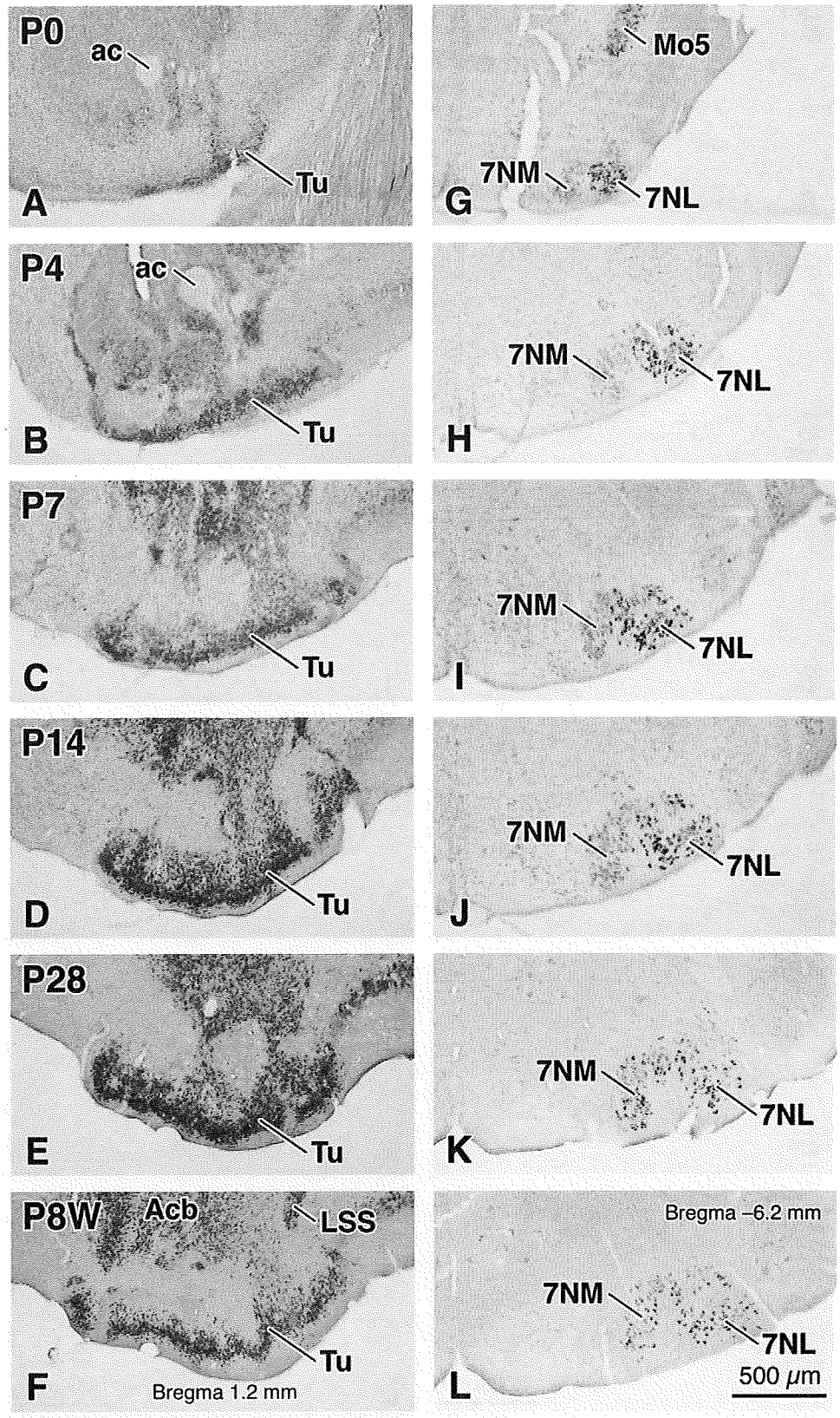


**Fig. 4.** Type 2a pattern of *Wfs1* mRNA signals in the mouse brain during postnatal development. (A–F) Changes in *Wfs1* mRNA signals in the olfactory tuberculum (Tu) during postnatal development. The day of birth is regarded as postnatal day 0 (P0). P4, P7, P14, P28, and P8W indicate postnatal days 4, 7, 14, and 28, and postnatal week 8, respectively. Brain sections of P0, P4, P7, P14, P28, and of P8W mice are shown in panels (A), (B), (C), (D), (E), and (F), respectively. The bregma level of a P8W-mouse section is represented at the lower middle in (F). (G–L) Changes in *Wfs1* mRNA signals in the facial nucleus during postnatal development. Brain sections of P0, P4, P7, P14, P28, and of P8W mice are shown in panels (G), (H), (I), (J), (K), and (L), respectively. The bregma level of a P8W-mouse section is represented at the upper right in (L). Note that *Wfs1* mRNA signals in the type 2a pattern are moderate, and of a relatively stable strength from P0 to P8W. Additionally, in the facial nucleus, the pattern of *Wfs1* mRNA signals during postnatal development is not homogeneous. In the lateral subdivision of the facial nucleus (7NL), the pattern is type 2a, whereas in the medial subdivision (7NM), it is type 1b. Upper and right sides of each panel are dorsal and lateral sides of each brain section, respectively. ac, anterior commissure; Acb, nucleus accumbens, LSS, lateral stripe of the striatum; Mo5, motor nucleus of the trigeminal nerve. Scale bar = 500 μm in (L) for (A–K).

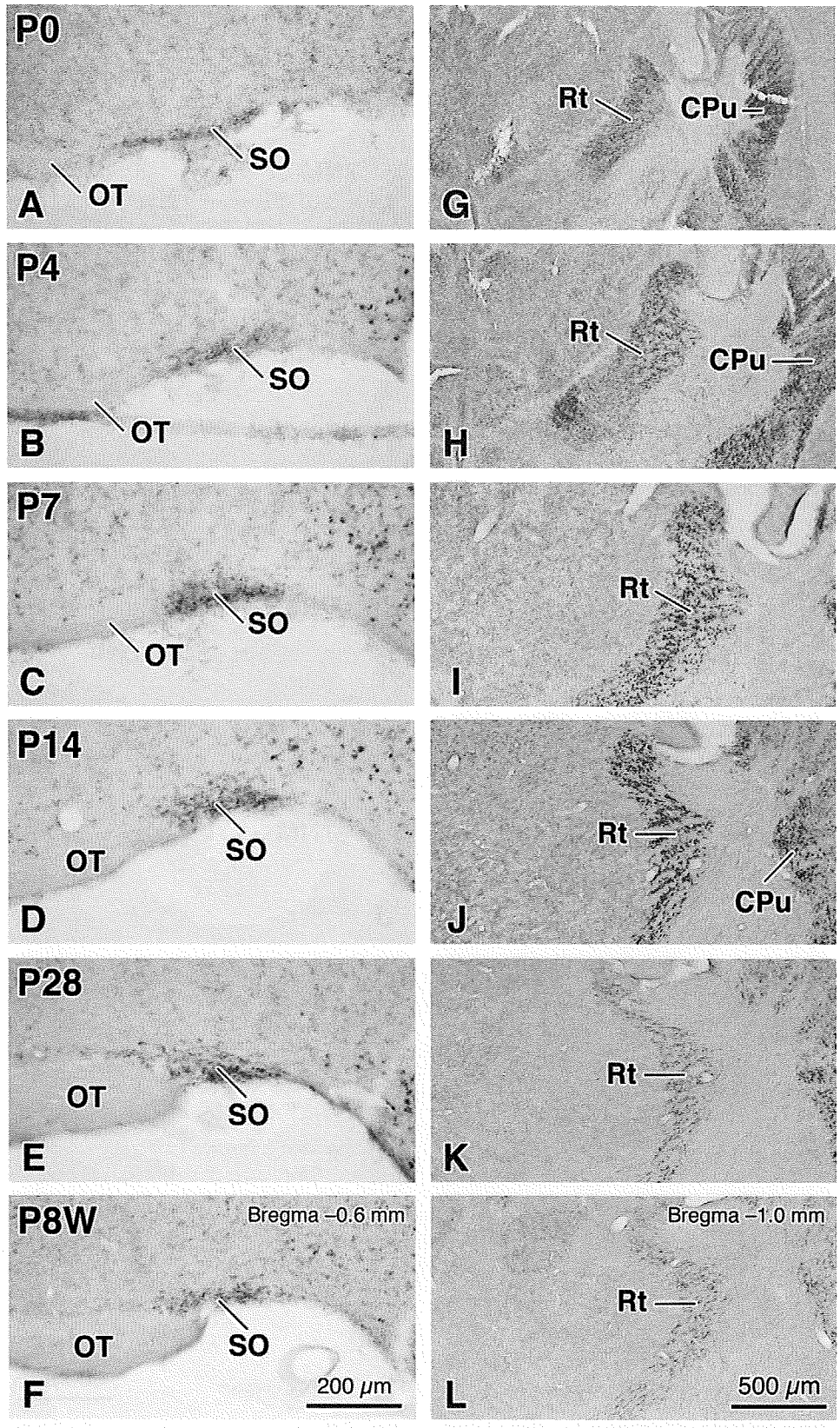


**Fig. 5.** Type 2b (A–F) and type 3a (G–L) patterns of *Wfs1* mRNA signals in the mouse brain during postnatal development. (A–F) Changes in *Wfs1* mRNA signals in the supraoptic nucleus (SO) during postnatal development. The day of birth is regarded as postnatal day 0 (P0). P4, P7, P14, P28, and P8W indicate postnatal days 4, 7, 14, and 28, and postnatal week 8, respectively. Brain sections of P0, P4, P7, P14, P28, and of P8W mice are shown in panels (A), (B), (C), (D), (E), and (F), respectively. The bregma level of a P8W-mouse section is represented at the upper right in (F). Note that *Wfs1* mRNA signals in the type 2b pattern are weak, and of a relatively stable strength from P0 to P8W. (G–L) Changes in *Wfs1* mRNA signals in the thalamic reticular nucleus (Rt) during postnatal development. Brain sections of P0, P4, P7, P14, P28, and of P8W mice are shown in panels (G), (H), (I), (J), (K), and (L), respectively. The bregma level of a P8W-mouse section is represented at the upper right in (L). Note that *Wfs1* mRNA signals in the type 3a pattern peak from P7 to P14 and show moderate strength at the peak. Upper and right sides of each panel are dorsal and lateral sides of each brain section, respectively. CPu, caudate putamen; OT, optic tract. Scale bar = 200 μm in (F) for (A–E), 500 μm in (L) for (G–K).

