, Beckmann JS,
53 Berg T, Bergmann S, Negro F, Telenti A, Bochud PY. Genetic variation in IL28B is
54
55
56
57
58
59
60
61
62
63
64
65

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65

Associated with Chronic Hepatitis C and Treatment Failure - A Genome-Wide Association
Study. *Gastroenterology* 2010 Jan 7.

FIGURE LEGENDS

Fig.1 Number of amino acid substitutions per sample in the sustained viral responders (SVR) and the non-sustained viral responders (non-SVR) group.

The numbers of variations, relative to a population consensus, that were unique to either SVR or non-SVR patients are shown for the full open reading frame (ORF) (Fig.1, left) and for each HCV protein (Fig.1, right).

Fig.2a Different amino acid usages at each viral amino acid position between the sustained viral responders (SVR) and the non-sustained viral responders (non-SVR) patients.

Amino acid variation was determined between SVR and non-SVR patients by Fisher's exact probability test. The longitudinal axis shows the $-\log P$ value.

Fig.2b Sequence alignment in the core region.

Dashes indicate amino acids identical to the consensus sequence and substituted amino acids are shown by standard single letter codes.

Fig.2c Sliding window analysis.

Viral regions affecting treatment outcome are shown as red spots. There are four hot spots: at core amino acid 110, amino acids 400-403 (i.e. the hyper variable region) in Envelope2 (E2) region, amino acids 724-743 in E2 and amino acids 2258-2306 in the nonstructural (NS)5A.

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65

Fig.2d Sequence alignment amino acids in the nonstructural (NS)5A around amino acids 2258 to 2306.

Dashes indicate amino acids identical to the consensus sequence and substituted amino acids are shown by standard single letter codes.

Fig.3 Correlation between pretreatment HCV RNA levels and the number of substitutions in the NS5A region aa 2258 to 2306.

Spearman's correlation coefficient by rank test is demonstrated.

Table

Table 1. Baseline Characteristics of All Patients (Group 1 and 2)

Characteristic	SVR (n = 58)			non-SVR (n = 20)			P value ^Δ
	Group 1 (n = 36)	Group 2 (n = 22)	Combined (n = 58)	Group 1 (n = 7)	Group 2 (n = 13)	Combined (n = 20)	
Gender(Male/Female)	20 / 16	9 / 13	29 / 29	4 / 3	5 / 8	9 / 11	0.80 [†]
Age(yrs)	50.0 ± 12.5*	57.3 ± 10.0	52.4 ± 12.1	55.0 ± 9.7	59.8 ± 6.4	58.1 ± 7.8	0.058 [†]
ALT(IU/l)	86.6 ± 86.6	71.2 ± 50.4	80.5 ± 74.2	52.9 ± 29.3	88.1 ± 90.1	75.8 ± 75.5	0.81 [‡]
Platelet($\times 10^3$ /mm ³)	20.8 ± 6.2	19.0 ± 5.2	20.1 ± 5.8	14.7 ± 7.1	19.1 ± 4.9	17.6 ± 6.0	0.11 [‡]
Fibrosis score(0-2 / ≥ 3) [§]	34 / 1	19 / 2	53 / 3	4 / 3	11 / 2	15 / 5	0.049 [†]
HCV RNA(KIU/ml)	750(2-3100)**	340(54-3600)	550(12-3600)	1300 (350-30000)	1400 (180-5000)	1300 (180-30000)	0.002 [†]
IFN dose($\geq 80\%$ / 60-80%) [¶]	28 / 4	21 / 1	49 / 5	4 / 3	11 / 2	15 / 5	0.12 [†]
Ribavirin dose($\geq 80\%$ / 60-80%) [¶]	27 / 5	17 / 5	44 / 10	4 / 3	5 / 8	9 / 11	0.003 [†]
RVR rate (%)	87.5	54.5	74.1	33.3	46.1	42.1	0.022 [†]
EVR rate (%)	100	100	100	66.7	100	89.4	0.07 [†]

* : mean ± SD ** : median (range) † : Fisher's exact probability test ‡ : Student t test || : Mann-Whitney's U test Δ : P values between all SVR (n = 58) vs. all non-SVR (n = 20)

