





ilers, raising the possibility that the causative gene for the Australian SCA15 family is allelic to that for the two Japanese SCA15 families.<sup>1</sup> However, some of the clinical features of the Japanese families are distinct from those of the Australian family as regards to the extracerebellar signs. Postural tremor of the head, arm, or trunk is more predominant in the Japanese patients than in the Australian patients.<sup>1</sup> Subsequently, additional families have been reported to link to the SCA15 locus.<sup>4</sup>

Recently, partial deletions of type 1 inositol 1,4,5-triphosphate receptor (*ITPR1*) and sulfatase modifying factor 1 (*SUMF1*) genes have been identified in the Australian SCA15 family and two British families with pure cerebellar ataxia, suggesting that *ITPR1* is the causative gene for SCA15.<sup>5</sup> Furthermore, a partial deletion of *ITPR1* has been identified in the Japanese SCA15 family.<sup>6</sup> However, it is unclear whether *ITPR1* is solely responsible for SCA15, because the deletions also involve *SUMF1*. Here, we report that the two families mapped to the SCA15 locus have the mutations in *ITPR1*, including a missense mutation, which strongly confirms that *ITPR1* is the causative gene for SCA15.

**METHODS SCA families.** The family members of the two Japanese families mapped to the SCA15 locus were analyzed in the present study. In addition, 54 unrelated dominant SCA families in which abnormal expansions of CAG repeat in the region of the gene for SCA1, SCA2, Machado-Joseph disease/SCA3, SCA6, SCA7, and dentatorubral-pallidum atrophy have been included are also analyzed for gene copy number analysis of *ITPR1*. High-resolution melting genotyping (HRM) was carried out on DNA samples after choosing affected members from the patients. The present study was approved by the Institutional Review Board of Nagoya University.

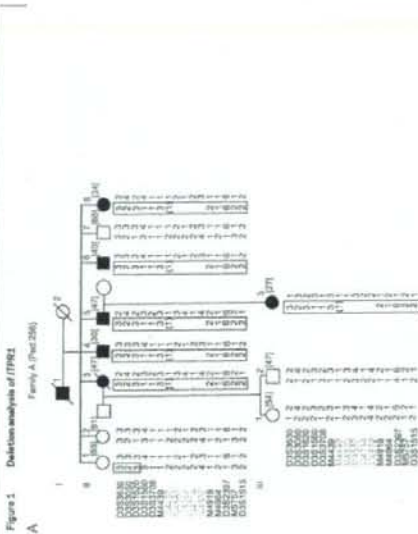
**Genetic analysis.** For five high-copy copyings, we established nine new microsatellite markers, namely, M4405, M4497, M4505, M4607, M4714, M4832, M4911, M4964, and M4972, in the region of 100,000 and 120,010 bp on chromosome 10q24.3. Genotyping was carried out using PCR techniques with the ABI PRISM 7700 Sequence Detection System (Applied Biosystems, Foster City, CA). We also employed the custom high-definition copy-based comparative genomic hybridization (CGH) microarrays (Agilent Technologies Inc., Palo Alto, CA) a region of approximately 54 Mb from *CNTN4* Gene ID: 152310 to 155190 was included in the microarray at an average interval of 200 bp for the probes. For gene expression analysis, RNA was extracted from cultured fibroblasts from an affected individual (II-10) and a normal individual. The total RNA (100 ng) from each *ITPR1* was subjected to the Affymetrix GeneChip technology (Affymetrix, Santa Clara, CA) and analyzed using the Affymetrix GeneChip software (version 3.0; Applied Biosystems). Detailed methods are available in our

Supplemental Appendix 1, available at [www.jneurosci.org](http://www.jneurosci.org).

**RESULTS Identification of deletion involving entire *ITPR1* in family A (Ped 256).** To investigate whether a common haplotype is shared among the affected individuals in the two Japanese SCA15 families linked to the SCA15 locus,<sup>1</sup> we conducted fine haplotype analyses based on the linkage analysis. We did not find any common founder haplotypes between these Japanese SCA15 families. However, all of the affected individuals in family A (Ped 256) lost heterozygosity from M4497 to M4832 (figure 1A). Furthermore, alleles from M4583 to M4832 were not examined from the affected individual II-5 to his affected daughter III-3 (figure 1A). These findings strongly suggest that the affected individuals in this family (Ped 256) had a heterozygous deletion in the region containing two genes, *ITPR1* and *SUMF1* (figure 1A). We performed quantitative real-time PCR analyses for *ITPR1* and *SUMF1*. The dosages of exons 2, 26, and 58 of *ITPR1* and exon 1 of *SUMF1* in the affected individuals were one-half those of unaffected individuals (figure 1B). These findings indicated that the affected individuals had the deletion of the entire *ITPR1* and exon 1 of *SUMF1*.