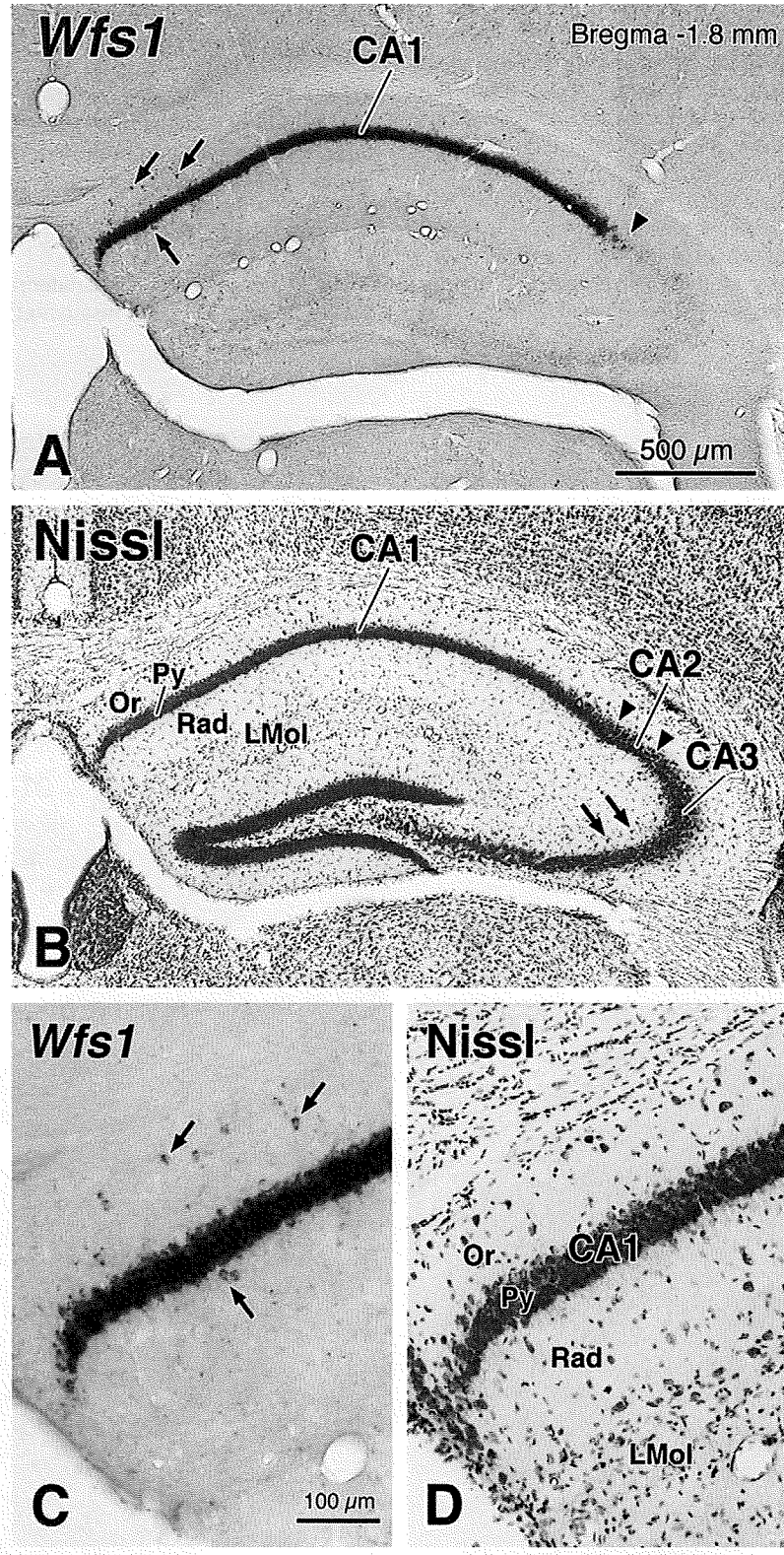


**Fig. 6.** *Wfs1* mRNA signals in the rostral part (Bregma = −1.8 mm) of the hippocampal formation in the young-adult mouse (postnatal week 8). (A and B) Mouse *Wfs1* mRNA signals (*Wfs1*, A), and cytoarchitecture (Nissl, B) in adjacent sections of the hippocampal formation hybridized with anti-sense cRNA probes of the mouse *Wfs1* 3′-terminus, and Nissl-stained with cresyl violet, respectively. Arrowheads indicate borders between each hippocampal field. Arrows in (A), and those in (B) show *Wfs1* mRNA-hybridized neurons in strata radiatum and oriens of the CA1 field, and small Nissl-stained cells scattered above the pyramidal cell layer of the CA3 field, respectively. (C and D) Higher magnification photomicrographs of mouse *Wfs1* mRNA signals (*Wfs1*, C) in the same section as in panel (A) and of cytoarchitecture (Nissl, D) in the same section as in panel (B). Arrows in (C) show the identical set of *Wfs1* mRNA-hybridized neurons pointed to by arrows in (A). Note that strong *Wfs1* mRNA signals are almost exclusively observed in the pyramidal cell layer of the CA1 field. In addition, *Wfs1* mRNA-hybridized neurons (arrows in A and C) are seen in strata oriens and radiatum of the CA1 field. CA1, CA1 field of the hippocampus; CA2, CA2 field of the hippocampus; CA3, CA3 field of the hippocampus; LMol, stratum lacunosum-moleculare; Or, stratum oriens; Py, pyramidal cell layer; Rad, stratum radiatum. Scale bars = 500 μm in (A) for (B), 100 μm in (C) for (D).

*3.2.2. PaS*

*3.2.2.1. Cytoarchitecture.* Areal demarcation and the laminar classification were based on Witter and Amaral (2004). From the cytoarchitectonic aspect, the PaS (Brodmann's area 49) is a multilayered structure in which there are more than three cortical layers. The layers of the PaS are subdivided into external and internal laminae, separated by a cell-free lamina (layer IV). The external lamina is composed of the molecular layer (layer I) and cell layers II and III, and the internal lamina, cell layers V and VI. Layers II and III comprise large, rather densely packed, lightly stained cells. There is no clear boundary between layers II and III of the external lamina. Layers V and VI consist of small, rather densely packed, moderately stained cells (Fig. 7B and D).

*3.2.2.2. Wfs1 mRNA signals.* Strong *Wfs1* mRNA signals were observed in cell layers II and III (the external lamina except for layer I). In the deep part of the external lamina, weak-to-moderate signals were also seen deeper down (Fig. 7).

*3.2.3. Entorhinal cortex*

*3.2.3.1. Cytoarchitecture.* Areal demarcation and the laminar classification were based on Insausti et al. (1997) and on Witter and

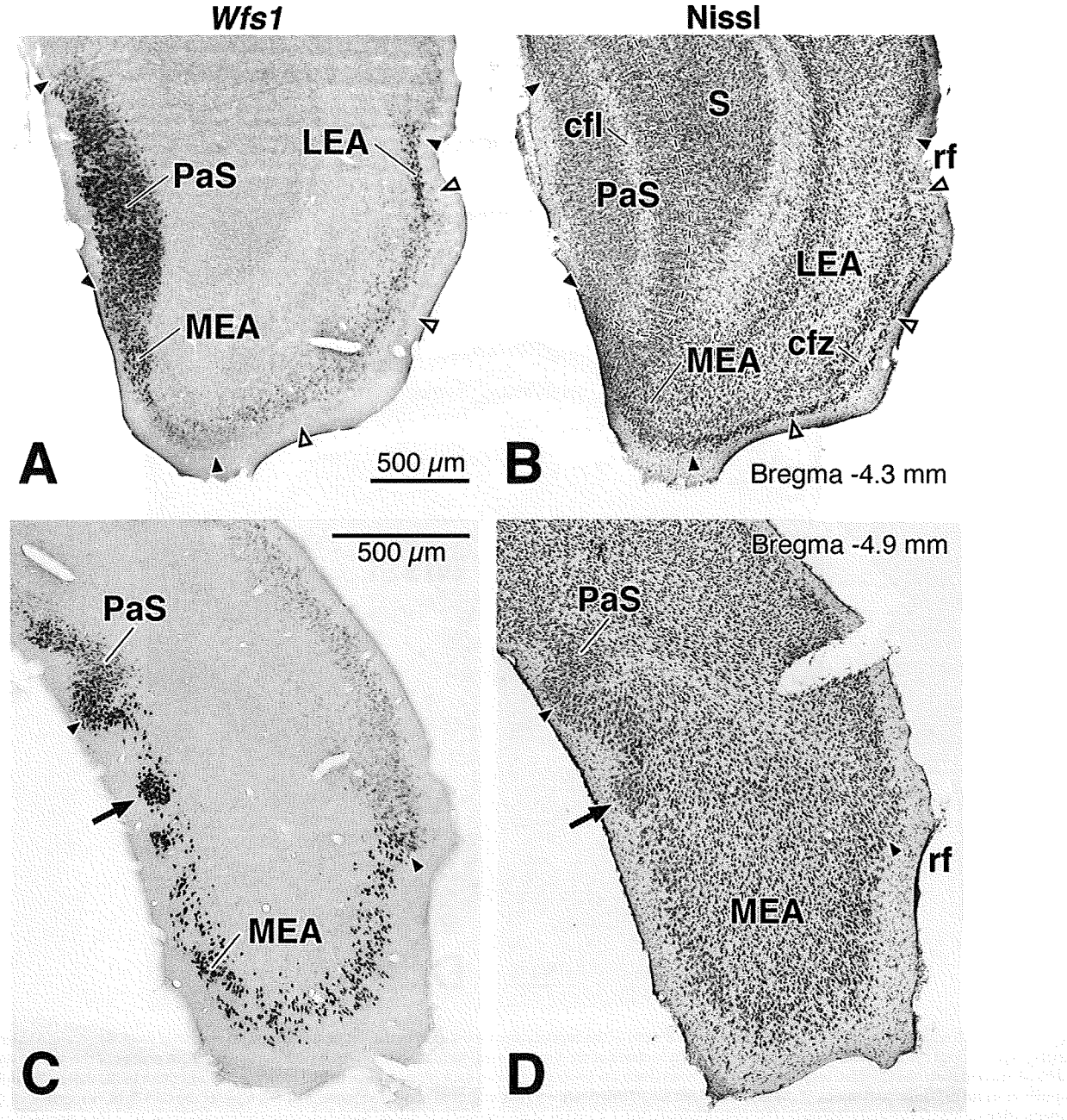


**Fig. 7.** *Wfs1* mRNA signals in the parasubiculum (PaS) and entorhinal cortex of the young-adult mouse (postnatal week 8). (A and B) Mouse *Wfs1* mRNA signals (*Wfs1*, A), and cytoarchitecture (Nissl, B) in adjacent sections of the rostral part (Bregma = −4.3 mm) hybridized with anti-sense cRNA probes of the mouse *Wfs1* 3′-terminus, and Nissl-stained with cresyl violet, respectively. The dashed line in (B) shows the border of the PaS. (C and D) Mouse *Wfs1* mRNA signals (*Wfs1*, C), and cytoarchitecture (Nissl, D) in adjacent sections of the caudal part (Bregma = −4.9 mm). Solid and open arrowheads indicate borders between each cortical area and the superficial boundary of layer II in the lateral entorhinal area (LEA), respectively. Arrows show an islet of cells in layer II of the medial entorhinal area (MEA). Note that strong *Wfs1* mRNA signals are observed in the PaS, MEA, and LEA. cfl, cell-free lamina; cfz, cell-free zone; rf, rhinal fissure; S, subiculum. Scale bars = 500 μm in (A) for (B), in (C) for (D).