Several clinical characteristics listed below were unavailable in some patients

§ : SVR : n = 56 (35 in group1, 21 in group2), non-SVR : n = 17 (7 in group1, 10 in group2) ¶ : SVR : n = 54 (32 in group1, 22 in group2)

Table 2a. Variations in each Amino Acid Position and SVR rate

Position	Group 1 (n = 43)	P value	Group 2 (n = 35)	P value	Combined (n = 78)	P value
Core aa 110	T	100% (19 / 19)	82.9% (13 / 14)	0.01	97% (32 / 33)	5E - 05
	non T	70.8% (17 / 24)	42.9% (9 / 21)	0.004	57.8% (26 / 45)	
p7 aa 773	V	77.4% (24 / 31)	53.6% (15 / 28)	0.16	66.1% (39 / 59)	0.002
	non V	100% (12 / 12)	100% (7 / 7)	0.03	100% (19 / 19)	
NS5A aa 2099	R	92.9% (13 / 14)	91.7% (11 / 12)	0.40	92.3% (24 / 26)	0.01
	non R	79.3% (23 / 29)	47.8% (11 / 23)	0.01	65.4% (34 / 52)	
NS5B aa 3013	L	78.9% (26 / 33)	47.8% (11 / 23)	0.17	66.1% (37 / 56)	0.008
	non L	100% (10 / 10)	91.7% (11 / 12)	0.01	95.5% (21 / 22)	

Table 2b. Number of Amino Acid Substitutions in each Region and SVR rate

Region	Group 1 (n = 43)	P value	Group 2 (n = 35)	P value	Combined (n = 78)	P value
E2 aa 400-403	mutation ≥2	89.3% (25 / 28)	100% (11 / 11)	0.002	92.3% (36 / 39)	0.0005
	mutation 0-1	73.3% (11 / 15)	45.8% (11 / 24)		56.4% (22 / 39)	
E2 aa 724-743	mutation ≥1	100% (28 / 28)	72% (18 / 25)	0.0002	86.8% (46 / 53)	0.0006
	no mutation	53.3% (8 / 15)	40% (4 / 10)		48% (12 / 25)	
ISDR(aa 2213-2248)	mutation ≥2	100% (15 / 15)	86.7% (13 / 15)	0.08	93.3% (28 / 30)	0.003
	mutation 0-1	75% (21 / 28)	46% (9 / 20)		62.5% (30 / 48)	
NS5A aa 2256-2306	mutation ≥5	100% (19 / 19)	84.2% (16 / 19)	0.01	92.1% (35 / 38)	0.0006
	mutation 0-4	70.8% (17 / 24)	37.5% (6 / 16)		57.5% (23 / 40)	

Table 3. Multivariate Logistic Regression Analysis

Factor	Odds (95% CI)	P value
Age	1.01 (0.91-1.13)	0.85
HCV RNA	1.00 (1.00-1.00)	0.09
Fibrosis score ≥3/0-2	2.37 (0.21-26.7)	0.48
RVR achievement	3.46 (0.54-22.1)	0.19
Ribavirin dose ≥ 80%	16.0 (1.66-163)	0.02
Core aa 110 T	24.7 (1.72-353)	0.02
NS5A aa 2258-2306 mutations 0-4/25	11.5 (1.23-108)	0.03

Table 4a. Baseline Characteristics of Patients with NS5A aa 2258-2306 mutations 0-4 or ≥5 (Group 1 and 2)

Characteristic	Mutation 0-4 (n = 40)	Mutation ≥5 (n = 38)	P value
Gender (Male/Female)	22 / 18	16 / 22	NS [†]
Age (yrs)	54.3 ± 11.4*	53.5 ± 11.5	NS [‡]
ALT (IU/l)	73.8 ± 70.3	85.3 ± 78.7	NS [‡]
Platelet (x10 ⁹ /mm ³)	16.0 ± 5.9	21.0 ± 5.7	0.03 [‡]
Fibrosis score (0-2 / ≥3) [§]	33 / 5	33 / 2	NS [†]
HCV RNA (KIU/ml)	1100 (99 - 30000) **	380 (12 - 5000)	0.02 [§]
IFN dose (≥80% / 60-80%) [¶]	31 / 8	33 / 2	NS [†]
Ribavirin dose (≥80% / 60-80%) [¶]	25 / 14	28 / 7	NS [†]
RVR rate (%)	65.8	62.9	NS [†]
EVR rate (%)	94.7	100	NS [†]
Relapse rate (%)	35.9	7.9	0.002 [†]
SVR rate (%)	57.5	92.1	0.0006 [†]

