添付資料3−6

OriV(vegetative replication origin)遺伝子領域の解析

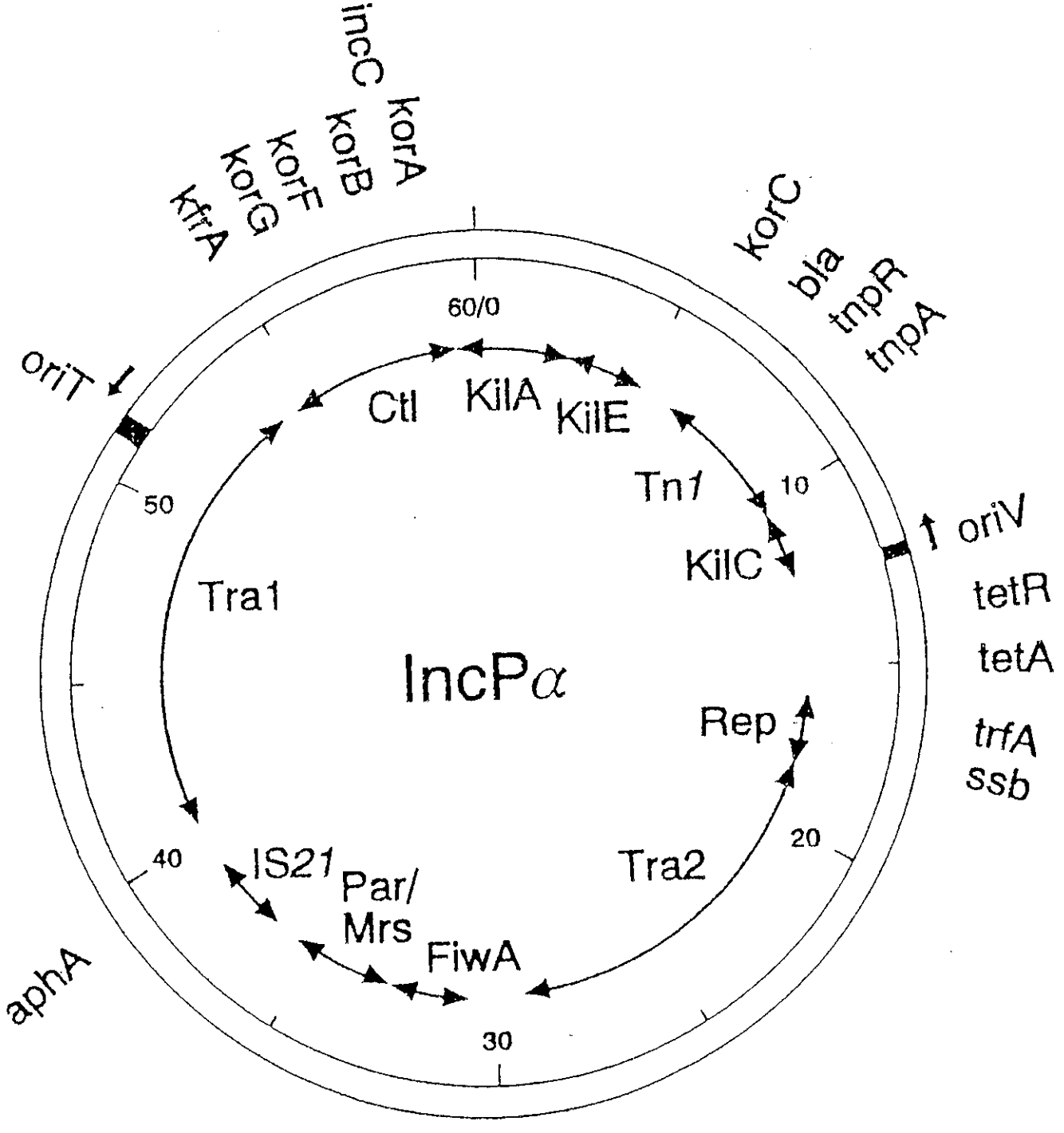
図は OriV(vegetative replication origin)領域のプラスミドが休止期の状態から DNA 複製を始める開始点を示したものである。TrfA は oriV の iteron に結合すると oriV は活性化され一方向のDNA 複製を開始する。またその間に蛋白質 DnaA が結合するサイト dnaA Box が3カ所にみられる。遺伝子 trfA は oriV を含む上流域に存在し、その蛋白質 TrfA は2種類 TrfA1, TrfA2 である。iteron1 と iteron10 の距離は 1090bp である。