Amaral (2004). In this study, the entorhinal cortex is subdivided into two areas, the MEA and the LEA. In the MEA, cells in layer II are primarily large-to-medium-sized, moderately packed, and moderately stained, while those in layer III are small-to-medium-sized and loosely packed (Fig. 7B and D). In the caudo-medial part of layer II, an islet of cells (arrow in Fig. 7D) was observed. Cells in the islet were medium-sized, rather densely packed, and lightly stained (Fig. 7D). In the rostro-medial part, which abuts the PaS, layer I is very thin and layers II and III contain densely packed cells that are small-to-medium-sized, and moderately stained (Fig. 7B).

In the LEA, layer II is separated from layer III by a narrow cell-free zone in much of the rostral part. Cells in layer II are very densely packed, while those in layer III are moderately or loosely packed. Layer III is thick and subdivided into a narrow moderately packed outer zone and a loosely packed inner zone. Since layer IV is very poorly developed or absent, layer V usually abuts layer III. Cells in layer V tend to be larger and more darkly stained than those in layer III (Fig. 7B).

*3.2.3.2. Wfs1 mRNA signals.* In the caudal part of the MEA, strong *Wfs1* mRNA signals were observed in layer II. These signals were almost confined to this layer (Fig. 7C and D). In layer II of the caudo-medial part, islets of strongly *Wfs1* mRNA-hybridized cells were seen (arrow in Fig. 7C). One of these islets corresponded to an islet of Nissl-stained cells (arrow in Fig. 7D). Strongly *Wfs1* mRNA-hybridized cells were densely packed in the islets, while those were scattered around the islets (Fig. 7C). In the rostro-medial part of the MEA, strongly-to-moderately *Wfs1* mRNA-hybridized cells were seen in layers II and III. In the rostro-lateral part of the MEA, weak *Wfs1* mRNA signals were detected in layer II (Fig. 7A and B).

In the LEA, strong *Wfs1* mRNA signals were observed in the outer zone of layer III. The distribution of these signals was confined to around the rhinal fissure (Fig. 7A and B). In the other part of the LEA, weak-to-moderate signals were seen in layer III deeper down. Different from the other multi-layered cortical areas, a very small number of *Wfs1* mRNA signals was detected in layer II (Fig. 7A and B).

## 4. Discussion

In the present study, we determined the patterns of change in the strength of *Wfs1* mRNA signals in each of the mouse brain structures from birth to early adulthood (P8W). There were three patterns. In type 1, signals were weak or absent in neonates but strong or moderate in young adults. This pattern was observed in the CA1 field, the PaS, and in the entorhinal cortex (MEA and LEA). In type 2, signals were of a relatively constant strength during development. This pattern was seen in limbic structures (e.g. S (subiculum) and Ce (central amygdaloid nucleus)) and brainstem nuclei (e.g. facial and chochlear nuclei). In type 3, signals peaked in the second week of age. This pattern was observed in the Rt (thalamic reticular nucleus). The present study also demonstrated layer-specific localization of *Wfs1* mRNA signals in the CA1 field, the PaS, and in the entorhinal cortex where strong signals were seen from P14 to early adulthood (P8W).

### 4.1. Comparison with previous findings

Our findings on *Wfs1* mRNA expression in the brain of young-adult mice were primarily compatible with previous studies in the mouse (Kato et al., 2008; Kawano et al., 2008; Luuk et al., 2008) and the rat (Takeda et al., 2001). In these studies, *Wfs1* expression was described in the cerebral cortex, the basal ganglia, the hypothalamus, the brain stem motor and sensory nuclei, the reticular formation, and in the cerebellar cortex, as well as in the CA1 field and in the amygdala. The present study showed that *Wfs1* mRNA signals were observed in these structures of the young-adult mouse. The findings indicate that *Wfs1* mRNA expression in these structures (present study) is similar to Wfs1 protein expression (Kato et al., 2008; Luuk et al., 2008), and is similar between the mouse (present study) and the rat (Takeda et al., 2001) in early adulthood.

### 4.2. Patterns of change in Wfs1 mRNA expression

In the following, we discuss each type of the patterns of change in the strength of *Wfs1* mRNA signals systematically.

#### 4.2.1. Type 1 pattern of change

*4.2.1.1. Type 1a.* Type 1a pattern was observed in the limbic cortex: the CA1 field, PaS, MEA, and LEA. The CA1 field is a part of the hippocampus proper, and the PaS, MEA, and LEA are parts of the parahippocampal cortical areas (Witter and Amaral, 2004). Detailed discussions about these structures are described separately in Section 4.3.

*4.2.1.2. Type 1b.* Type 1b pattern was observed in the motor, limbic, and olfactory cortices (MoCII, CgII, and Pir), basal nuclei that are parts of the limbic system (LS, and Acb), and in the sensory and motor brainstem nuclei (Me5, 7MN, and Amb). The cingulate cortex is one of the largest components of the limbic system and is characterized by diffuse projections from the anteromedial thalamic nucleus (Palomero-Gallagher and Zilles, 2004). It is involved in motivational aspects of learning tasks (Gabriel et al., 1980) and contributes to motor functions via numerous efferents to subcortical motor systems (Palomero-Gallagher and Zilles, 2004). The Pir (piriform cortex) is a part of the primary olfactory cortex, since the Pir receives direct projections from the MOB (main olfactory bulb) (Shipley et al., 2004). The LS (lateral septal nucleus) is characterized by massive glutamatergic afferents from the hippocampus proper and the subiculum, and by massive bidirectional connections with the rostral brainstem, especially with the hypothalamus and the ventral midbrain. The LS contributes to emotional behaviors (Risold, 2004). The Acb (nucleus accumbens) is a limbic part of the striatum. This nucleus receives extensive inputs from limbic structures, such as the hippocampus and amygdala, as well as from the prefrontal areas subserving limbic and autonomic functions, i.e. orbital, infralimbic, prelimbic, and agranular insular cortices. The Acb reciprocates its dopaminergic input, and in addition, innervates most of the dopaminergic neurons projecting to the associative and motor structures (Joel and Weiner, 2000). The Me5 (mesencephalic trigeminal nucleus) is one of the sensory relay nuclei, and plays a role in proprioception during mastication and the integration of jaw movements (Waite, 2004). The Amb (nucleus ambiguus) is one of the branchial motor nuclei in the brainstem, and innervates the striated muscles of the pharynx, esophagus, and larynx (Loewy and Spyer, 1990; Saper, 2000). It is possible that the Me5 and the Amb contribute to feeding. Further details concerning the 7NM are described separately in Section 4.4.

*4.2.1.3. Type 1c.* Type 1c pattern was observed in layer II of the sensory cortical areas except for the olfactory area (SoCII, AuCII, and ViCII), and in the SC. There are some striking similarities between the sensory cortical areas and the SC: both structures have layered architecture, the both structures receive few olfactory inputs, and the both structures contribute to process sensory information including visual, somatosensory, and auditory modalities (Sefton et al., 2004).

#### 4.2.2. Type 2 pattern of change

*4.2.2.1. Type 2a.* Type 2a pattern was observed in the limbic structures (S, Tu, BSTL, IPAC, and Ce), the caudal part of the CPu, and

in the oromotor nuclei relevant to feeding (Mo5, 7NL, and 12N). The S (subiculum) is a part of the hippocampal formation and is the major origin of the fornix (Witter and Amaral, 2004). The Tu (olfactory tuberculum) is referred to as a part of the primary olfactory cortex, since the Tu receives direct projections from the MOB. In addition, the Tu is regarded as a part of the ventral striatum, the limbic part of the striatum (Shipley et al., 2004). The BSTL (lateral bed nucleus of the stria terminalis) and the IPAC (interstitial nucleus of the posterior limb of the anterior commissure) are parts of the central division of the extended amygdala. This means that characteristics of the BSTL and the IPAC are similar to those of the Ce (central amygdaloid nucleus): the BSTL and the IPAC maintain close structural, cytochemical, and hodological relationships with the Ce (de Olmos et al., 2004). The Ce is believed to be an important output region of the amygdala, at least for the expression of innate emotional responses and associated physiological responses. The expression of these responses involves connections from the medial subdivision of the Ce to brainstem areas that control specific behaviors and physiological responses (LeDoux, 2007).

In general, the CPu (dorsal striatum or neostriatum) is subdivided into medial and lateral from the anato-functional aspect of view. The lateral CPu is regarded as motor striatum, and the medial CPu is regarded as associative striatum (Joel and Weiner, 2000). In addition, anatomical differences between the rostral and caudal CPu were also reported in the rodent striatum. The distribution of $\mu$ (mu) opiate receptors demonstrated that spatial organization of patch and matrix compartments in the rat striatum was different between rostral and caudal parts: patches were numerous and of large size in the rostral part, while they were rare and of small size in the caudal part (Desban et al., 1993). As for corticostriatal projections to the matrix in the rat striatum, patterns of axonal arborization were different between the rostral and caudal parts: the extended axonal arborizations were primarily confined to the rostral part, conversely, the focal axonal arborizations were observed most obvious in the caudal part (Kincaid and Wilson, 1996). Since there are anatomical differences between the rostral and caudal parts of the rodent CPu, it is possible to accept that the type 2a pattern of change in the mouse CPu was confined to the caudal part. Further details concerning the oromotor nuclei (Mo5, 7NL, and 12N) are described separately in Section 4.4.