* : mean ± SD, † : Fisher's exact probability test, ‡ : Student t test, § : Mutation 0-4 : n = 38, mutation ≥5 : n = 35,

** : median (range), ¶ : Mann-Whitney's U test, ¶ : Mutation 0-4 : n = 39, mutation ≥5 : n = 35

Table 4b. Baseline Characteristics of Patients with Core 110 T or N/S (Group 1 and 2)

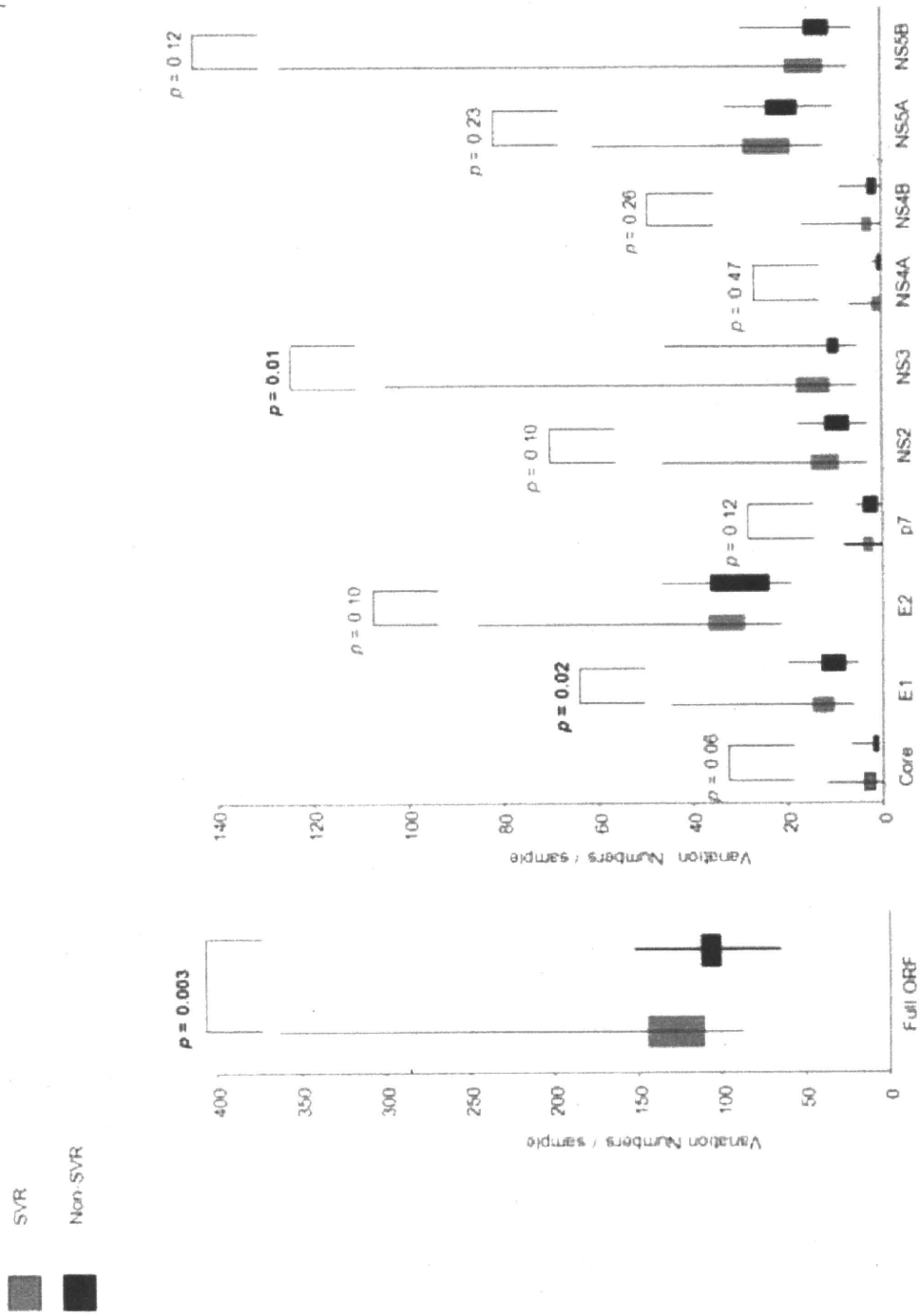
Characteristic	Core 110 T (n = 33)	Core 110 N/S (n = 45)	P value
Gender (Male/Female)	18 / 15	20 / 25	NS [†]
Age (yrs)	50.4 ± 13.0*	56.4 ± 9.5	0.032 [†]
ALT (IU/l)	64.5 ± 46.2	88.8 ± 86.2	NS [†]
Platelet (x10 ⁹ /mm ³)	19.3 ± 4.9	19.5 ± 6.6	NS [†]
Fibrosis score (0-2 / ≥3) [§]	30 / 1	36 / 6	NS [†]
HCV RNA (KIU/ml)	580 (54 - 3600) **	980 (12 - 30000)	NS
IFN dose (≥80% / 60-80%) [†]	26 / 3	38 / 7	NS [†]
Ribavirin dose (≥80% / 60-80%) [†]	23 / 6	30 / 15	NS [†]
RVR rate (%)	72.4	59.1	NS [†]
EVR rate (%)	100	95.5	NS [†]
Relapse rate (%)	3.0	38.6	9E-05 [†]
SVR rate (%)	97.0	57.8	5E-05 [†]