iteron1 と iteron10 は逆向きに塩基配列が並び、iteron1 から iteron9 までは同方向に塩基配列が並んでいる。また iteron4 と iteron5 の間の距離が他と比べて大きいことから(間に dnaA が2つ入っている)、ループには役割を分担する2つの iteron ブロックがあると考えられる。バンドのパターン変化を示すものと考えられる。

写真は iteron1 と iteron10 を用いて遺伝子増幅プライマーとし、PCR 増幅を行ったものである。マグネシウム濃度を 1.5mM と一定にし、アニーリング温度を45℃、50℃、55℃、60℃に上昇させていった。徐々にバンド数が減少していった。

B. midousuji は発育温度が62℃以上であることから、このような温度シークエンスを行った。

Stringency が高い状況でバンドが出現していることから、*B. midousuji* に iteron 遺伝子塩基配列が存在するものと考えられる。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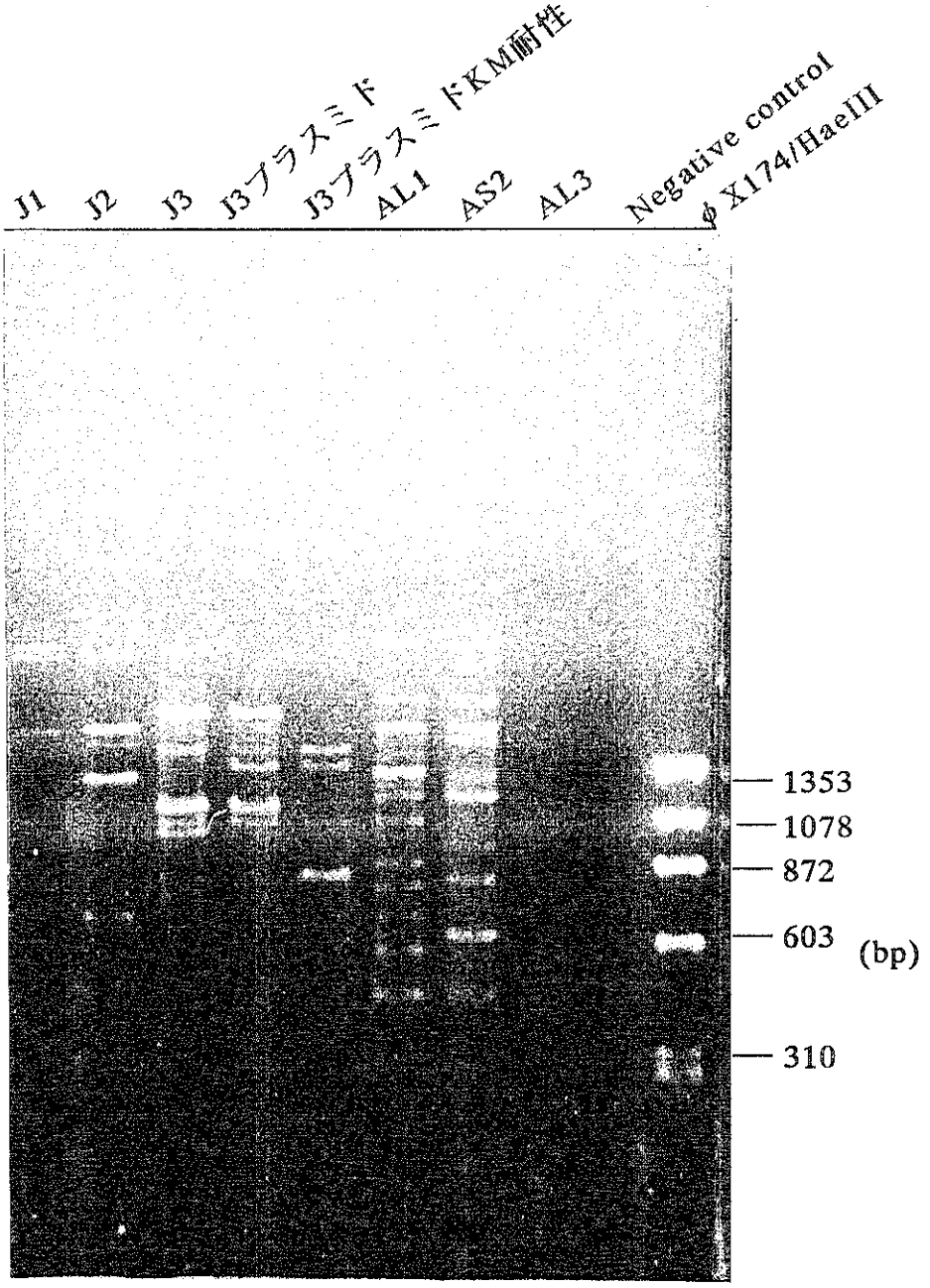