*4.2.2.2. Type 2b.* Interestingly, brain structures potentially relevant to the clinical symptoms of Wolfram syndrome showed the type 2b pattern of change. Detailed discussions concerning the clinical symptoms are described separately in Sections 4.5–4.7. In addition, brain structures, where atrophic changes were observed in Wolfram syndrome patients, also represented the type 2b pattern. For example, the main and accessory olfactory bulbs (MOB and AOB) showed the type 2b pattern in the mouse. In Wolfram syndrome patients, atrophic changes were observed in the olfactory bulb and tracts (Genís et al., 1997; Shannon et al., 1999). Further details concerning the atrophic changes are given in Section 4.8.

*4.2.3. Type 3 pattern of change*

*4.2.3.1. Type 3a.* The Rt (thalamic reticular nucleus), which showed the type 3a pattern, forms a thin neuronal sheet at the rostral, dorsolateral, lateral, and ventrolateral edges of the dorsal thalamus (Groenewegen and Witter, 2004). Groenewegen and Witter (2004) noted that the Rt was strategically "placed" between the dorsal thalamus and the cerebral hemisphere: all incoming and outgoing fibers of the thalamus have to pass through the Rt, and most of the giving off collaterals terminates at a restricted part of the Rt. Thalamic reticular neurons are all GABAergic and express parvalbumin (Mitrofanis, 1992). The prevailing interpretation of the functional role of the Rt is that it serves attentional brain mechanisms (e.g., "searchlight hypothesis") (Crick, 1984; Guillery et al., 1998; McAlonan et al., 2000). The Rt is important for the control of the firing mode of thalamocortical projection neurons and, in this way, for the selection of the information that is transferred from the thalamus to the cerebral cortex. The Rt plays an important role as pacemaker during synchronized firing of thalamocortical cells (Groenewegen and Witter, 2004).

*4.2.3.2. Type 3b.* Type 3b pattern was observed in layer V of the motor (MoCV), sensory (SoCV, AuCV, and ViCV), and of the limbic cortices (CgV, and RSCV) and in layer II of the limbic cortex (RSCII). Interestingly, *Wfs1* mRNA signals in layer II were observed in the motor, sensory, and cingulate cortices in early adulthood, while those were not seen in the retrosplenial cortex. Together with the anterior cingulate cortex, the retrosplenial cortex is involved in the motivational aspects of learning tasks and contributes to motor functions via numerous efferents to subcortical motor systems (Palomero-Gallagher and Zilles, 2004). In addition, many observations support a significant role of the retrosplenial cortex in visuospatial functions. There is massive visual input to the retrosplenial cortex, and major projections from the postsubiculum which is involved in coding for head position in space (Taube et al., 1990; Vogt et al., 2004).

Interestingly, *Wfs1* mRNA expression in layer V of the motor and sensory cortices (type 3b) synchronized with that in the Rt (type 3a). It is not known why the expression in these structures synchronized each other. It should be noted that layer V in the motor and sensory cortices indirectly connect with the Rt by way of the higher order thalamic nuclei (Gabreëls et al., 1998). For example, layer V neurons in the visual cortex send their axons to the lateral posterior nucleus (LP), a higher order nucleus of the visual thalamus (Sefton et al., 2004). Then LP neurons project to the Rt (Groenewegen and Witter, 2004). The indirect connections between layer V and the Rt may provide clues as to the synchronization.

*4.3. Strong Wfs1 mRNA signals in the CA1 field, PaS, and entorhinal cortex*

*4.3.1. CA1 field*

The CA1 field is a part of the hippocampus proper. According to an excellent review by Witter and Amaral (2004), the CA1 field has connections with various intrahippocampal, cortical, and subcortical structures. The CA1 field receives intrahippocampal projections from the CA3 field (Schaffer collaterals), and from the CA2 field (Ishizuka et al., 1990). There are only weak associational connections (Tamamaki et al., 1987; Amaral et al., 1991) and weak commissural connections (Van Groen and Wyss, 1990b) in the CA1 field. Cortical inputs to the CA1 field arise from the entorhinal, perirhinal, and postrhinal cortices, which compose the parahippocampal region. The CA1 field receives subcortical projections from the septum, the amygdala, and from the thalamus. It also receives light noradrenergic, serotonergic, and dopaminergic inputs from the brainstem nuclei (Swanson et al., 1987). In addition to the afferent connections, the CA1 field has efferent connections with various intrahippocampal, cortical, and subcortical structures. The major projection arising from the CA1 field is a projection to the adjacent subiculum. With regard to cortical efferents, the CA1 field sends axons back to the parahippocampal region including the entorhinal, perirhinal, and postrhinal cortices. The CA1 field also projects to the retrosplenial, prelimbic, and infralimbic cortices. Subcortical outputs from the CA1 field terminate in the septum, nucleus

accumbens, olfactory structures including the olfactory bulb, the hypothalamus, and in the amygdala (Van Groen and Wyss, 1990b; Witter and Amaral, 2004). Since strong *Wfs1* mRNA signals were observed in the pyramidal layer, the *Wfs1* gene might contribute to these neuronal relays in this layer. However, it is unclear whether *Wfs1* mRNA-hybridized pyramidal cells are involved in all of these neuronal relays. Further studies by using tract-tracing methods are required to clarify the fiber connections of *Wfs1* mRNA-hybridized neurons in the CA1 field.

The principal neuronal cell type of the CA1 field is the pyramidal cell (Witter and Amaral, 2004). Since the pyramidal cell makes up the vast majority of neurons in the pyramidal cell layer (Witter and Amaral, 2004), and since *Wfs1* mRNA signals were seen in most of the cells of this layer (present study), the signals were probably located in pyramidal cells. In addition to the pyramidal cell, there are several types of non-pyramidal cells in strata oriens, radiatum, and lacunosum-moleculare of the CA1 field. The vast majority of these neurons are immunoreactive for GABA (γ-aminobutyric acid; Ribak et al., 1978), and most of these cells are considered to be local circuit neurons (interneurons; Witter and Amaral, 2004). Since *Wfs1* mRNA-hybridized cells were also observed in strata radiatum and oriens of the CA1 field (present study), it is suggested that *Wfs1* mRNA would be detected in interneurons of these strata. However, it is not known whether *Wfs1* mRNA signals are present in interneurons of the pyramidal cell layer. Further studies are required to clarify whether *Wfs1* mRNA is expressed in interneurons of the pyramidal cell layer in the CA1 field.

Functional studies suggested that the septal hippocampus is necessary for spatial learning and memory (Moser et al., 1993; Witter and Amaral, 2004), whereas the temporal hippocampus appears to be essential for normal fear-related behavior in rats (Kjelstrup et al., 2002; Witter and Amaral, 2004). Since *Wfs1* mRNA signals in the CA1 field were observed in both the septal and temporal levels, the *Wfs1* gene might contribute both to spatial learning and memory, and to normal fear-related behavior. In addition, distribution of the signals was not homogeneous in the CA1 field: strong signals were observed in the septal hippocampus while weak-to-moderate signals were seen in the temporal hippocampus (present study). The functional difference between the septal and temporal hippocampi may help to explain the difference in the strength of the signals between the two hippocampi.

#### 4.3.2. PaS

The PaS is one of the parahippocampal areas. In the mouse, *Wfs1* mRNA signals were confined to layers II and III (the external lamina). Afferent fibers to these layers arise from various intrinsic, hippocampal, parahippocampal, cortical, and subcortical structures in the rat (Witter and Amaral, 2004). The PaS gives rise to both intrinsic associational connections (Köhler, 1985; Caballero-Bleda and Witter, 1993), and a commissural projection (Köhler, 1985; Van Groen and Wyss, 1990a). The PaS receives a hippocampal input from the subiculum (Swanson et al., 1978; Köhler, 1985; Van Groen and Wyss, 1990a,c), and a weak parahippocampal input from the entorhinal cortex (Köhler, 1986, 1988; Van Groen and Wyss, 1990a,c). The PaS also receives weak cortical projections from the retrosplenial cortex and the occipital visual cortex (Vogt and Miller, 1983; Van Groen and Wyss, 1990a). Subcortical afferents to the PaS arise from the septum, the endopiriform nucleus (Van Groen and Wyss, 1990a,c; Eid et al., 1996; Behan and Haberly, 1999), amygdala (Van Groen and Wyss, 1990a; Petrovich et al., 1996; Pikkarainen et al., 1999; Kemppainen et al., 2002), and the thalamus. Thalamic inputs to the PaS arise from the anteroventral and anterodorsal nuclei, laterodorsal nucleus, and nucleus reuniens (Herkenham, 1978; Wouterlood et al., 1990; Shibata, 1993; Van Groen and Wyss, 1995). The PaS receives serotonergic projections from the raphe nuclei (Köhler et al., 1981; Köhler and Steinbusch, 1982; Van Groen and Wyss, 1990a,c), and noradrenergic projection from the locus coeruleus (Swanson et al., 1987; Witter and Amaral, 2004).

In addition to receiving afferent fibers, the PaS sends efferent fibers to hippocampal, parahippocampal, and subcortical structures (Witter and Amaral, 2004). The PaS gives rise to hippocampal projections to the dentate gyrus, the hippocampus proper, and to the subiculum (Köhler, 1985; Van Groen and Wyss, 1990a). It sends parahippocampal projections to the presubiculum (Köhler, 1985; Van Groen and Wyss, 1990a) and to the entorhinal cortex (Köhler, 1985; Van Groen and Wyss, 1990a; Caballero-Bleda and Witter, 1993), and gives rise to a modest thalamic projection to the anterodorsal nucleus. This nucleus is the exclusive target of the extrahippocampal projections in the rat PaS (Van Groen and Wyss, 1990a; Witter and Amaral, 2004). As described above, the PaS is involved in several neuronal relays. Probably the most unique characteristic of the PaS is its relay from the anterior thalamic nucleus to the hippocampal formation. This relay provides a route by which thalamic input might influence very early stages of hippocampal information processing (Witter and Amaral, 2004). The *Wfs1* gene possibly contributes to this information processing.