**Identification of breakpoint sequence in *ITPR1*.** To confirm the deletion of *ITPR1*, we performed aCGH analysis using oligonucleotide probes spanning the region from *CNTN4* to DSS1303 on chromosome 10q24.3. The *R* ratios for the affected individuals (II-5, II-6, and II-8) and two unaffected individuals (II-7 and III-2) in family A. The log<sub>2</sub> *R* ratios for the affected individuals for the probes from the nucleotide position 4,176,024 to 4,887,327 were decreased to  $-1$ , whereas those for the probes from the nucleotide position 4,142,899 to 4,871,481 and from the nucleotide position 4,887,693 to 5,242,899 were  $-0$ , confirming the extent of the deletion (figure 1B). In contrast, we did not observe any changes in this region in an affected individual in family B (Ped 2216). Furthermore, aCGH analysis was applied to 54 unrelated dominant SCA families; however, no deletion of *ITPR1* or *SUMF1* was detected in those families.

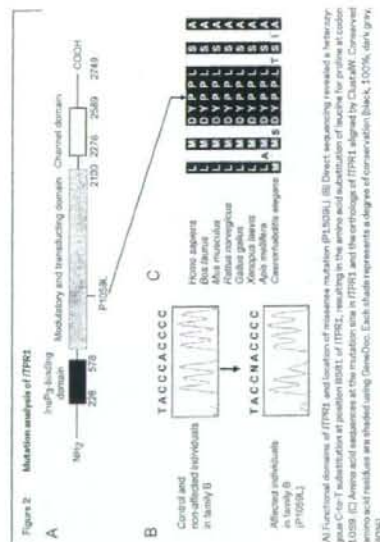
To determine the breakpoints, we developed the primers for each read and performed PCR, obtaining a  $\sim 2,300$  bp fragment from the affected individuals, but none from the unaffected individuals (figure 2A). The sequence analysis of this junction fragment revealed that no significant homology was observed when the junction sequence was aligned with the reference genomic sequence at the proximal and distal breakpoints and the sequences at proximal and distal breakpoints showed a two nucleotide overlap (figure 2B and C). RepeatMasker (<http://www.repeatmasker.org/>) revealed that



**Figure 1.** Deletion analysis of *ITPR1*. **A**, Pedigree analysis of family A (Ped 256). Genotypes for markers M4497, M4583, M4607, M4714, M4832, and M4972 are shown. **B**, Gel electrophoresis image of PCR products for *ITPR1* and *SUMF1* in affected and unaffected individuals. The scale bar represents the size of the DNA fragments in kilobases (kb).

the distal breakpoint was embedded within an AT dinucleotide repeat. The proximal breakpoint was embedded immediately before the *Alu* element. The deletion in this family is thus 41,4018 bp in size, including the entire *ITPR1* and exon 1 of *SUMF1*. Chromosomal deletion is mainly mediated by two mechanisms: nonallelic homologous recombination (NAHR) or nonhomologous end joining (NHEJ).<sup>7</sup> In the case of NAHR, the chromosomal rearrangement can be between large highly homologous low-copy repeat (LCR) structures. AT-rich palindromes, and pericentromeric repeats (figure 2C).<sup>8</sup> In addition, the sequence at breakpoint showed 2–5 nucleotide overlap, which is frequently observed in chromosomal rearrangements

compared the 1-Mb genomic sequence surrounding *SUMF1* and *ITPR1* against itself using PipMaker.<sup>9</sup> The sequence analysis of the junction in our case and those in previously reported cases showed that distal breakpoints were scattered within a  $\sim 65$ -kb region and proximal breakpoints were scattered within a  $\sim 225$ -kb region (figure 2C). These breakpoints are frequently embedded within or beside repetitive sequences, however, some of the breakpoints were embedded within LCR structures, AT-rich palindromes, and pericentromeric repeats (figure 2C).<sup>8</sup> In addition, the sequence at breakpoint showed 2–5 nucleotide overlap, which is frequently observed in chromosomal rearrangements