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J2
J3
J3プラスミド
J3プラスミドKM耐性
AL1
AS2
AL3
Negative control
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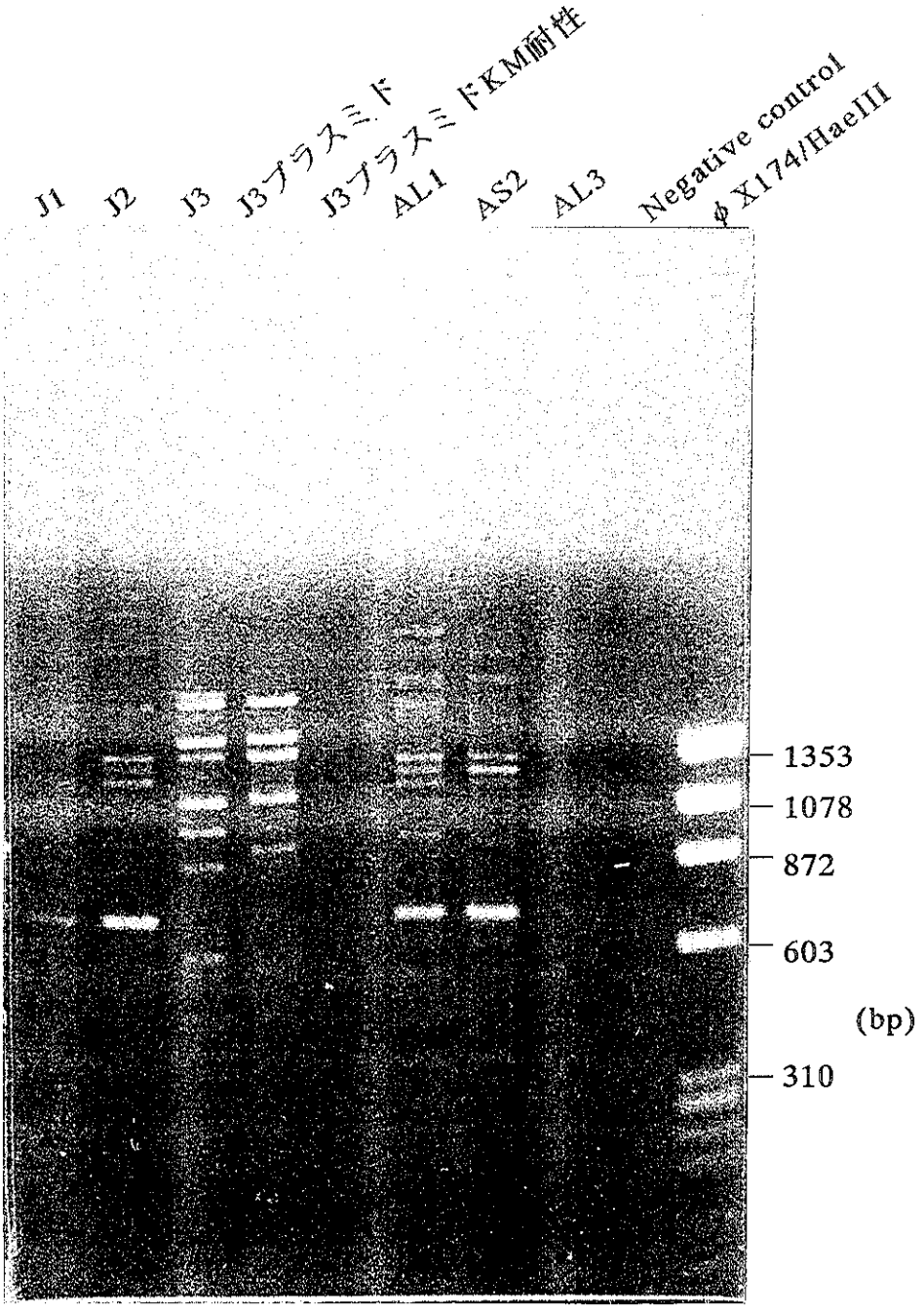
1353
1078
872
603
(bp)
310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(bp)
