031 LABORATORY R & D LEADS TO MEOR FIELD PILOT IN FUYU-OILFIELD, CHINA

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Abstract

A MEOR field test is being conducted in Fuyu-oilfield, China to increase oil recovery from a mature reservoir through the waterflood for over 20 years. Most of the feasibility tests have been almost conducted and the surface facility has been constructed at the field. The microorganisms for injection have been already selected through feasibility tests in laboratory. Recent works include the optimization of microbial incubating conditions and the development of advanced monitoring techniques of microorganisms.

The metabolism of gas producing microorganisms among the screened candidates were significantly affected by replenishment of phosphate. Based on this result, two flooding tests were conducted to evaluate oil recovery increased by such a small amount of additive. As a result, additional oil recovery was improved twice as much (from 9.6 to 19.4% S_{or}) by the addition of phosphate. Therefore, a cheap locally available artificial fertilizer which includes rich phosphate will be used as an additive at the operation.

One of objectives in our research is to clarify the oil recovery mechanisms by means of microorganisms. Hence, the new techniques which included the gene engineering analysis were applied to detect each microorganism individually under the existence of many microorganisms. Moreover, another monitoring method was suggested to understand microbial metabolic activity of carbon dioxide. In this method, the amount of produced CO_2 could be estimated with the concentration of 2,3-butanediol in formation water. The preceding techniques will be used at the field pilot to investigate *in situ* microbial conditions.

Indigenous microorganisms in the whole cores drilled at the middle of a test block were investigated with the established monitoring technology which included an identification of ribonucleic acid (RNA) gene. This investigation

suggested that there were many kinds of microorganisms in the cores and their population in the high permeable cores were higher than those in the lower permeable cores. In addition, strains of microorganisms sampled from the high oil-saturated cores were less than those of microorganisms collected from the low oil-saturated cores. These results mean this advanced technology has a potential to define the reservoir characteristic such as water injection profile by the microbial distribution.

Introduction

The oil consumption in the world will amount to 104.6 million B/D in 2015, according to the prediction by Energy Information Administration, U.S. Department of Energy in 1997¹⁾. Especially, the growth of the consumption in developing Asia area is larger than those of other areas. The forecasted value (24.9 million B/D) in 2015 is more than twice compared with the current results (11.1 million B/D) in 1995, because the future rapid economic growth is expected in this area. Therefore, the development of the technology to fulfill the future oil requirements is a must. Because the number of mature oil fields are increasing, the redevelopment technologies for such aged reservoirs (IOR/EOR methods) are becoming more important. Here, our focusing technology is MEOR (microbial EOR) process among various IOR/EOR methods. This process was suggested by Beckman²⁾ in 1926 and has been studied at both laboratories and many fields³⁾. In JNOC/TRC (Japan Natl. Oil Corp./Technology Research Center), the research on MEOR has been conducted since 1987. Moreover, the field pilot project has been started since 1996 as an international collaborative research and development project between JNOC and JPGCL (Jilin Petroleum Group Co. Ltd.). The feasibility study had been already done in the first year of

this project, i.e. field selection, screening of microorganisms and planning of the test scheme⁴⁾. The objectives of the field trial are (1) the improvement of oil recovery in the field, (2) the evaluation of well screened microorganisms in a real reservoir, and (3) the clarification of oil recovering mechanisms.

This paper includes following two topics. At first, the incubating conditions were optimized to get the maximum effect on the oil recovery (for the first objective). This technical and economical challenge was done using a phosphate additive through the quantitative evaluation of microbial oil recovery. Secondly, the advanced monitoring methods were developed to get informations of microbial growth and their metabolism in the reservoir, because the understanding of *in situ* conditions is a must for the second and third objectives.

Pilot Test Field, Blocks and Microorganisms as Candidates for Injection

Pilot test field and blocks. Pilot test field is Fuyu oil field in Jilin province, China which were selected based on the general screening criteria of MEOR applications and its suitable reservoir conditions for useful microorganisms preserved in JNOC/TRC.