#### 4.3.3. Entorhinal cortex

*4.3.3.1. Fiber connections of the superficial layers of the entorhinal cortex.* The entorhinal cortex (MEA and LEA) is a part of the parahippocampal cortex. According to the review by Witter and Amaral (2004), fibers of the so-called perforant pathway take their origin mainly from entorhinal-cortical neurons located in layers II and III, where *Wfs1* mRNA signals were observed in the mouse. These layers receive inputs from a variety of cortical structures including the ipsilateral and contralateral entorhinal cortex (Burwell and Amaral, 1998b). Extrinsic cortical afferents to the superficial layers originate from the hippocampal and parahippocampal regions. Hippocampal fibers to the layers arise from the subiculum, and parahippocampal afferents originate from the perirhinal and postrhinal cortices, the presubiculum (Naber et al., 1997; Burwell and Amaral, 1998a,b), and from the PaS (Köhler, 1985; Van Groen and Wyss, 1990a; Caballero-Bleda and Witter, 1993). Finally, a substantial input to the superficial layers originates from the olfactory structures, in particular from the olfactory bulb, the anterior olfactory nucleus, and the piriform cortex (Haberly and Price, 1978; Kosel et al., 1981). In addition, the superficial layers receive subcortical afferents from the telencephalon, the thalamus, the hypothalamus, and the brainstem. Telencephalic inputs arise from the medial septal nucleus, nucleus of the diagonal band, and from the amygdala (Price et al., 1987; Pitkänen et al., 2000). The major thalamic input originates from nucleus reunions (Herkenham, 1978; Wouterlood et al., 1990; Wouterlood, 1991). The hypothalamic input arises from the supramammillary nucleus (Haglund et al., 1984). The brainstem input originates from the ventral tegmental area, the central and dorsal raphe nuclei (Azmitia and Segal, 1978; Köhler and Steinbusch, 1982), locus coeruleus (Moore et al., 1978), and from nucleus incertus, a CRH (corticotropin releasing hormone) receptor-rich nucleus (Goto et al., 2001; Witter and Amaral, 2004).

In addition to these afferent connections, the superficial layers have efferent connections not only with the hippocampal formation (the perforant pathway), but also with parahippocampal, limbic, paralimbic, and olfactory regions of the cortex (Insausti et al., 1997) and with the septal region (Alonso and Köhler, 1984). Perforant path fibers terminate in the dentate gyrus, the CA3 and CA1 fields, and in the subiculum (Witter and Amaral, 2004), and the perforant pathway is most likely glutamatergic (Fonnum,

1970). Parahippocampal projections from the superficial layers terminate in the presubiculum, the PaS (Köhler, 1986, 1988; Van Groen and Wyss, 1990a,c), and in perirhinal area 35 (Insausti et al., 1997; Burwell and Amaral, 1998a). The superficial layers emit projections to the infralimbic cortex, the ventral taenia tecta, the prelimbic, orbitofrontal, and agranular insular cortices (Wyss and Van Groen, 1992; Condé et al., 1995; Insausti et al., 1997), and the olfactory area (de Olmos et al., 1978; Insausti et al., 1997). Additionally, many layer II neurons in the MEA project to the septal region (Alonso and Köhler, 1984; Witter and Amaral, 2004). Thus, it is possible that *Wfs1* mRNA-hybridized cells in layers II and III of the entorhinal cortex are involved in a wide variety of neuronal relays through the perforant pathway described above. Since neurons in these layers are key elements in the temporal lobe memory system (Klink and Alonso, 1997), the *Wfs1* mRNA-hybridized cells contribute to learning and memory. However, it is unclear whether majority of perforant pathway neurons in these layers express *Wfs1* mRNA. Further studies by using tract-tracing methods are required to clarify the fiber connections of *Wfs1* mRNA-hybridized neurons in the entorhinal cortex. Such studies will uncover whether the *Wfs1* mRNA-hybridized cells contribute to learning and memory as projection neurons (perforant pathway neurons) or interneurons.

*4.3.3.2. The islet of cells in layer II of the MEA.* The present study demonstrated the islet of cells in layer II of the mouse MEA. A majority of the cells in the islet were strongly hybridized with *Wfs1* mRNA. This evidence is supported by the finding that highly Wfs1-positive cell clusters were distributed in the mouse MEA (Luuk et al., 2008; Kawano et al., unpublished observations). Although Woznicka et al. (2006) demonstrated that "distinct spherical groups of small cells are situated at the border of layer I/II" in the caudal part of the canine MEA, there have been few descriptions of the islet in both the mouse and the rat (Insausti et al., 1997; van Groen, 2001; Witter and Amaral, 2004). Further studies are required to clarify hodological, neurophysiological, histochemical, and immunohistochemical details of the islet. In such studies, *Wfs1* mRNA will be a useful marker for the islet.

*4.3.3.3. A small number of Wfs1 mRNA signals in layer II of the LEA.* A laminar distribution of *Wfs1* mRNA and protein in layer II was present in most of the mouse cortical areas (Kawano et al., 2008; Luuk et al., 2008; Kawano et al., unpublished observation) as described in the rat (Takeda et al., 2001). In the LEA, *Wfs1* mRNA signals were observed in layer III, however, only a small number of the signals was detected in layer II. This evidence suggests that the laminar distribution of *Wfs1* mRNA signals in the LEA is unique to that in the multi-layered cortex. Thus *Wfs1* mRNA might be a useful marker to distinguish the LEA from other cortical areas including the MEA.

### 4.4. Facial nucleus

In the facial nucleus, the pattern of change in the strength of *Wfs1* mRNA signals differed between the 7NM (type 1b) and the 7NL (type 2a). This difference might be attributable to the myotopical organization in the nucleus. The facial nucleus in rodents is myotopically organized from birth to adulthood: neurons in the 7NM innervate the auricular muscles, whereas those in the 7NL send their axons to muscles in the orbital region, the perioral region, and in the proboscis (muscles involved with orofacial function) (Ashwell, 1982; Ashwell and Watson, 1983; Travers, 2004). It is not known why the type 1b pattern is seen in the 7NM, however, it is possible that the type 2a pattern in the 7NL is attributable to the orofacial function especially feeding, since the same pattern of change (type 2a) was seen in the Mo5 (motor nucleus of the trigeminal nerve) and in the 12N (hypoglossal nucleus), which play important roles in feeding.

### 4.5. Diabetes insipidus

Arginine vasopressin-synthesizing neurons are distributed in the SO (supraoptic nucleus) and the PVNm (magnocellular part of the paraventricular hypothalamic nucleus) (Armstrong, 2004). *Wfs1* mRNA signals in these nuclei showed the type 2b pattern (Figs. 1, 3G–L; Table 1). This finding suggests that the diabetes insipidus in Wolfram syndrome patients is attributable to dysfunctional neurons in these nuclei resulting from loss-of-function mutations in the *WFS1* gene.

Neuropathological studies showed loss of neurons in the SO and in the paraventricular hypothalamic nucleus (Genís et al., 1997; Shannon et al., 1999). In addition, Gabreëls et al. (1998) examined brains of three Wolfram syndrome patients by using immunohistochemistry for both the vasopressin and for the vasopressin precursor, and described in the patients with diabetes insipidus, not only a loss of the vasopressin in neurons of the paraventricular hypothalamic nucleus, but also a defect in processing of the vasopressin precursor in this nucleus. Thus, the WFS1 protein may function in the survival of neurons and in vasopressin precursor-processing from birth to early adulthood in the SO and/or the PVNm.

### 4.6. Sensorineural hearing loss

The *WFS1* gene is responsible for both sensorineural deafness in Wolfram syndrome patients (Minton et al., 2003) and autosomal dominant low frequency sensorineural hearing loss (Bespalova et al., 2001; Young et al., 2001). In the mouse brain, *Wfs1* mRNA signals in the cochlear nucleus and inferior colliculus showed the type 2b pattern, and those in the auditory cortex, the type 1c or 3b pattern. In the cochlea, Wfs1 protein was invariably expressed in inner hair cells and spiral ganglion cells from birth to postnatal day 35 (Cryns et al., 2003). Thus, it is suggested that the *Wfs1* gene contributes to both the development and maintenance of cells in the auditory system including the cochlea. It is also suggested that not only dysfunctional inner ear cells but also dysfunctional neurons in the auditory-related structures of the brain attribute to both the sensorineural deafness in Wolfram syndrome patients and autosomal dominant low frequency sensorineural hearing loss.

### 4.7. Psychiatric symptoms in Wolfram syndrome patients

Swift et al. (1990) reported that 41 of 68 Wolfram syndrome patients (60%) had episodes of severe depression, psychosis, or organic brain syndrome, as well as impulsive verbal and physical aggression. These symptoms were very severe in 17 patients (25%), of whom 12 required admission to a psychiatric hospital and 11 attempted suicide. Based on this evidence, they proposed that the *WFS1* gene predisposed homozygotes to psychiatric illness (Swift et al., 1990). Subsequently, molecular neuropsychiatric studies suggested a role for the *WFS1* gene in the pathophysiology of impulsive suicide (Sequeira et al., 2003), and an association between mutations of the *WFS1* gene and hospitalization for psychiatric illness (Swift and Swift, 2005). In addition, the *Wfs1* gene was suggested to be a putative biomarker for post-traumatic stress disorder by a behavioral study using rats (Kesner et al., 2007), and the *Wfs1* knockout mouse showed bipolar disorder-like behavioral phenotypes, such as retardation in emotionally triggered behavior, decreased social interaction, and altered behavioral despair depending on experimental conditions (Kato

et al., 2008). Conversely, several molecular neuropsychiatric studies have found no evidence of a supporting role for the *WFS1* gene in psychiatric disorders, particularly major depression and bipolar disorder (Furlong et al., 1999; Evans et al., 2000; Middle et al., 2000; Ohtsuki et al., 2000; Kato et al., 2003; Kawamoto et al., 2004). As described here, it is not known whether mutations of the *WFS1* gene contribute significantly to the incidence of psychiatric illness. The present study showed that weak *Wfs1* mRNA signals were distributed in the raphe nuclei and nucleus coeruleus from birth to early adulthood. It is possible that the functions of the raphe nuclei and of the nucleus coeruleus in Wolfram syndrome patients are impaired by loss-of-function mutations in the *WFS1* gene. The dysfunction may predispose the patients to major depression and bipolar disorder, since these nuclei are strongly related to these mood disorders (Kandel, 2000). In addition, the present study demonstrated that strong-to-moderate *Wfs1* mRNA signals were widely distributed in the limbic structures including the hippocampus and the amygdala, and in the rostral part of the cerebral cortex from P14 to early adulthood. It is possible that the psychiatric symptoms in Wolfram syndrome patients are attributable to dysfunctional neurons in these structures arising from loss-of-function mutations in the *WFS1* gene.