**Figure 2** Mutation analysis of ITPR1. **A**, Schematic diagram of ITPR1 protein structure showing the NTP-binding domain (residues 258-276), the modulatory and transducing domain (residues 277-289), and the channel domain (residues 290-294). A mutation is indicated at residue 276. **B**, Electropherograms showing the wild-type sequence (TACCACCCC) in control individuals and the mutant sequence (TACCNACCCC) in affected individuals. **C**, Amino acid sequence of ITPR1 with the mutation at residue 276 (N → A) highlighted in red.

mediated by NHEJ (figure 2C).<sup>10,11,12</sup> Taken together, the results indicate that ITPR1 deletion is mediated by NHEJ.

**Consequences of ITPR1 and SOMP1 deletion at mRNA level.** The quantitative real-time PCR analysis using mRNA from cultured fibroblasts from an affected individual (14) revealed that the mRNA expression levels of ITPR1 exons 5–6, ITPR1 exons 25–26, ITPR1 exons 44–45, and SOMP1 exons 6–7 of the affected individual were one-half those of the normal control, indicating that ITPR1 and SOMP1 from the deleted allele were not expressed (figure 4).

**Identification of a nonsense mutation in ITPR1 in family B (F04216).** We performed multisequence analysis of the entire exon and splice junctions in ITPR1 and SOMP1 of the affected individuals in family B and identified one nonsense mutation, C881>T (resulting in substitution of leucine for proline; p1059L), in exon 25 of ITPR1 in all the affected individuals in the heterozygous state, whereas unaffected individuals did not have this substitution (figure 2, A and B). This nucleotide change was not observed in 254 normal chromosomes in Japanese controls. We found no nucleotide substitutions in SOMP1. p1059L was located in the modulatory and transducing domain in ITPR1 (figure 2A). Amino acid sequence alignments of ITPR1 using ClustalW<sup>13</sup> revealed that the proline residue at codon 1059 is highly conserved among species (figure 2C).

**DISCUSSION** In this study, we found the total deletion of ITPR1 and the decrease in ITPR1 mRNA

level in patients with ITPR1 deletion. ITPR1 is a major ionotropic glutamate receptor, which mediates Ca<sup>2+</sup> release from the endoplasmic reticulum in various neurons, including CA1, basal ganglia, and the thalamic neurons, particularly Purkinje neurons.<sup>14,15</sup> Intracellular Ca<sup>2+</sup> homeostasis is important for maintaining the function of neurons, particularly Purkinje neurons.<sup>16</sup> Indeed, mice homozygous for null ITPR1 develop ataxia and epilepsy without apparent morphologic abnormalities.<sup>17,18</sup> On the other hand, mice heterozygous for null ITPR1 develop mild motor dysfunction in the cerebellum.<sup>19</sup> Thus, the haploinsufficiency of ITPR1 may result in dysfunction confined to Purkinje neurons, and the complete loss of ITPR1 results in dysfunction in both cortical and Purkinje neurons. The finding indicates that Purkinje neurons are particularly vulnerable to the gene dosage of ITPR1. Indeed, none of the individuals with ITPR1 with ITPR1 mutation had epilepsy or abnormal electroencephalograms and clinical phenotype was limited to cerebellar ataxia with tremor even in the heterozygous state.<sup>19</sup> The neuropathologic findings of individuals with ITPR1 deletion as missense mutations will confirm this speculation.

Dysregulation of intracellular Ca<sup>2+</sup> homeostasis by haploinsufficiency or nonsense mutation of ITPR1 results in dysfunction of Purkinje neurons, and ultimately might result in degeneration of Purkinje neurons in humans. The study of the molecular mechanism underlying Purkinje cell degeneration caused by ITPR1 will provide new insight into the mechanisms of ataxia and eventually the development of new therapeutic approaches for preventing the degeneration of Purkinje neurons.