This field was discovered in 1959 and developed by China Jilin Province Oilfield Administrative Bureau (this name was changed to a new one at the end of 1996; JPGCL). This sandstone reservoir is shallow, at approximately 300–500 m in depth and has 13 formations (roughly four zones) with thin alternations of sandstone and shale. Total reservoir area is 120 km². The reservoir characteristics are : permeability = 100–300 md, porosity = 22–26 %, temperature = 28–32 °C and pressure = 20–30 atm. The second recovery by waterflood process has been conducted over the field since 1973. The inverted nine spot flooding pattern in the early period had to be changed to the line drive pattern, because of early break through. This pattern has been continued to date.

The target blocks for the field trial are “East 24-26” and “East 24-23” located in the east area of this field. These blocks are neighbours, but are made independent of each other by faults. The relevant characteristics of these two blocks (East 24-23 and East 24-26) are : depth, 300–450 m and 320–450 m; thickness (net), 15.2 m and 14.8 m; permeability, 240 md and 230 md; porosity, both 26%; temp., both 28.0 °C; salt content of oil,

both 1373 mg L⁻¹; specific gravity of oil (at 50/4 °C), 0.854 and 0.851; kinematic viscosity of oil, 31.3 and 29.3 mPa·s; well spacing, both approximately 100 m; and water cut (as of the end of 1995), 68% and 70%, respectively. The data of salt content, specific gravity and viscosity come from well No. 24-22 and No. 24-26.

Microorganisms as candidates for injection.

Following four kinds of microorganisms, i.e. *Enterobacter cloacae* TRC-322⁵⁾, *Bacillus subtilis* TRC-4118⁶⁾, *Bacillus licheniformis* TRC-18-2-a⁵⁾ and *Enterobacter cloacae* TU-7A, have been already selected as candidates for injection, through the early feasibility studies which included fundamental incubating tests, compatibility tests between reservoir-originated microorganisms and the selected from a competitive point of view, and oil recovery tests using Berea sandstone⁴⁾.

TRC-18-2-a has all productivities (gas, acid, surfactant and polymer) and were isolated from drilling cuttings in a domestic drilling site. TRC-322 is gas producing microorganism and its origin is the formation water of a domestic oil field. TRC-4118 was discovered from an activated-sludge in a domestic sewage treatment facility which is not a conventional origin at MEOR research, but this microorganism is the best surfactant producer. TU-7A provided from Tohoku University was collected from soil (containing spilled oil) near well site in another domestic oil field. Its main ability is a gas productivity.

Optimization of Incubating Conditions of Gas Producing Microorganisms

Effects of phosphate as an additive at incubating experiments. The phosphorous component generally has the effective influence upon microorganisms. In fact, our recent flask-experiments showed the effectiveness of additional phosphate on metabolism of gas producing microorganisms; *Enterobacter cloacae* TRC-322 and TU-7A. Experimental conditions were 30 °C of cultivation temperature, a week of cultivation period and 100 ml of media in 120-ml vials (sealed and displaced the head space with purified nitrogen gas). The amount of total produced gas of TRC-322 increased from 47 ml to 132 ml by supplement, and TU-7A similarly increased the gas production from 45 ml to 138 ml. The former gas amount were measured with medium M (molasses), the latter were measured with medium MP (molasses and phosphate).

Components of these media were : M, 40-g molasses in 1-L distilled water; and MP, 40-g molasses and 0.1-g K_2HPO_4 in 1-L distilled water. This result showed the definite effectiveness and has a useful implications ; it will be effective to supply additives such as cheap local available fertilizers which have an abundance of phosphorus.

Effects of phosphate at flooding experiments. The preceding incubation tests showed positive results. Here, following flooding experiments were carried out to evaluate effects of phosphate on the oil recovery by TRC-322.