*: mean ± SD, †: Fisher's exact probability test, ‡: Student t test, §: Core 110 T: n = 31, Core 110 N/S: n = 42,

** : median (range), || : Mann-Whitney's U test, ¶ : Core 110 T: n = 29

Figure 1
[Click here to download high resolution image](#)

Kadokura et al
 Fig 1



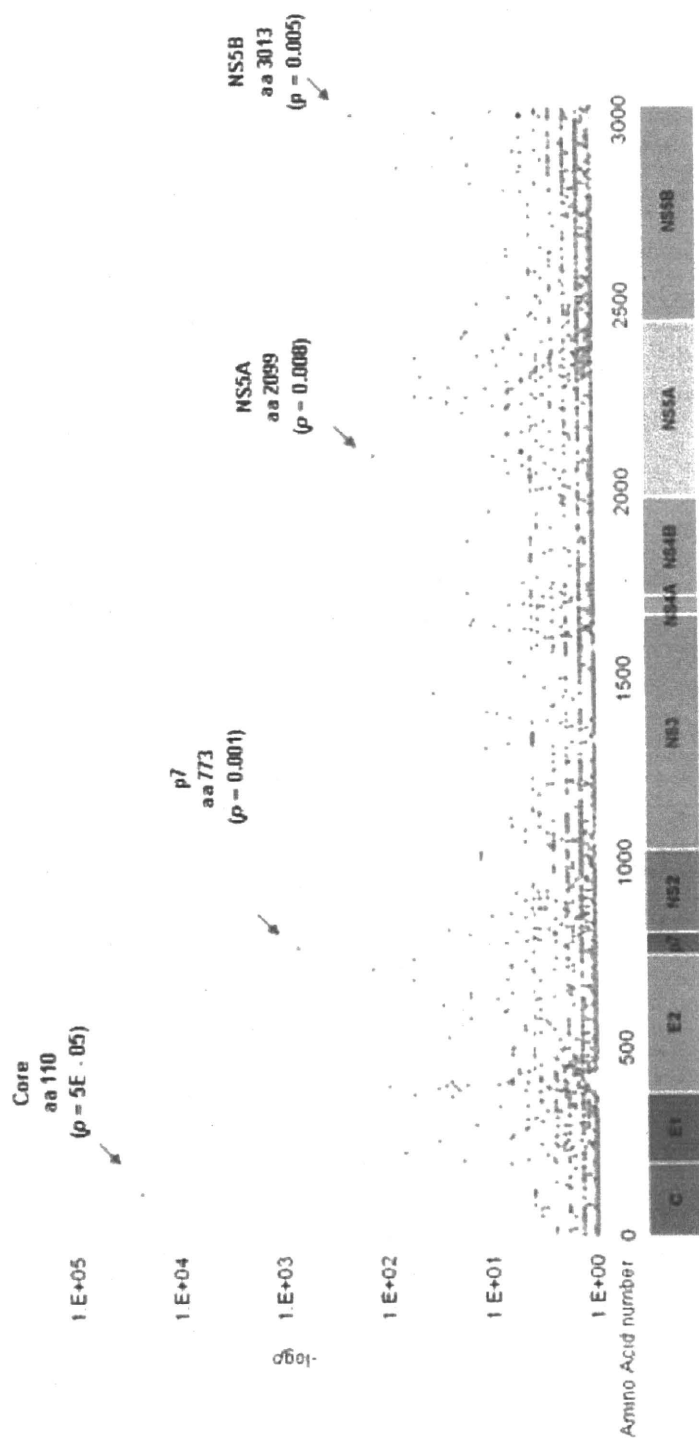


Figure 2c