### *4.8. Relationship between Wfs1 mRNA expression and neuroradiological and neuropathological evidence*

Neuroradiological (Rando et al., 1992; Scolding et al., 1996; Ito et al., 2007) and neuropathological (Genís et al., 1997; Shannon et al., 1999) examinations have been carried out in brains of Wolfram patients. The principal findings of these examinations were brainstem atrophy, cerebellar atrophy, and optic atrophy. Mild atrophic changes in the cerebral cortex and hypothalamus were also described. The present study showed that strong-to-moderate *Wfs1* mRNA signals were widely seen in the limbic structures (e.g. CA1, MEA, LEA, PaS, S, Tu, BSTL, IPAC, and Ce) from P7 to early adulthood. However, these structures were not affected in Wolfram syndrome patients (Genís et al., 1997; Shannon et al., 1999). Although *Wfs1* mRNA signals in the cerebellar cortex were weak from P4 to early adulthood (type 2b), cerebellar atrophy was demonstrated in Wolfram syndrome patients (Rando et al., 1992; Scolding et al., 1996; Genís et al., 1997; Shannon et al., 1999; Ito et al., 2007).

To reconcile the results with the neuroradiological and neuropathological evidence, the following possible interpretations are offered. In the cerebellum, functions of the WFS1 protein are essential for the survival of neurons expressing weak *WFS1* mRNA signals. In the limbic structures, functions of the WFS1 protein are not necessary for the survival of neurons expressing strong-to-moderate *WFS1* mRNA signals and/or functions of the mutant WFS1 protein are counteracted in these neurons by 'functionally-related proteins of WFS1 (WFS1-frps)', which compensate for functions of the normal WFS1 protein. Thus pathological changes do not occur in the limbic structures, but do occur in the cerebellum.

Interestingly, several nuclei potentially relevant to the symptoms of Wolfram syndrome, such as the SO and PVNm, potentially relevant to diabetes insipidus; the Co and IC, potentially relevant to sensorineural hearing loss; and the LC and raphe nuclei, potentially relevant to psychiatric symptoms, also showed the type 2b pattern the same as the cerebellum. These results support the notion that functions of the WFS1 protein are essential for the survival of neurons expressing weak *WFS1* mRNA signals in symptom-relevant nuclei, the WFS1-frps are not expressed in the neurons, and these factors lead to pathological changes in the symptom-relevant nuclei of Wolfram syndrome patients.

### *4.9. Conclusion*

There were three patterns of change in the strength of *Wfs1* mRNA signals in each of the mouse brain structures during the postnatal development. Out of the three patterns, several nuclei potentially relevant to the symptoms of Wolfram syndrome showed the type 2b pattern, in which the signals were weak and of a relatively constant strength during development. Based on these results, the present study provided a hypothesis that functions of the WFS1 protein are essential for the survival of neurons expressing weak *WFS1* mRNA signals in symptom-relevant nuclei, the WFS1-frps are not expressed in the neurons, and these factors lead to pathological changes in the symptom-relevant nuclei of Wolfram syndrome patients. To test this hypothesis experimentally, the availability of the *Wfs1* knockout mouse could offer opportunities for further investigation. These studies in the next step are necessary to determine the exact physiological role of the Wfs1 protein in the brain, and to obtain more insights into its pathophysiological roles in the endocrinological, otological, neurological, and psychiatric symptoms of Wolfram syndrome.

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ORIGINAL ARTICLE

# Construction of a prediction model for type 2 diabetes mellitus in the Japanese population based on 11 genes with strong evidence of the association

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**Prediction of the disease status is one of the most important objectives of genetic studies. To select the genes with strong evidence of the association with type 2 diabetes mellitus, we validated the associations of the seven candidate loci extracted in our earlier study by genotyping the samples in two independent sample panels. However, except for *KCNQ1*, the association of none of the remaining seven loci was replicated. We then selected 11 genes, *KCNQ1*, *TCF7L2*, *CDKAL1*, *CDKN2A/B*, *IGF2BP2*, *SLC30A8*, *HHEX*, *GCKR*, *HNF1B*, *KCNJ11* and *PPARG*, whose associations with diabetes have already been reported and replicated either in the literature or in this study in the Japanese population. As no evidence of the gene–gene interaction for any pair of the 11 loci was shown, we constructed a prediction model for the disease using the logistic regression analysis by incorporating the number of the risk alleles for the 11 genes, as well as age, sex and body mass index as independent variables. Cumulative risk assessment showed that the addition of one risk allele resulted in an average increase in the odds for the disease of 1.29 (95% CI=1.25–1.33, $P=5.4\times10^{-53}$). The area under the receiver operating characteristic curve, an estimate of the power of the prediction model, was 0.72, thereby indicating that our prediction model for type 2 diabetes may not be so useful but has some value. Incorporation of data from additional risk loci is most likely to increase the predictive power.**
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## INTRODUCTION

Genome-wide association studies (GWASs) have identified novel susceptibility genes for type 2 diabetes mellitus in Caucasians.[1–5] *TCF7L2*, *CDKAL1*, *CDKN2A/B*, *IGF2BP2*, *SLC30A8* and *HHEX* have been widely replicated as susceptibility genes for type 2 diabetes in Asian populations[6–12] as well as in populations of European ancestry.[13,14] We recently identified *KCNQ1* as a novel susceptibility gene, as well as seven other candidate susceptibility loci in a multistage GWAS for type 2 diabetes in the Japanese population, in which a total of 1612 cases and 1424 controls and 100 000 single nucleotide polymorphisms (SNPs) were included.[15] *KCNQ1* was found to confer risk of type 2 diabetes with a relatively large effect size in Asian populations (odds ratio (OR) for Japanese, Chinese and Korean individuals of 1.42),[15] which was similar to that demonstrated earlier for *TCF7L2* in the Japanese population.[6]

Follow-up of GWASs includes analysis of second-tier genes, meta-analysis for specific populations, as well as analysis of gene–gene or gene–environment interactions. A large-scale meta-analysis[16] and an analysis of gene–gene interaction for susceptibility genes[17] have been performed for type 2 diabetes in populations of European ancestry.

In this study, we attempted to confirm in independent subject panels of Japanese and Hong Kong Chinese individuals the associations of the seven candidate susceptibility loci that we identified in addition to *KCNQ1* in our GWAS of type 2 diabetes.[15] However, as described in this article, we failed to replicate the associations of the seven loci with diabetes. We then attempted to extract genes with strong evidence of the associations with diabetes, and selected 11 genes, including *KCNQ1*. As we did not detect any gene–gene interaction between the 11 genes, we then attempted to construct a prediction model for this disease by using the data from the 11 genes, as well as age, gender and body mass index (BMI) as independent variables to obtain a comprehensive understanding of the genetic background of diabetes in the Japanese population.

## MATERIALS AND METHODS

### Validation of the results from a multistage GWAS in the Japanese population

**Study subjects.** We assembled two independent subject panels for our replication study: replication-Japanese and replication-Chinese. The 1000 cases and 1000 controls for the replication-Japanese panel were recruited by the Study Group of the Millennium Genome Project for Diabetes Mellitus. The inclusion criteria for diabetic patients were (i) an age at disease onset of 30–60 years and (ii) the absence of antibodies to GAD. Types of diabetes other than type 2 were excluded on the basis of clinical data. The criteria for controls included (i) an age of $>50$ years, (ii) no past history of a diagnosis of diabetes and (iii) an $HbA_{1c}$ content of $<5.8\%$.

For the replication-Chinese panel, subjects of southern Han Chinese ancestry, who resided in Hong Kong, were recruited. The cases consisted of 1416 individuals with type 2 diabetes selected from the Prince of Wales Hospital Diabetes Registry;[5,18] 626 of these subjects had early-onset diabetes (age at diagnosis of $<40$ years) and a positive family history, whereas the remaining 790 patients were randomly selected from the registry. Patients with classic type 1 diabetes with acute ketotic presentation or a continuous requirement for insulin within 1 year of diagnosis were excluded. The controls consisted of 1577 subjects with normal glucose tolerance (fasting plasma glucose concentration of $<6.1\,mmol\,l^{-1}$); 596 of these individuals were recruited either from the general population participating in a community-based screening program for cardiovascular risk or from hospital staff, whereas the remaining 981 subjects were recruited from a population-based screening program for cardiovascular risk in adolescents.[19] The clinical characteristics of the subjects in each panel are summarized in Supplementary Table 1A. The study protocol was approved by the local ethics committee of each institution. Written informed consent was obtained from each subject.

**Study design and statistical analysis.** For the validation of the results from our earlier multistage GWAS,[15] seven SNPs (rs2250402, rs2307027, rs3741872, rs574628, rs2233647, rs3785233 and rs2075931) were genotyped in the two panels either by sequence-specific primer–PCR analysis followed by fluorescence correlation spectroscopy[20] or by real-time PCR analysis with TaqMan probes (Applied Biosystems, Foster City, CA, USA). Differences in allele frequency between cases and controls for each SNP were evaluated by $\chi^2$ with one degree of freedom. Meta-analysis was performed by the Mantel–Haenszel method (fixed-effects models) with the 'meta' package of the R-Project (http://www.r-project.org). A $P$-value of $<0.05$ was considered statistically significant.

### Examination of gene–gene interaction and construction of a prediction model

**Study subjects.** In total, 2424 cases and 2424 controls of the Japanese population obtained by combining the second and third screening panels in our original study[15] and the replication-Japanese panel of this study were included in this analysis (analysis-panel). The criteria for the second and third screening panels were described in the earlier report.[15] The clinical characteristics of the subjects are summarized in Supplementary Table 1B.