Figure 1 shows experimental apparatus. The main equipment in this system has a holder containing Berea sandstone core, a membrane filter (0.45 μ m), a pump and a fraction collector. The Berea sandstone core (1.5 inch in diameter and 1 ft in length) is covered with a rubbersleeve, and set in a holder. The core holder and vessels (for brine, oil and microbial suspension) are placed in an oven to be maintained at the specified temperature (30 °C). A confining pressure of 50–60 kg cm⁻² is applied on the core. The profiles of pressure are monitored with two pressure measurement tools which are connected to inlet and outlet lines. Fluids, (except microbial solution), oil and brine are injected through a 0.45 μ m membrane filter to prevent contamination.

Crude oil produced from target block was used as residual oil. This is a stocktank oil with the following properties ; its specific gravity is 0.87 at 20/4 °C and viscosity is 30 mPa·s. In addition, synthetic brine (specified according to the components of formation water) is used, and its composition is, in mg L⁻¹: NaCl, 1210; KCl, 23; NaHCO₃, 2820; CaCl₂·2H₂O, 187; MgCl₂·6H₂O, 114; FeCl₃·6H₂O, 4; KH₂PO₄, 10; NaHSO₄·H₂O, 3; and it is made up with distilled water. Two media; MSB (molasses solution based on synthetic brine) and MPSB (molasses solution with phosphate based on synthetic brine) were used as media for injection. The concentration of molasses and (NH₄)₃PO₄ in these media were 40 g L⁻¹ and 2 g L⁻¹, respectively. The latter was specified according to the chemical analysis of locally available fertilizer which was to be applied in the field test.

This flooding experiments were conducted as the tertiary mode. After 10 and a half days cultivation at 30 °C, the driving synthetic brine was injected to recover the residual oil.

The results are presented in Table 1 and Figures 2–4. The monitoring of pressure profile during

shut-in showed pressurization by gas (carbon dioxide) in both cases. The maximum pressure were 43 psi at MSB and 77 psi at MPSB. The latter was approximately twofold as high as the former. It was presumed that the metabolism of CO₂ was accelerated by phosphorous. The additional oil recovery after microbial injection were 9.6% (medium MSB) and 19.4% (medium MPSB) of the residual oil. The addition of (NH₄)₃PO₄ could contribute towards improving oil recovery, and the effectiveness was more than twice.

The Development of Advanced Monitoring Techniques for the Field Trial

One of our important objectives in the field pilot is to make clear the oil recovery mechanisms by microorganisms. Therefore, both activities of microorganisms themselves and their metabolism must be observed.

Monitoring methods of microbial growth. The former observation will be carried out by the PCR-RFLP (polymerase chain reaction - restriction fragment length polymorphisms) method^(7,8) and FISH (fluorescence *in situ* hybridization) method^(9,10), and these techniques have been already established⁽¹¹⁾. The application of PCR-RFLP method makes all kinds of microorganisms measurable among mixed condition diacritically. In addition, according to the FISH analysis, the target microorganisms (i.e. four kinds of candidates; TRC-322, TRC-4118, TRC-18-2-a and TU-7A) can be detected selectively and rapidly from sample of produced water which includes other kinds of microorganisms.

Monitoring methods of microbial metabolism. The latter consists of following measurements and/or analysis; i.e. (1) pressure profile during shut-in and the components of produced gas for the investigation of gas producing microorganism's activities, (2) pH for acid metabolism, (3) IFT for biosurfactant production, and (4) viscosity for biopolymer production. The measuring target of (2)–(4) items is the water phase in produced fluids. In addition, the collected water will be analyzed with gas chromatography-mass spectrometry (GC-MS). Moreover, viscosity of oil will be measured and its composition will be analyzed with GC-MS to investigate the degradation by microorganisms.