 Click here to download high resolution image

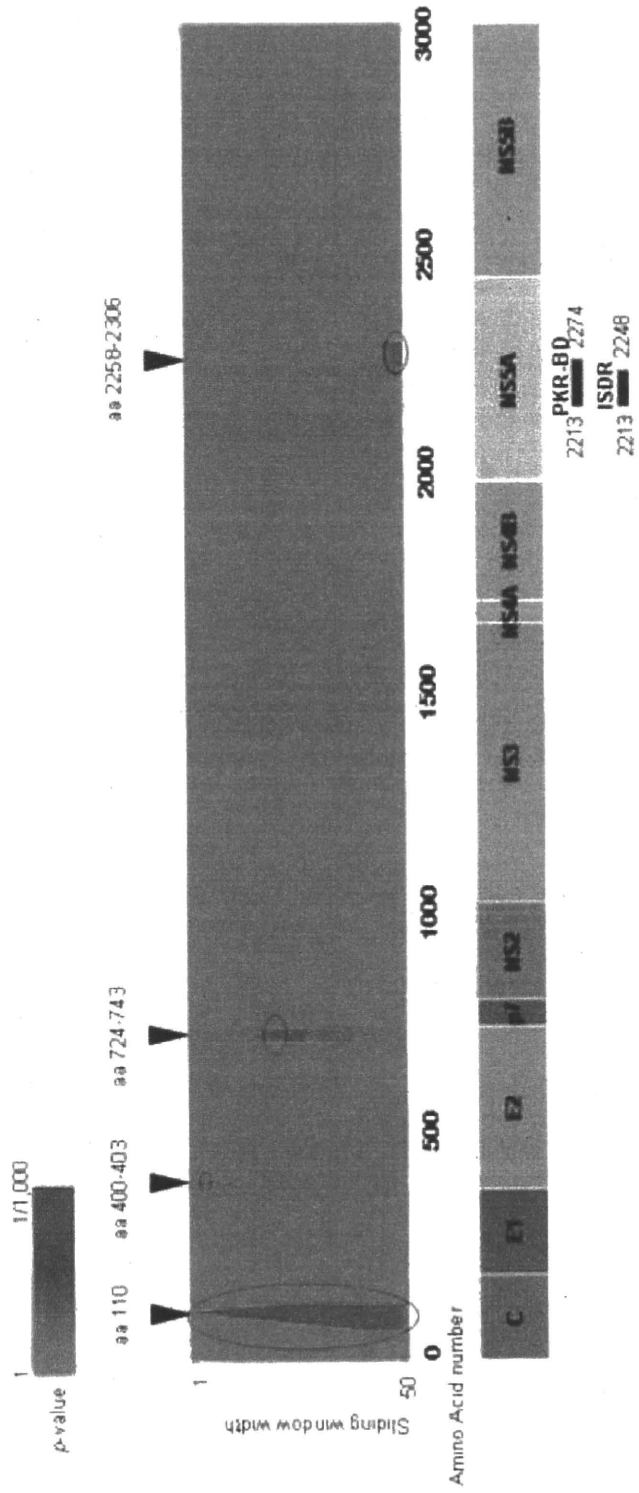


Figure 2d
 Click here to download high resolution image

Kadokura et al
 Fig. 2d

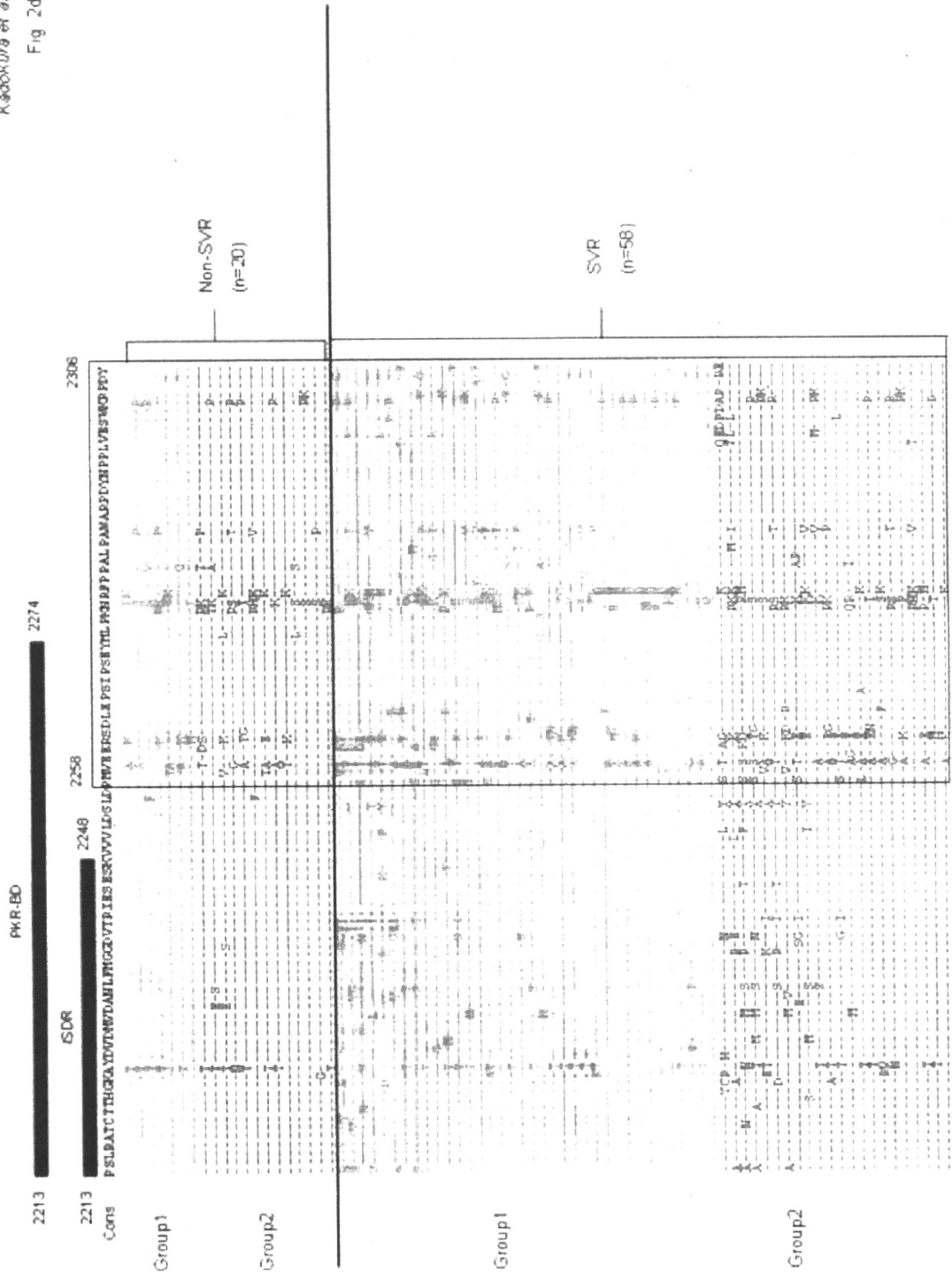