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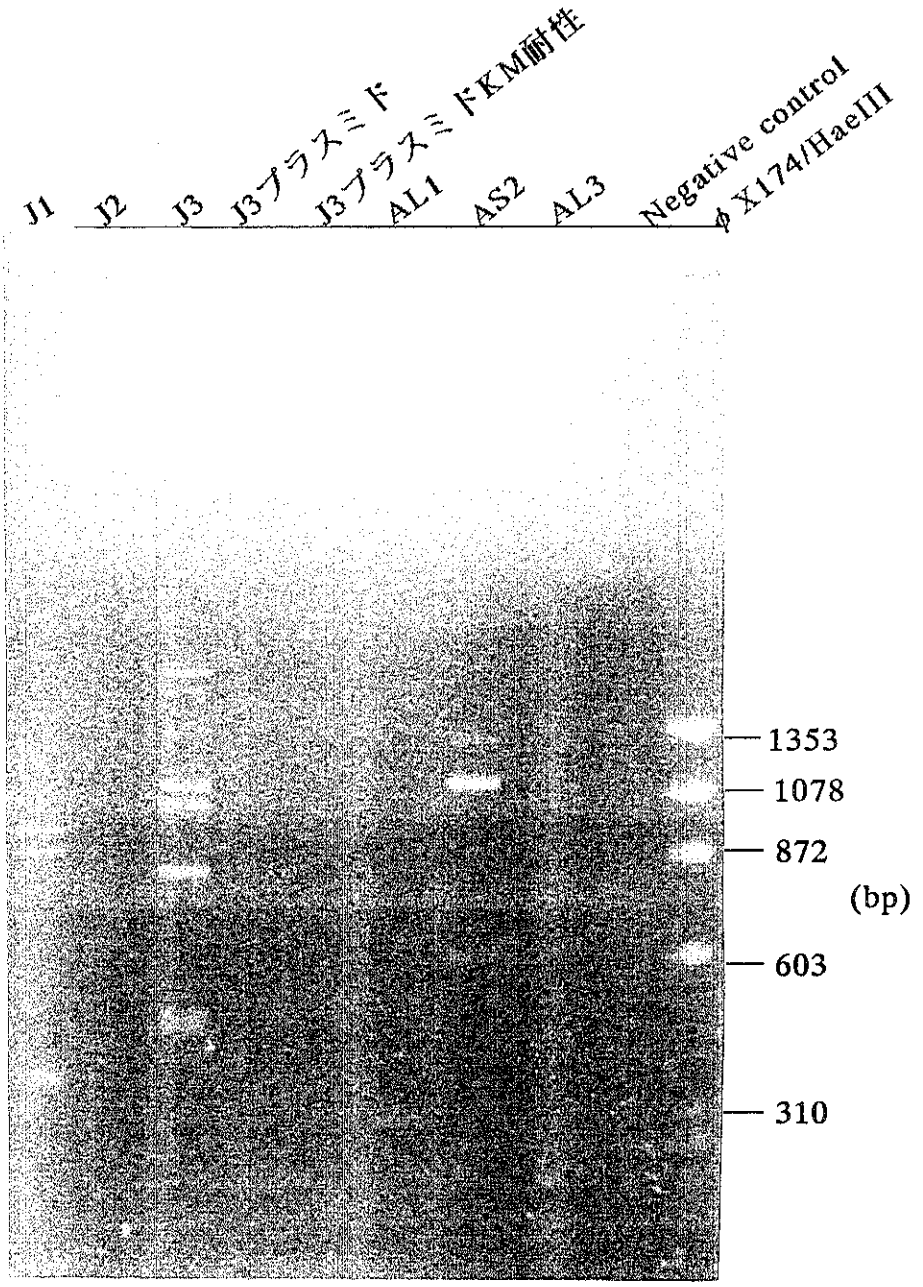
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(bp)
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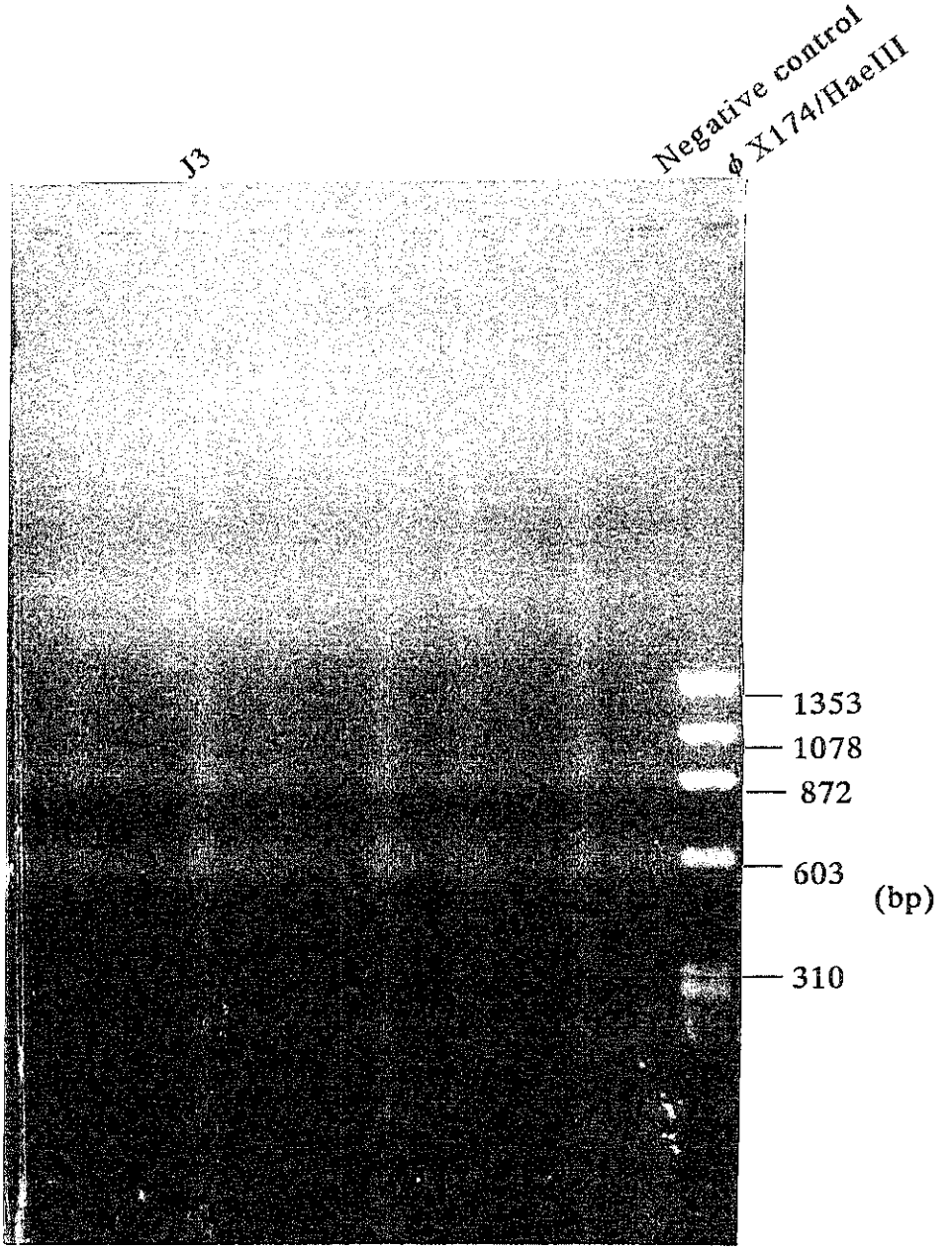
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添付資料3—7