**Electronic database information.** NCBI accession numbers: *Homo sapiens* ITPR1, AA030942.2; *Rattus norvegicus* ITPR1, NP\_777246.1; *Altaea maritima* ITPR1, NP\_049715.2; *Reno* ortholog ITPR1, NP\_0107256.1; *Gadus pallus* ITPR1, XP\_414438.2; *Xenopus laevis* ITPR1, NP\_001084015.1; *Apo* ortholog ITPR1, XP\_392236.3; *Caenorhabditis elegans* ITPR1, NP\_010203741.

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## TDP-43 Mutation in Familial Amyotrophic Lateral Sclerosis

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Amyotrophic lateral sclerosis (ALS) is a fatal neurodegenerative disease. Accumulating evidence has shown that G31A/TGG>G31C/CAG mutation in TDP-43 in the human genome is associated with ALS. We previously reported that TDP-43-positive abeta-like inclusions in the lower motor neurons, whose findings are indistinguishable from those of sporadic ALS. In three affected individuals in two generations of one family, we found a single base-pair change from A to G in position 1028 in TDP-43. We identified in a G1028/G mutation a novel mutation, A1028G, in TDP-43. Our findings indicate a new pathogenic site that molecular pathogenesis of ALS.

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Amyotrophic lateral sclerosis (ALS) is a fatal and incurable neurodegenerative disorder. One of the neuropathological hallmarks of ALS is the presence of ubiquitinated neuronal cytoplasmic inclusions (NCIs) in lower motor neurons.<sup>1,2</sup> Recently, the 43kDa TDP-43 DNA-binding protein (TDP-43) has been identified as the major component of NCIs in sporadic ALS (SALS) and sporadic dementia 1 (SOD1)-negative familial ALS (FALS), as well as sporadic and familial frontotemporal lobar dementia (FTLD).<sup>3–6</sup> Furthermore, the abnormal-molecular-weight fragments of TDP-43 were

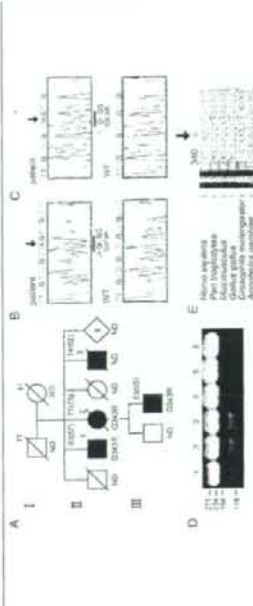
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found in affected individuals (Fig. 1A, Subject 11-2) and a control subject.<sup>7</sup> We also analyzed genomic DNA from SALS patients and a sporadic FALS case with related disorders: frontotemporal lobar degeneration with ubiquitin-positive inclusions (FTLUI) in 1 case, FTLD with motor neuron disease (FTLD-MND) in 2 cases, and primary lateral sclerosis in 1 case. We amplified all the exons of TDP-43 (NM\_007373) with the use of a series of primers, followed by sequence reaction. This study was approved by the Institutional Review Board of Nagoya University.

**TDP-43 Immunohistochemistry**  
For immunohistochemistry (see Fig. 1B, Subject 11-2), the distribution of TDP-43-immunoreactive NCIs in the brain was examined by immunohistochemical analysis. We prepared 4- $\mu$ m-thick paraffin-embedded sections. These sections were immunostained by the avidin-biotin-peroxidase complex method with the use of a Vectastain ABC kit (Vector Laboratories, Burlingame, CA) and a rabbit polyclonal antibody against TDP-43 (10743-1-AP; 1:1000; ProteinTech Group, Chicago, IL).

**Plasmid Construction**  
A 1028G mutation in TDP-43 was constructed by site-directed mutagenesis. Human TDP-43 complementary DNA (cDNA) was isolated from the human whole-brain