Here, a new method is suggested to evaluate approximate amount of carbon dioxide produced

by TU-7A. Most of gas components produced by TU-7A was carbon dioxide according to the chemical analysis. The representative metabolic pathway to produce CO₂ is the butanediol fermentation shown as follows;

Hence, it is possible to estimate the amount of gas produced by TU-7A in the reservoir by the measurement of 2,3-butanediol concentration in the produced water. Figure 5 shows both measured value and calculated one (based on the analysis of 2,3-butanediol) of carbon dioxide during the incubation of TU-7A (conditions were: temp., 30 °C; and medium, 100-ml M in 120-ml vials). The both profiles are well matched, and this result means this monitoring technique to be useful for the investigation of CO₂ producing activity.

Investigation of indigenous microorganisms in a cored well¹²⁾ Much of recent reservoir data from the core analysis was a must for this field trial. Therefore, a new well "I-15" was drilled in the middle of a target block "East 24-23" (Fig.6). The location of I-15 was decided to take representative reservoir data in the target block. The target reservoir consists of 13 layers, and total reservoir thickness (including shale formation) amounts to 150 m. During the coring of all 150-m reservoir section, many pieces of the reservoir core were collected to investigate reservoir-originated microorganisms. The samples were collected from eight points of sandstone formation, and named #1 to #8 in the order of sampling (Fig.9). Three pairs of samples belonging to three series of sandstone layers, respectively, for instance, the pair of #1 (359 m) and #2 (360 m) samples were collected from a sandstone column between 358.8–362.36 m at No.4 coring run. Similarly, the pairs of #3 (374 m) and #4 (378 m), #5 (408 m) and #6 (410 m) were obtained from series of 373.95–378.9 m column at No.5 coring run and 407.6–411.1 m column at No.8 coring run, respectively. The last pair of #7 (419 m) and #8 (420 m) sample were collected from two columns at No.9 run. Only in this case, there was a very thin shale between these two samples. Except these pieces for biological investigation, three whole cores; Jnoc 1, 2 and 3 were collected from the same three columns which contained #1–#6 piece samples. The whole cores were brought to Japan for special core analysis. The sampling method of pieces was

as follows (Fig.7); (1) cutting a whole core, (2) immediately, scratching pieces from middle part of cylindrical face of core into sterile petri dishes by a pickel which was sterilized with flaming, (3) sealing petri dishes. The reason to take samples from middle points of cylinder was to prevent contamination of non-reservoir-originated microorganisms which might invade into the core from the surface with drilling mud. The indigenous microorganisms were extracted from collected pieces as follows (Fig.8); (1) milling the pieces with sterile mortar, (2) putting 2 g of milled samples into 5 ml of sterile water, (3) setting reservoir-originated microorganisms free from the rock surface by the super sonic waving treatment (each 1 minute treatment of super sonic waving and standing was done by turns 10 cycles), (4) extracting suspended microorganisms from the water. These extracted microorganisms were isolated by the preceding effective gene engineering technique, i.e. PCR-RFLP method. As a result, 60 kinds of microorganisms were isolated. Their viable cell counts are shown in Table 2. Total strains and total viable cell number (the unit is cells g⁻¹) in each sample were: #1, 18, 3.3×10⁵; #2, 14, 5.7×10⁵; #3, 6, 2.7×10³; #4, 7, 1.4×10³; #5, 18, 9.1×10³; #6, 8, 4.1×10⁴; #7, 11, 1.4×10⁵; and #8, 28, 1.6×10⁶, respectively. Moreover, the investigation of correlation between each sample in three pairs (#1–#2, #3–#4 and #5–#6) showed that the same 6, 2 and 3 kinds of microorganisms existed in both samples of each pair, respectively. The CCAL data (permeability to air and porosity) of whole cores were as follows: Jnoc 1, K_v=292 md, K_h=266 md, φ=27.6%; Jnoc 2, K_v=4.9 md, K_h=20 md, φ=23.1%; and Jnoc 3, K_v=113 md, K_h=248 md, φ=25.2%. The correlation between the biological data and CCAL data suggested the followings; (1) porous and high permeable cores (#1, #2, #5 and #6) included more microorganisms than tight and low permeable ones (#3 and #4), (2) number of strains in porous and high permeable zones were more than those in tight and low permeable ones, and (3) number of the same kinds of microorganisms in the pair of #1 and #2 was more than those in pair of #3–#4 and #5–#6, because the former vertical permeability (K_v=292 md) was higher than the latter (K_v=4.9 md and 113 md), hence, microorganisms could transport through porous media easily in the high permeable column. Moreover, the correlation between log data and biological ones were discussed here. According to the induction log, resistivity of each sampling