平成10 年度の生活安全総合研究推進事業(外国への日本人研究者派遣事業)による米国コロンビア大学地球環境研究所(Lamont Earth Observatory)でのニューヨーク、ジャマイカ湿地帯環境改善計画シンポジウム(The Jamaica Bay Meeting)での口頭発表抄録 （1999年2月1日）

Human Health, Biodiversity and Industrial Pollution in Jamaica Bay, NY

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Anthropogenic pollution of the marine environment has significant adverse effects on endangered species, and on suitability for human recreational use. Industrial pollution is also very likely to impact adversely on human health as regards both environmental exposures to teratogens and carcinogens, as well as exposures to toxic algal blooms and human infectious agents. The restoration of the Jamaica Bay National Seashore presents itself as a possible paradigm for highly-urbanized salt march ecosystems throughout the industrialized world. Since this ecosystem has been, and continues to be, heavily impacted by exogenous contaminants it provides an excellent opportunity to study the nature of the relationship between biodiversity and pollution.

One aspect of the proposed study would require assessment of biodiversity of macrofauna and macroflora, and its often inverse correlation with increasing levels of pollution. This study would require extensive sampling of soil and water, and testing for industrial contaminants including metals, solvents, polychlorinated biphenyls (PCB), dioxin, polyaromatic hydrocarbons (PAH), and other xenobiotics. Localized sampling of macroflora and macrofauna would permit assessment of bioaccumulation of specific target chemicals, including mercury, lead, dioxin, PCB and PAH. These studies would require significant expenditures for mass spectrometric analyses of soils, water, and biological samples.

In this way connections could possibly be made linking specific areas of pollution,including their geophysical characters, and oceanographic properties to bioaccumulation in certain elements of the food chain. Only by understanding these relationships could specific steps could be proposed to address problematic components of the ecosystem.

From the anthropocentric perspective, the obvious area of investigation would be

determination of the impacts of sewage seepage, storm runoff, and sludge disposal on levels of pathogenic microflora (e.g. coliform bacteria and hepatitis viruses). Traditional bacteriological laboratory methods, and also molecular biology techniques such as the polymerase chain reaction (PCR), would be required for this aspect of the study. In addition, the various sources of pollution may impact on nutrient loading, decline in predators, loss of natural filters, and introduced species, to contribute to red tides and other kinds of harmful algal blooms. Thus, in addition to concerns about infectious agents and unanswered questions of long-term toxicities due to increased cancer and birth defects in local communities, there is a very real concern for acute toxicity in humans including gastrointestinal and neurological symptoms.

A quantitative assessment of these complex biophysical processes on human health would require mathematical modeling including the potential impacts of chaos theory, and application of traditional risk assessment methods.

Finally, an area that is perhaps least well understood is the ability of marine ecosystems, and in particular salt marshes where biodegradative processes are highly active to naturally buffer exogenous impacts. Our specific interest centers on microfauna including species of Bacillus to mediate biodegradation of environmental contaminants. Our recent studies indicate that thermophilic bacteria isolated from compost are capable of digesting organic (fish carcasses) and as well as inorganic (plastics) pollutants. Specific plasmid-encoded genes were found to be responsible for these various biodegradative properties, and these were linked to antibiotic resistance genes. Our studies also suggest that bacteriological toxicity toward algae could potentially be a natural method for buffering against anaerobic conditions. The possibility exists that similar bacteriological systems may exist in industrially impacted salt march ecosystems. Studies of bacterial evolution indicate that under certain environmental conditions processes in addition to random mutation may drive genotypic and phenotypic changes.