Figure 2b
Click here to download high resolution image

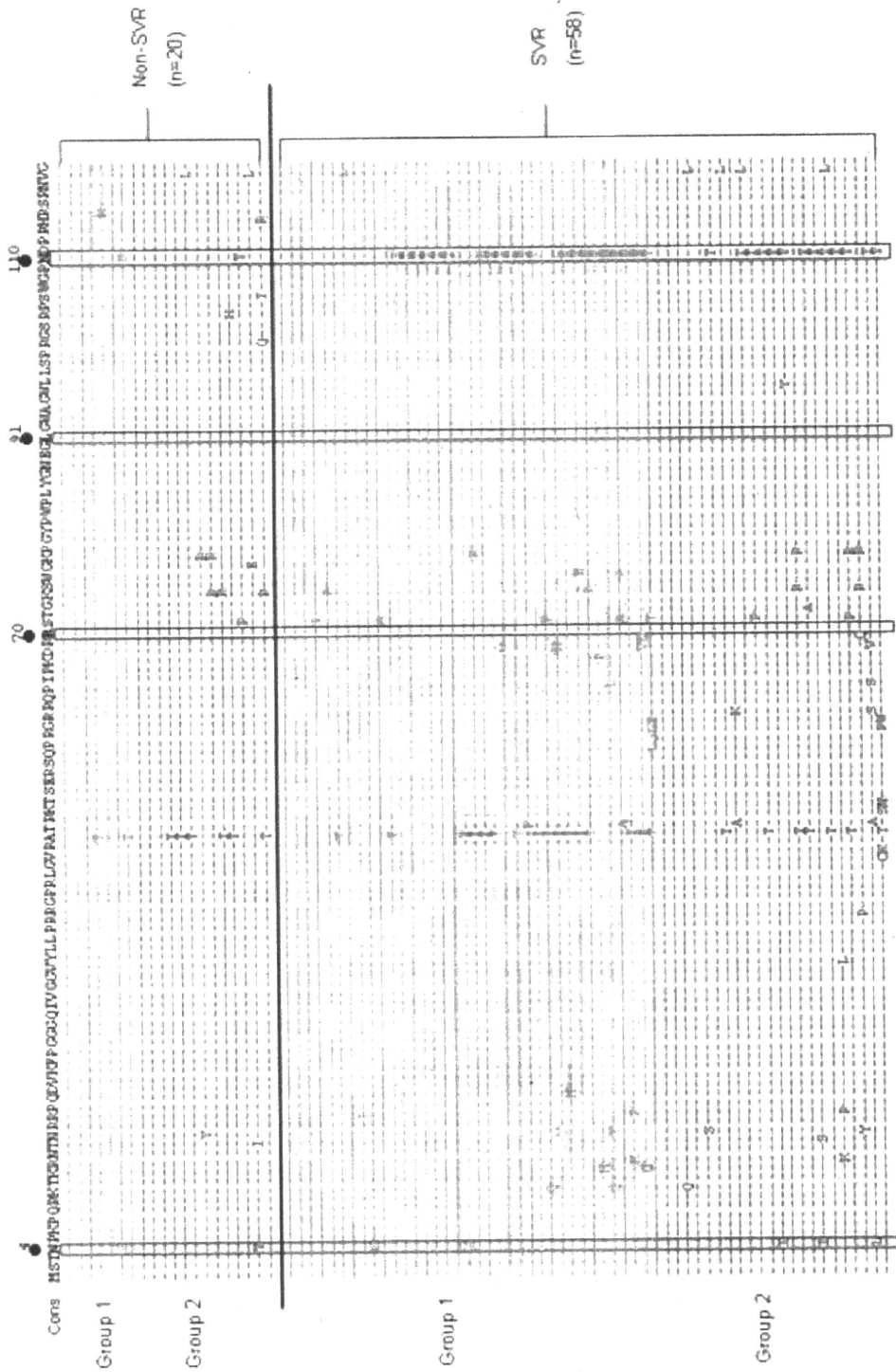


Figure 3
Click here to download high resolution image