point were 8.3, 14.5, 12.3, 32.9, 88.3, 83.1, 37.8 and 21.9 Ωm in order of sample number (Fig.10). (The resistivities had large difference between #1-#2 pair and #5-#6 pair.) The values in #5 and #6 were 6-10 times higher than those in #1 and #2. Hence, it was presumed that the oil saturation of #5 and #6 cores were higher than those of #1 and #2. The cell counts of #1 and #2 were 10-100 times higher than those of #5 and #6. This result is quite reasonable, because microorganisms generally exist in the water phase.

The preceding correlations suggested that the characteristics of reservoir condition could be presumed by biological data, even if there were no CCAL and no log data in the target section. For instance, the porous, high permeable and/or flooded out zone might be estimated by a highly concentrated microbial section. In addition, the existence of the same kinds of microorganisms might be a useful standard whether the section was high permeable or not, and whether the boundary existed between sampling points or not.

Conclusions

1. The oil recovery by *E. cloacae* TRC-322 was increased from 9.6 % S_{or} to 19.4 % S_{or} by the supplementation of phosphate.
2. Two kinds of monitoring techniques ; PCR-RFLP and FISH methods were applied to investigate *in situ* microbial growth.
3. According to the investigation of collected core pieces with PCR-RFLP method, population of indigenous microorganisms and number of strains in high permeable and porous formations were higher than those in low permeable and tight zones. In addition, water saturated zones have more microorganisms than those oil saturated. Because the vertical permeability affected microbial transportation. in the vertical direction, the number of the same microorganisms between neighbour cores in low K_v zone differed from those of high K_v significantly.
4. A new monitoring technique was established to evaluate carbon dioxide producing activity. The total amount of produced CO_2 gas was estimated by the 2,3-butanediol analysis in the produced water.

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References

1. "International Energy Outlook 1997," Energy Information Administration, U.S. Department of Energy (ed.), DOE/EIA-0484(97), 118, April 1997
2. Beckman, J.W., "Action of Bacteria on Mineral Oil," *Ind. Eng. Chem. News Ed.* 4:3, 1926
3. Lazar, I.I., "MEOR Field Trials carried out over the World during the Last 35 Years," *Microbial Enhancement of Oil Recovery - Recent Advances ; proceedings of the 1990 international conference on microbial enhanced oil recovery*, E.C.Donaldson (ed.), Elsevier, 1991
4. Yonebayashi, H., Ono, K., Enomoto, H., Chida, T., Hong, C-X. and Fujiwara, K. : "Microbial Enhanced Oil Recovery Field Pilot in a Waterflooded Reservoir," SPE 38070, 1997
5. Yonebayashi, H., Yoshida, S., Enomoto, H., and Ono, K. : "Isolation and screening of microorganisms for the microbial enhanced oil recovery," *J Indo Microbiol* (the original paper is submitted to the journal), 1997
6. Yonebayashi, H., Yoshida, S., Enomoto, H., and Ono, K. : "Isolation of microorganisms from activated-sludge and compost for MEOR," *J Indo Microbiol* (the original paper is submitted to the journal), 1997
7. Saiki, R.K., Sharf, S., Faloona, F., Mullis, K.B., Horn, G.T., Erlich, H.A. and Arnheim, N. : "Enzymatic Amplification of Globin Genomic Sequences and Restriction Site Analysis for Diagnosis of Sickle Cell Anemia," *Science*, 230, 1350-1354, 1985
8. Saiki, R.K., Gelfand, D.H., Stoffel, S., Sharf, S.J., Higuchi, R., Horn, G.T., Mullis, K.B., Erlich, H.A. : "Primer-Directed Enzymatic Amplification of DNA with a Thermostable DNA Polymerase," *Science*, 239, 487-491, 1988
9. Amann, R.L., Krumholz, L. and Stahl, D.A. : "Fluorescent-Oligonucleotide Probing of Whole Cells for Determinative, Phylogenetic, and Environmental Studies in Microbiology," *J. Bacteriol.*, 172, 762-770, 1990
10. Amann, R.L., Binder, B.J., Olson, R.J., Chisholm, S.W., Devereux, R. and Stahl, D.A. : "Combination of 16S rRNA-Targeted Oligonucleotide Probes with Flow Cytometry for Analyzing Mixed Microbial Populations" *Appl. Environ. Microbiol.*, 56, 1919-1925, 1990
11. Fujiwara, K., Tanaka, S., Yonebayashi, H., and Enomoto, H., "Rapid Detection Technique of Injected *Enterobacter* species for Microbial Enhanced Oil Recovery Field Pilot," *Bioscience, Biotechnology, and Biochemistry* (the original paper is submitted to the journal), 1997
12. Fujiwara, K., Ohtsuka, M., Tanaka, S., Ichimura, N., Yonebayashi, H., Enomoto, H. and Hong, C-X., "Investigation of Microorganism in Reservoirs for Microbial Enhanced Oil Recovery Field Pilot," *Appl. Environ. Microbiol.* (the original paper is submitted to the journal), 1997