Taken together these findings suggest the need for investigation of the biodiversity of microflora at various sites within the marshlands with various human impacts. This study would also require bacteriological and molecular biological techniques such as PCR.

口頭発表に対する Raymond N. Sambrotto, Senior Research Scientist, Lamont-Doherty, EarthObservatory (sambrott@ldeo.columbia.edu 61 Rt. 9W/ P.O. Box 1000Palisades, NY 10964 U.S.A. phone: 914-365-8402 fax: 914-365-8150)から Environmental Genetics Laboratory at Lamont, Columbia University 開設の通知

Title: Development of a Genetic Analysis Facility at Lamont and its Application to Environmental Problems

Introduction and rationale:

There has been an explosive growth in the capabilities and applications of biotechnology over the last two decades. Many of what were once cutting edge laboratory techniques in the analysis of DNA have quickly been transformed into almost routine procedures. Most of these advances have been driven by medical applications, as the entire human genome will soon be mapped ahead of schedule.

We propose to establish the capabilities to extract, amplify and make preliminary analyses of DNA here at Lamont. These capabilities already exist on the Columbia campus at the Biology Dept. and Medical School.

However, unlike these other labs., the Lamont Genetic Analysis Facility will be devoted to environmental samples. The scientific return on this investment can be enormous, and the costs for establishing such a facility are not great. Space exists in Sambrotto's lab. (with minor modification) for this facility.

Applications:

- Analysis of microbial populations associated with polluted soils and sediments (O'Driscoll and Hoshina).

- Cladistic studies of marine and estuarine plankton (Sambrotto)

- Cladistic studies of endangered or other critical populations (CERC).

Funding sources:

- EPA

- NSF, particularly their BioComplexity Program. The estimated budget for research projects in this area alone is $45M, and the President's request to Congress for next year suggests significantly

greater funding.

- NIH (in collaboration with health researchers).

添付資料3－8

参考文献

ベンゼン環の水酸化反応に係わる酵素遺伝子の論文リスト

1. Eiji Masai ,Katsumi Sugiyama ,Naoko Iwashita et.,al The *bph*DEF *meta*-cleavage pathway genes involved in biphenyl/polychlorinated biphenyldegradation are located on a linear plasmid and separated from the intial *bphACB* genes in *Rhodococcus* sp. strain RHA1. GENE 187(1997)141-149

2. Jean Armengaud, Birgitta Happe, Kenneth N. Timmis Genetic Analysis of Dioxin Dio xygenase of *Sphingomonas* sp. Strain RW1:Catabolic GenesDispersed on the Genome Journal of Bacteriology 180: (15) 3954-3966, 1998

3. Jean Armengaud, Kennith N. Timmis, Rolf-Michael Wittich A Functional 4-Hydroxys alicylate/Hydroxyquinol Degradative Pathway Gene Cluster Is Linked to the Initial Dibenzo-*p*-Dioxin Pathway Genes in *Sphingomonas* sp. Strain RW1
Journal of Bacteriology 181: (11) 3452-3461, 1999

4. Jean Armengaud, Kenneth N. Timmis Molecular characterization of Fdx1, a putida redoxin-type[2Fe-2S] ferredoxin able to transfer electrons to the dioxin dioxygenase of *Sphingomonas* sp. RW1 Eur. J. Biochem. 247, 833-842, 1997

ベンゼン環の解裂に係わる酵素遺伝子*BphC* に関する論文リスト

1. Xue Peng, Eiji Masai, Yoshihiro Katayama et., al. Characterization of the *meta*-cleavag emeta Compound Hydrolase Gene Involved in Degradation of the Lignin-Related Bipheny lStructure by *Sphingomonas paucimobilis* SYK-6. Applied and Enviromental Microbiology 65: 62789-2793, 1999

2. Shin-ichi Sato, Naoki Ouchiyama, Toshiaki Kimura et.,al Cloning of Genes Involved in Carabazole Degradation of *Pseudomonas* sp. Strain CA10: Nucleotide Sequences of Genes and Characterization of *meta*-cleavage Enzymes and Hydrolase Journal of bacter iology 179: (15) 4841-4849 , 1997