**Selection of the loci included in this study.** Prediction of the phenotypes on the basis of genetic polymorphisms should include the genetic data from the loci with strong evidence of the association. Starting from 15 genes described in earlier reports, we selected 11 genes with strong evidence of the association on the basis of the data in the literature and on the results of the replication experiments in this study. Process of the selection of the 11 genes will be described in detail in Results.

**Statistical methods.** Multiplicative gene–gene interaction was evaluated for each pair of the 11 genes using an interaction term in addition to the terms for the pair of the genes in the logistic regression model. The genotypes for each locus were coded by 0, 1 and 2. Correction for multiple testing was performed by Bonferroni's method.

As there was no evidence for the presence of gene–gene interactions, we attempted to construct a phenotype prediction model by incorporating the number of risk alleles for the 11 loci as an independent variable in addition to age, gender and BMI. The Cochran–Armitage test was used to examine the trend of the increase in the odds by increasing the number of the risk alleles. To construct a prediction model, the log of odds was expressed by the linear combination of the independent variables. Coefficients for the variables were estimated by the logistic regression analysis after making disease (cases) or nondisease (controls) as the dependent variable. Using the coefficients estimated by the logistic regression analysis, we constructed a phenotype prediction model. To evaluate the prediction model, receiver operating characteristic (ROC) curves[21] for the sensitivity and specificity of the prediction model with or without adjustment for age, sex and BMI were generated, and the area under the curve (AUC) was calculated from the ROC curve.

## RESULTS

### Validation of the results from a multistage GWAS in the Japanese population

We identified earlier 10 loci associated with type 2 diabetes by three-staged GWAS starting from 100 000 SNPs. Among the 10 loci, 3 SNPs were located in an intron of *KCNQ1*, and the association of this gene with diabetes was confirmatory.[15] To validate the other seven loci for the association with type 2 diabetes, we analyzed them in two independent replication panels of Japanese and Han-Chinese individuals (Table 1, Supplementary Table 2). Only one SNP, rs2250402, which is located in *EIF2AK4*, was found to be significantly associated in the replication-Japanese panel ($P$=0.039, OR=1.17, 95% CI=1.01–1.36). However, neither this SNP ($P$=0.41, OR=1.05) nor any of the other six SNPs showed such an association in the replication-Chinese panel. Meta-analyses for these SNPs showed that rs2307027 in *KRT4* and rs3785233 in *A2BP1* yielded $P$-values of $<0.05$ and ORs between 1.12 and 1.13 (Table 1). When the original second and third screening

**Table 1 Association study for the candidate susceptibility genes for type 2 diabetes selected by multistage screening in the Japanese population**

| *SNP ID* | *Chr* | *Gene* | *Risk allele* | *Panel* | *RAF (DM)* | *RAF (NC)* | *P* | *OR* | *95% CI* |
|---|---|---|---|---|---|---|---|---|---|
| rs2250402 | 15 | *EIF2AK4* | C | Replication-Japanese | 0.23 | 0.20 | 0.04 | 1.17 | 1.01–1.36 |
| | | | | Replication-Chinese | 0.24 | 0.23 | 0.41 | 1.05 | 0.93–1.19 |
| | | | | Meta-analysis | | | 0.05 | 1.10 | 1.00–1.20 |
| rs2307027 | 12 | *KRT4* | C | Replication-Japanese | 0.18 | 0.17 | 0.17 | 1.12 | 0.95–1.32 |
| | | | | Replication-Chinese | 0.14 | 0.13 | 0.16 | 1.11 | 0.96–1.29 |
| | | | | Meta-analysis | | | 0.05 | 1.12 | 1.00–1.25 |
| rs3741872 | 12 | *FAM60A* | C | Replication-Japanese | 0.25 | 0.24 | 0.18 | 1.11 | 0.96–1.28 |
| | | | | Replication-Chinese | 0.23 | 0.22 | 0.21 | 1.08 | 0.96–1.22 |
| | | | | Meta-analysis | | | 0.07 | 1.09 | 0.99–1.20 |
| rs574628 | 20 | *ANGPT4* | G | Replication-Japanese | 0.60 | 0.61 | 0.46 | 0.95 | 0.84–1.08 |
| | | | | Replication-Chinese | 0.65 | 0.65 | 0.59 | 1.03 | 0.93–1.15 |
| | | | | Meta-analysis | | | 0.96 | 1.00 | 0.92–1.08 |
| rs2233647 | 6 | *SPDEF* | G | Replication-Japanese | 0.86 | 0.87 | 0.70 | 0.97 | 0.81–1.16 |
| | | | | Replication-Chinese | 0.94 | 0.93 | 0.54 | 1.07 | 0.87–1.31 |
| | | | | Meta-analysis | | | 0.90 | 1.01 | 0.88–1.16 |
| rs3785233 | 16 | *A2BP1* | C | Replication-Japanese | 0.18 | 0.16 | 0.19 | 1.12 | 0.95–1.32 |
| | | | | Replication-Chinese | 0.13 | 0.12 | 0.10 | 1.14 | 0.97–1.34 |
| | | | | Meta-analysis | | | 0.04 | 1.13 | 1.01–1.27 |
| rs2075931 | 1 | Intergenic | A | Replication-Japanese | 0.67 | 0.66 | 0.85 | 1.01 | 0.89–1.16 |
| | | | | Replication-Chinese | 0.73 | 0.74 | 0.27 | 0.94 | 0.84–1.05 |
| | | | | Meta-analysis | | | 0.48 | 0.97 | 0.89–1.06 |

Abbreviations: Chr, chromosome; OR, odds ratio for risk allele frequency.
Assignment of risk alleles was based on the original study.[15] Numbers of cases versus control subjects in the replication-Japanese and replication-Chinese panels were 1000 versus 1000 and 1416 versus 1577, respectively. RAF (DM) and RAF (NC) denote risk allele frequencies in cases and controls, respectively. *P* values were calculated for allele frequency. Meta-analysis was performed by the Mantel–Haenszel method (fixed-effects models). *P*-values for the test of heterogeneity among panels joined in the Mantel–Haenszel tests were all >0.05.

panels were included in the meta-analyses, these two loci, as well as the SNPs in *EIF2AK4* (rs2250402) and *FAM60A* (rs3741872), gave *P*-values of <0.001 and ORs between 1.15 and 1.18 (Supplementary Table 3). However, the *P*-values did not reach the proposed significance of GWAS ($=5\times10^{-7}$).

### Selection of polymorphisms for the prediction model

To construct a reliable prediction model for diabetes, polymorphisms with strong evidence of association should be used. From the previous literature, we selected 15 genes (including one intergenic marker), that is, *SLC30A8*, *HHEX*, *LOC387761*, *EXT2*, *CDKN2A/B*, *GCKR*, *IGF2BP2*, *CDKAL1*, *FTO*,[1–5] *TCF7L2*,[22] *KCNJ11*,[23] *PPARG*,[24] *WFS1*,[25] *HNF1B*[26] and *KCNQ1*,[15] as candidate genes to be included in both gene–gene interaction analysis and construction of a prediction model. Starting from 23 SNPs in these 15 genes, we selected 11 SNPs in 11 genes according to the following process. There is sufficient evidence of the associations of *KCNQ1* and *TCF7L2* genes with diabetes as supported by replication studies in the Japanese population.[6,15,27] In addition, *SLC30A8*, *HHEX*, *CDKN2A/B*, *IGF2BP2* and *CDKAL1* associated with the disease in the European population were found in our earlier study to be associated with the disease in the Japanese population as well.[7–9]

To further extract genes with strong evidence of the association with diabetes, we attempted to replicate the associations reported earlier using our own data (analysis panel with 2424 cases and 2424 controls). For the 19 SNPs in *SLC30A8*, *HHEX*, *LOC387761*, *EXT2*, *CDKN2A/B*, *GCKR*, *IGF2BP2*, *CDKAL1*, *FTO*, *TCF7L2*, *KCNJ11*, *PPARG* and *KCNQ1*, we extracted genotyping data from our earlier studies[6–9,15,27–29] and, if necessary, genotyped additional subjects to obtain a data set for 2424 cases and 2424 controls of the Japanese population (analysis panel). The SNPs in *WFS1* (rs6446482, rs734312) and *HNF1B* (rs7501939, rs4430796) were genotyped for this study in the same individuals. SNPs with *P*-values for the test of deviation from the Hardy–Weinberg equilibrium of <0.01 were excluded for further analysis. When two SNPs were located in the same genomic region, the one with the lower *P*-value for the association test was selected for further analysis. *GCKR*, for which we earlier reported the marginal association with type 2 diabetes,[7] was found to be associated with the disease in this enlarged Japanese panel ($P=1.7\times10^{-5}$; Supplementary Table 4). *KCNJ11* and *PPARG*, which have been included in the genes associated with diabetes in Caucasians, showed marginal associations ($P=0.066$ and $P=0.075$, respectively; Supplementary Table 4) in our panel. Two SNPs in *WFS1* and two SNPs in *HNF1B* were newly genotyped in the analysis panel. Although no association was apparent between *WFS1* and type 2 diabetes, both SNPs in *HNF1B* exhibited *P*-values of <0.05 (Supplementary Table 4). From these data, we included 11 SNPs in 11 genes as described above for the source of genotype data to be analyzed in both the examination of gene–gene interaction and the prediction of phenotypes.

### Gene–gene interaction

We evaluated multiplicative gene–gene interaction for each pair of the 11 loci as described in Materials and methods. Two combinations, rs1801282 (*PPARG*) ×rs1470579 (*IGF2BP2*) (nominal $P=0.0025$) and rs1801282×rs3802177 (*SLC30A8*) (nominal $P=0.018$), showed *P*-values of less than 0.05 (Supplementary Figure 1). However, these *P*-values were not significant when Bonferroni's correction for multiple testing was applied (significance level, $0.05/55=9.1\times10^{-4}$). Although *PPARG* and *IGF2BP2* are located on the same chromosome (3p25 and 3q28, respectively), it is unlikely that loci on different arms of the same chromosome show significant linkage disequilibrium. *SLC30A8* is located on a different chromosome (8q24.11) from

*PPARG*. The reason why nominal *P*-values of these combinations showed less than 0.05 may be because of the low minor allele frequency of rs1801282.