**Fig. 1.** Detection of TDP-43 mutation in familial amyotrophic lateral sclerosis (FALS). (A) Pedigree family pedigree. Q43AR, A1028G change in genomic DNA in heterozygous state. Age at death or onset age and age at disease onset (y) are indicated. (B) DNA sequence of genomic polyoma virus (PCV) protein. Arrows indicate A1028G in the patient. The resulting Q43AR is absent at the site of the substitution of the patient. (C) DNA sequencing chromatograms. The resulting Q43AR is absent at the site of the substitution of the patient. (D) PCR products of A1028G mutation in TDP-43. (E) PCR products of PCR products in three generations in one pair are indicated on the left. Lane 1 to 7 indicate patient lanes 3 to 7 indicate normal control subject. (F) Sequence alignment of TDP-43 in affected persons. An arrowhead indicates of Homo sapiens NP\_031401.1; Puv (polydora) XP\_001133199.1; Mus musculus NP\_663331.2; Gallus gallus XP\_417612.1; Drosophila melanogaster NP\_227081.1; and Anopheles gambiae XP\_595683.2 were multiply aligned with the site of the change program, version 1.01. (G) The numbering on top of the alignment corresponds with the human amino acid sequence. Arrows indicate A1028G, which is the site of Q43AR in individual 11-2 in our study.













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段材料子について日本呼吸器学会は解熱、白血球数の正常化とレントゲン所見の改善傾向、CRPの最高値の30%以下への低下をあげています。

### おわりに

VAPを繰り返すALNS患者さんへの手帳は不良でしたが、そのような患者さんでも気管食道の灌漑を行うことによりVAPの発症率は著しく減少します。私たちの施設ではこの3年間、VAPで亡くなった患者さんはおられません。呼吸器感染症は神経難病患者さんにとって時に命を脅かす大きな問題です。呼吸器やスクイージングによる肺の圧迫などによって呼吸器感染症に発展することが大切です。さらには栄養状態を保つこと、肺性浮腫の温床となる肺病を作らないこと、入浴や清拭で身体を清潔に保つことなどの全身管理の管理も忘れてはいけません。感染症発症した場合には、早期に治療を開始すること、少い間に治療を始めることが、加齢での回復に結びつきます。患者さんへのフォローを最前線におさえ、結果を可視にします。発熱や痰の増加など感染症の発症を疑わせる症状が認められた時はなるべく早期に対応する必要があります。

(原稿 直筆)









イカメアは、男性の性的傾向を抑制し変化させることにより、両性の倫理的側面を模倣する事柄として「フクロエシックス」(男性生殖腺をフェロモンスと呼ぶことからの派生)とも呼ばれる。必要になるかもしれないなど述べているが、脳神経学の科学性に疑問を呈する立場から言えば、脳神経学は単に生物倫理や医療倫理の応用問題に過ぎないこととなるだろう。

一方で、脳神経学の独自の価値を強調する立場からは、脳科学者マイケル・ガラーゴの「よりよいより価値な変化がある。彼は、『脳のなかの脳』脳神経学辞典」の中で次のように述べている。

「これまでのところ、脳神経学における議論は、何よりも科学者ではなく人々の中心になってきた。そもそも脳神経科学者がこの両性の間をなかの脳に及び及びた。また、脳は脳神経学をこの定義した。一側面、正解、死、生活習慣、生活習慣といった、人々の健康や幸福にかかわる問題で、土台となる脳メカニクスについての知識に基づいて書ける分野である。」

つまり、これまでは哲学や倫理学で扱われてきた脳神経学に関わる問題は、脳科学の手法によって客観的に解明できるという主張である。これは、哲学や倫理学に代する形に報告に等しいだろう。

脳神経学という学問分野が1つの領域として確立しているのか、それとも脳神経学は倫理学の一部として受け取られているのか、あるいは脳神経学の脳科学的側面によって倫理学そのものが脳科学に飲み込まれるのか、さまざまな可能性が本来に覆いかぶかっている。最後のものは可能性が低いだろう。

だが、どんな呼び名を採ろうとしても、どんなアプローチ法を採ろうとしても、確実なことは、脳神経学を生かしたらとらえて、脳科学と社会をめぐる問いは、1つのチャレンジであり続けるだろうといえることだ。

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## ホスピス/緩和ケアの概念と実践についての国際比較研究

—英国・アイルランドのホスピス訪問を通して—

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Key Words: ホスピス, 緩和ケア, 英国, アイルランド, 国際比較