3. Frank J. Mondello, Michael P. Turcich, John H.Lobos et.,al Identification and Modification of Biphenyl Dioxygenase Sequences That Determine the Specificity of Polychlorinated Biphenyl Degradation. Applied and Enviromental Microbiology 63: (8) 3096-3103 ,1997

4. Hideto TAKAMI, Toshiaki KUDO, Koki HORIKOSHI Isolation of Extradiol Dioxygena se Genes That Are Phylogenetically Distant from Other *meta*-cleavage Dioxygenase Genes Biosci. Biotech. Biochem. 61: (3) 530-532,1997

5. Juan A.Asturias, Lindsay D.Eltis, Matthias Prucha et.,al., Analysis of Three 2,3-Dih ydroxybiphenyl 1,2-Dioxygenases Found in *Rhodococcus globerulus* P6 The Journal of Bi ological Chemistry 269: (10) 7807- 7815, 1994

6. Vivian H. Plellizari, Serguei Bezorodnikov, and John F. Quensen, et.al., Evaluation of Strains Isolated by Growth on Naphthalene and Biphenyl for Hybridization of Genes t o Dioxygenase Probes and Polychlorinated Biphenyl-Degrading Ability. Applied and Envir

onmental Microbiology 62: (6) 2053-2058, 1996

7. Seungil Han, Lindsay D.Eltis, Kenneth N.Timmis et.,al Crystal Structure of the Biphenyl-Cleaving Extradiol Dioxygenase from a PCB-degrading Pseudomonad. Science 270: 976-980, 1995

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発表関連

○ダイオキシン会議'99　於イタリア　ベニス　平成11年9月12日～17日

Bacterium capable of biodegradation of dioxin-like substances, Sadayori Hoshina, David H. Figurski, I.Bernard Weinstein, Hiroshi Gohda and Tohru Furuichi,Organohalogen Compounds,vol.40, pp503-505,1999

First step toward biodegradation of dioxins by means of a reactor,Kunichika Nakamiya, Sadayori Hoshina, Ikuo Souta, Kazuei Ishii and Tohru Furuichi,Organohalogen Compounds,vol.40,pp535-538,1999

○第１０回廃棄物学会研究発表会　於埼玉県大宮　平成11年10月26日～28日

バイオリアクターによるダイオキシン分解,中宮邦近、石井一英、古市徹、保科定頼、惣田昱夫,第１０回廃棄物学会研究発表会講演論文集,880-882,1999

好熱菌によるダイオキシン類分解実験および遺伝子解析,保科定頼、河野緑、郷田浩志、古市徹,第１０回廃棄物学会研究発表会講演論文集,883-885,1999

PCB分解菌によるダイオキシン類の分解とその特徴,惣田昱夫、古市徹、石井一英、中宮邦近,第１０回廃棄物学会研究発表会講演論文集,886-888,1999

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以降は雑誌/図書等に掲載された論文となりますので、
「研究成果の刊行に関する一覧表」をご参照ください。

「研究成果の刊行に関する一覧表」

Bacterium capable of biodegradation of dioxin-like substances, Sadayori Hoshina, David H. Figurski, I.Bernard Weinstein, Hiroshi Gohda and Tohru Furuichi,Organohalogen Compounds,vol.40, pp503-505,1999

First step toward biodegradation of dioxins by means of a reactor,Kunichika Nakamiya, Sadayori Hoshina, Ikuo Souta, Kazuei Ishii and Tohru Furuichi,Organohalogen Compounds,vol.40,pp535-538,1999

バイオリアクターによるダイオキシン分解,中宮邦近、石井一英、古市徹、保科定頼、惣田昱夫,第１０回廃棄物学会研究発表会講演論文集,880-882,1999

好熱菌によるダイオキシン類分解実験および遺伝子解析,保科定頼、河野緑、郷田浩志、古市徹,第１０回廃棄物学会研究発表会講演論文集,883-885,1999

PCB 分解菌によるダイオキシン類の分解とその特徴,惣田昱夫、古市徹、石井一英、中宮邦近,第１０回廃棄物学会研究発表会講演論文集,886-888,1999