Fig.1 Flooding Apparatus

Fig. 2 Pressure Response during Incubation of *Enterobacter cloacae* TRC-322 with Two Kinds of Media; MSB and MPSB.

Fig.3 Oil Recovery, Differential Pressure and Oil Rate vs. Pore Volume Produced at Flooding Experiment using TRC-322 with Molasses and Phosphate.

Fig.4 Oil Recovery, Differential Pressure and Oil Rate vs. Pore Volume Produced at Flooding Experiment using TRC-322 with Molasses.

Fig.5 Calculated Carbon Dioxide Amount based on 2,3-butanediol Analysis vs. Measured one using TU-7A.

Fig.6 Location Map of Fuyu Oilfield and Targeting Blocks

Fig.7 Sampling Method of Reservoir's Rock containing Microorganisms.

Fig.8 The Extraction Method of Indigenous Microorganisms from the Collected Rock Samples.

Figure 9 Sedimentological Core Log in Well I-15 showing Collected Samples for the Investigation of Indigenous Microorganisms.

The legend are as follows : 1, shale ; 2, shale; 3, alternation of sandstone and shale; 4, sandstone; 5, conglomerate; 6, faint; 7, moderate; 8, strong; 9, in fracture only; 10, parallel lamination; 11, (weak); 12, cross stratification; 13, current ripples; 14, calcareous concretion; 15, mud clust; 16, soft rock deformation. The graduations of grain size mean mud, very fine, fine, medium, coarse, very coarse, granule and pebble, in order from left to right.

Figure 10 Induction, Sonic, Gamma Ray and SP Log Values showing Sampling Points for the Investigation of Indigenous Microorganisms.

Notes : The unit of gamma ray log; JG is local original unit. One JG is approximately equivalent to 600 pulse per minute.