**要旨** 本研究は、ヨーロッパ緩和ケア協会 (EAPC) による2005年の国際レポート<sup>1)</sup>、欧州議会の政策的支援を受けて行われた PALLIUMプロジェクト<sup>2)</sup>による2005年の報告書<sup>3)</sup>等による文献検討と、英国・アイルランドのホスピス訪問によるインタビューから、ホスピス/緩和ケアの概念と実践について国際比較分析を行い、日本における緩和ケアのあり方の検討に資することを目的とした。その結果、英国・アイルランドでの緩和ケアの定義、対象、運営時間、告知のあり方、看取りのあり方等において、文化的背景に基づき多様性がみられた。そして、トータルパレイン<sup>4)</sup>に対するケアに必要な諸要素として、「互恵を促すこと」、「多職種で患者様を囲むこと」、「コミュニケーション・スキルを高めること」、「患者と共にあること」、「自然であること」、「患者が自分のコントロールを取り戻すこと」が見出され、文化を考慮した日本の緩和ケア構築の必要性への示唆を得た。

## 1. 緒言

2002年、世界保健機構 (以下WHO) は、生命を脅かす疾患による苦悶に直面している患者とその家族に対し、より早期から、よく生きるための諸問題を解決するためのアプローチとしての緩和ケア<sup>5)</sup>を定議した。これは、わが国の2004年の「第3次がん10年戦略<sup>6)</sup>」(2007年)、「がん対策基本法」に反映されている。これにより緩和ケア教育・研究が推進され、2007年には文部科学省が「がん予防・検診・診断・治療」を推進した。原に診療報酬では、緩和ケアナース加算、緩和ケア研修加算が導入され、日本における緩和ケアが広がりをみせている。

しかし、日本における緩和ケアは、充分な理解の下に開始されてはいない。緩和ケアが発祥したヨーロッパにおいても、今日、その概念・定義および組織・機能をめぐって、多岐性と共通性が見られ、緩和ケアのあり方をめぐって、いくつかの議論が議論されている。そこで、緩和ケア先進国であるイギリス・アイルラ

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2. ヨーロッパ緩和ケア協会 (EAPC) による国際報告書 (The EAPC Task Force on the Development of Palliative Care in Europe)<sup>1)</sup>

この報告は、WHO委員会による、アンケート調査によるヨーロッパ各国現在及び各国の緩和ケアの現状の報告であり、インターネットにて公開されているものである。

3. 緩和ケアに関する日本・英国・アイルランドの各国文献  
4. 英国とアイルランドのホスピス訪問と、スタッフに行ったインタビューデータ

## III. 結果・考察

## 1. ホスピス・緩和ケアの歴史

ホスピスは、中世ヨーロッパで誕生した。当時は、病人や孤児、貧民、病者などに安らぎと援助を施すための施設であった<sup>7)</sup>。19世紀に入り、世界で初めて、末期病者のためのホスピスが開設された。それは、1827年にアイルランドのダブリンにおいて、マザー・マリア・エイクレンヘッド (図1) により設立された修道女会 The Irish Sisters of Charity が設立した Our Lady's Hospice (聖母マリア・ホスピス) である。この修道女



図1 マザー・マリア・エイクレンヘッド (聖母マリア・ホスピスにて肖像撮影)

表1 各国の初期のホスピス・緩和ケアの成り立ち

設立年	国名	施設名	特徴
1870年	アイルランド	聖母マリア・ホスピス	入居型ホスピス
1890年	オーストラリア	清心ホスピス	病院併設型
1905年	イギリス	聖ジョセフ・ホスピス	入居型ホスピス
1907年	イギリス	聖クリストファー・ホスピス	入居型ホスピス
1975年	カナダ	ロイヤルビクトリア病院	緩和ケア病棟
1977年	スウェーデン	モックラ病院ホームケア部門	ホームケアサービス
1980年	イタリア	国立ミラノがん研究所ペインコントロール部門 およびパトリオ二二基金	ホームケアサービス
1981年	日本	聖隷三井病院	院内設立型ホスピス
1983年	ドイツ	ケルン大学病院緩和ケアユニット	大学病院緩和ケア病棟
1984年	スウェーデン	サンダーゴール・バルチチセラ病院緩和ケア	病院がん部門の緩和ケア病棟
1984年	日本	慶応義塾大学病院	院内併設型ホスピス
1985年	ベルギー	ブリュッセル・聖ルーク大学病院緩和ケアユニット	緩和ケア病棟ホームケアサービス
1991年	オランダ	フリユネン・ヨハネ病院	入居型ホスピス