Table 1 Conditions and Results of Flooding Experiments using TRC-322				
No.			1	2
Porosity	ϕ	[%]	23	23
Permeability	K_w	[md]	742	716
Initial Oil Saturation	S_{oi}	[%]	73	72
Residual Oil Saturation after Water Flooding	S_{or}	[%]	45	47
Medium			MSB	MPSB
Bacterial Counts in Injected Fluid	$\times 10^4$	[cells/ml]	7.9	1.3
Cultivation Time		[days]	10.5	10.5
Cultivation Temperature		[°C]	30	30
Oil Recovery after Microbial Flooding		[% S_{or}]	9.6	19.4

Table 2 Isolates from Reservoir Cores and Viable Cell Number of Each Strains

Strains ^a	Core Samples Number							
	#1	#2	#3	#4	#5	#6	#7	#8
201	3.6x10 ⁴				1.3x10 ²			3.9x10 ⁴
202					4.6x10 ²			
203		1.5x10 ⁴						6.4x10 ⁴
204	1.1x10 ⁵	4.1x10 ⁴			2.8x10 ²	1.6x10 ⁴		4.1x10 ⁵
205	3.9x10 ³	5.9x10 ⁴	6.7x10 ²	2.1x10 ²				
206	2.9x10 ³		1.0x10 ³		3.2x10 ²		4.9x10 ⁴	
207	6.9x10 ⁴	4.6x10 ⁴		5.1x10 ²	2.9x10 ²	6.8x10 ³		2.3x10 ⁴
208								3.5x10 ⁴
209		2.8x10 ⁵						9.6x10 ⁴
210	7.3x10 ³	2.2x10 ³						
211	2.3x10 ³			1.4x10 ²			1.2x10 ⁴	3.6x10 ⁴
212		1.6x10 ³	3.1x10 ²	1.1x10 ²		1.7x10 ⁴	3.1x10 ⁴	7.9x10 ⁴
213					2.2x10 ²		1.4x10 ⁴	1.1x10 ⁵
214					4.4x10 ²			
215				2.1x10 ²	2.8x10 ²	1.3x10 ²	1.4x10 ⁴	3.9x10 ⁴
216	1.9x10 ⁴	7.7x10 ⁴	4.4x10 ²					5.0x10 ⁵
217			2.9x10 ²					1.8x10 ⁴
218	3.6x10 ³							
219		4.1x10 ⁴					1.1x10 ³	1.1x10 ³
220	2.8x10 ³	4.8x10 ³			6.3x10 ³		1.9x10 ³	6.9x10 ⁴
221		2.1x10 ³						
222	6.1x10 ³							
223	3.3x10 ³				1.9x10 ²		5.8x10 ²	
224								1.3x10 ²
225						2.9x10 ²		
226								2.9x10 ²
227					1.0x10 ¹			
228					1.7x10 ²			
229					1.0x10 ¹			
230					5.0x10 ¹			
231					3.7x10 ¹			
232					1.4x10 ²			
233	3.9x10 ⁴							7.3x10 ⁴
234					8.0x10 ¹			
235					3.0x10 ¹			
236						3.2x10 ³		1.1x10 ²
237						2.0x10 ¹		
238						1.0x10 ¹		
239	6.6x10 ³							
240	5.9x10 ³							
241	2.1x10 ³							
242	7.1x10 ³							
243	2.2x10 ²							
244		1.6x10 ³						
245		5.5x10 ²						1.1x10 ²
246		4.3x10 ²						
247			1.0x10 ²					
248				1.1x10 ²				
249				1.2x10 ²				
250							2.2x10 ³	5.8x10 ³
251							2.9x10 ³	
252							6.3x10 ³	
253								3.6x10 ²
254								1.3x10 ²
255								4.6x10 ²
256								2.9x10 ²
257								2.1x10 ²
258								1.2x10 ²
259								1.4x10 ²
260								3.1x10 ²
Total Number of Strains ^b	18	14	6	7	18	8	11	28
Total Viable Cell Number ^c	3.3x10 ⁵	5.7x10 ⁵	2.7x10 ³	1.4x10 ³	9.1x10 ³	4.1x10 ⁴	1.4x10 ⁵	1.6x10 ⁶

Unit: cells/g

^a Strains isolated from 8 kinds of reservoir cores. Strains number are renamed in sequence from the difference recognized by the PCR-RFLP method.

^b Total number of strains isolated from each of reservoir cores.

^c Total viable cell number isolated from each of reservoir cores.