### Cumulative risk assessment for type 2 diabetes on the basis of susceptibility genes

As there was no evidence of gene–gene interaction between 11 SNPs of 11 genes, *SLC30A8*, *HHEX*, *CDKN2A/B*, *GCKR*, *IGF2BP2*, *CDKAL1*, *TCF7L2*, *KCNJ11*, *PPARG*, *KCNQ1* and *HNF1B*, they were included in the prediction model as independent variables with the additive effect (additive effect in the liability and multiplicative effect in the odds) without interaction terms. Effective numbers of cases and controls whose genotypes for the 11 loci were successfully obtained were 2316 and 2370, respectively. The Cochran–Armitage trend test gave a *P*-value of $4.7\times10^{-56}$ for the trend in the increase in the odds for cases relative to controls with an increasing number of risk alleles for the 11 susceptibility loci (Supplementary Table 5). We then estimated ORs for type 2 diabetes in subjects with different numbers of risk alleles on the basis of the multiplicative model by logistic regression analysis with adjustment for age, sex and BMI. The ORs for type 2 diabetes in subjects with 7–18 risk alleles in comparison with those harboring 0–6 risk alleles are shown in Figure 1. An increase of one risk allele resulted in an average increase in the odds of 1.29 (95% CI=1.25–1.33, $P=5.4\times10^{-53}$, logistic regression analysis).

To predict disease status for type 2 diabetes in a given individual, we constructed a prediction model on the basis of the number of risk alleles or the liability value calculated from the number of risk alleles as well as age, sex and BMI. The coefficients to calculate the liability value were estimated with the logistic regression model. To estimate the predictive power of the model, we generated ROC curves as described in Materials and methods. The AUC was 0.63 when only the number of risk alleles was used for the prediction. When age, sex and BMI were also included, the AUC increased to 0.72 (Figure 2). Meanwhile, an AUC value for the ROC curve based on only age, sex and BMI was 0.68, which was better than that based on only the number of risk alleles (data now shown). The model incorporating age, sex and BMI as well as the number of risk alleles thus showed moderate power for the prediction of type 2 diabetes. The best accuracy was 0.66 at the threshold between non-diabetic and diabetic status of 0.52 (non-diabetic status=0, diabetic status=1), for which the specificity and the sensitivity were 0.71 and 0.61, respectively.

## DISCUSSION

By the validation of the results from our multistage GWAS, we detected only marginal associations of *EIF2AK4*, *KRT4* and *A2BP1* with type 2 diabetes in meta-analyses with two subject panels of Japanese or Chinese individuals. Relations of *KRT4* (keratin 4 gene) and *A2BP1* (ataxin-2-binding protein 1 gene, also known as *FOX1*) to glucose or lipid metabolism are unknown. Deletion of *EIF2AK4* (eukaryotic translation initiation factor 2 alpha kinase 4 gene, also known as *GCN2*) in mice resulted in liver steatosis during leucine deprivation as a result of unrepressed expression of lipogenic genes.[30] The functionally related gene, *EIF2AK3* (also known as *PERK* or *PEK*), has been shown to cause diabetes mellitus both in humans (Wolcott–Rallison syndrome, OMIM604032) and in rodent models.[31,32] Taken together, *EIF2AK4* may be a good candidate for the diabetes susceptibility gene. The sample size required for a statistical power of 0.80 with equal numbers of cases and controls is 10 505 when the frequency of the risk allele, OR and type I error probability are assumed to be 0.20, 1.10 (the value for *EIF2AK4* in the meta-analysis in Table 1) and 0.05, respectively. Further studies of these genes in other Asian populations as well as in other ethnic groups are needed for confirmation of their association with type 2 diabetes. Given this uncertainty, we did not include these genes in the assessments of cumulative risk and gene–gene interaction.

Among tens of type 2 diabetes susceptibility genes identified by recent GWASs in Caucasians, the associations of six genes, that is, *TCF7L2*, *CDKAL1*, *CDKN2A/B*, *IGF2BP2*, *SLC30A8* and *HHEX*, have been replicated in Asian populations as well as in populations of European ancestry. A recent meta-analysis in Japanese subjects also supported the associations.[12] In this study, we performed replication study, and, on the basis of the results, we added five more genes, that is, *KCNJ11*, *PPARG*, *GCKR*, *KCNQ1* and *HNF1B*, for the cumulative risk assessment for type 2 diabetes. Thus, the SNPs of *HNF1B*, which were earlier associated with type 2 diabetes in Chinese as well as in Caucasians,[26] showed the association with the disease in the Japanese

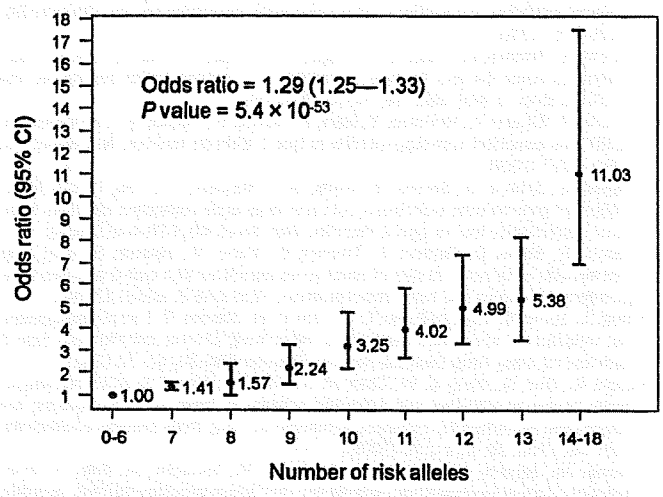


**Figure 1** Odds ratios for subjects with different numbers of risk alleles for 11 susceptibility loci for type 2 diabetes. The cumulative effect of the 11 loci on type 2 diabetes was tested by counting the number of risk alleles associated with type 2 diabetes with a logistic regression model with adjustment for age, sex and BMI. The ORs for subjects with each number of risk alleles are expressed relative to individuals with 0–6 risk alleles.

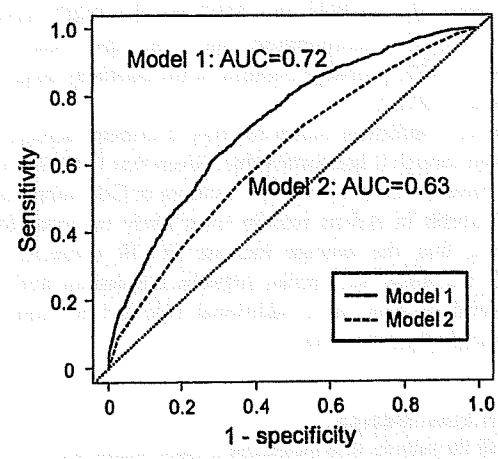


**Figure 2** ROC curves for the prediction model on the basis of the number of risk alleles for 11 susceptibility loci for type 2 diabetes. The prediction model for type 2 diabetes was constructed using the logistic regression model, and ROC curves for the model were generated. In model 1, the number of risk alleles was used as an independent variable together with age, sex and BMI as covariates, whereas only the number of risk alleles was used as an independent variable in model 2.

population in this study. In addition, the *C* allele of rs780094 in *GCKR* was associated with increased risk of type 2 diabetes in this study, which is consistent with a recent study in Caucasians.[33] The associations of *KCNJ11* and *PPARG* with diabetes were marginal in this study; however, they were included for the prediction model, as the associations were replicated in some studies of Caucasians.

Our gene–gene interaction analysis showed no significant interaction for any of the 55 possible pairs of genes when corrected for multiple testing. When the significance level was set at 0.05, two pairs were judged to be significant. However, such gene–gene interactions were not supported from the functional point of view. A large-scale study may provide more convincing evidence for such interactions.

As no confirmatory evidence for gene–gene interaction was observed, we treated the 11 genes as independent variables in the prediction model. The addition of one risk allele was estimated to increase the odds by an average of 1.29 according to the multiplicative model. This value is similar to that (1.24) estimated for type 2 diabetes in Caucasians.[17] Two earlier cumulative risk assessments for type 2 diabetes in Asian populations with relatively small numbers of associated loci yielded values of 1.17 and 1.24 for the fold increase in risk for each additional risk allele.[11,34] In our prediction model for type 2 diabetes, the AUC for the ROC curve was lower than that in the earlier study[17] based on 15 loci in Caucasians (0.72 and 0.86, respectively). However, the number of loci in our study (11 loci) was lower than that in the study for Caucasians. The inclusion of additional loci in our model should improve its ability to predict type 2 diabetes in Asian populations. Several reports of the prediction of type 2 diabetes using ~18 loci were recently described for populations of European ancestry.[35–38] A prediction based on 18 loci gave an AUC value of 0.80 for the ROC curve,[35] whereas the corresponding values for a population-based prospective study were 0.68,[36] 0.615[37] and 0.75.[38] They concluded that genetic variations associated with diabetes had a small effect on the ability to predict the development of type 2 diabetes as compared with clinical characteristics alone. In fact, the AUC value (0.72) based on both the genetic variations and the clinical characteristics was slightly better than that based on only the clinical characteristics (0.68). We admit that the evidence of the association with diabetes is a little weaker for *KCNJ11* and *PPARG* in the Japanese population than for the other nine genes. If *KCNJ11* and *PPARG* were excluded from the analysis, the AUC for the ROC curve in the prediction model incorporating age, sex and BMI remained unchanged at 0.72, probably because of the relatively large effects of *KCNQ1* and *TCF7L2*.

Finally, our prediction model for type 2 diabetes achieved limited success even though it has some value. Given that GWASs for diabetes in Asians have not been as extensive as those in Caucasians, many risk loci for diabetes in Asians remain most likely to be undiscovered. Considering that the average increase in OR conferred by each additional risk allele was similar between Caucasians and Japanese, incorporation of data from additional risk loci is most likely to increase the predictive power.

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INTERNAL MEDICINE

□ CASE REPORT □

# Peginterferon (PEG-IFN) Plus Ribavirin Combination Therapy, but neither Interferon nor PGE-IFN Alone, Induced Type 1 Diabetes in a Patient with Chronic Hepatitis C

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## Abstract

Interferon (IFN) therapies, including IFN, peginterferon (PEG-IFN) and ribavirin (RBV) plus PEG-IFN combination, are widely used for patients with chronic hepatitis C. We encountered a patient with chronic hepatitis C in whom previous IFN or PEG-IFN alone had not induced type 1 diabetes (T1D), while the addition of RBV to PEG-IFN did induce T1D. The patient had HLA types conferring highly susceptibility to T1D. Thus, adding RBV to PEG-IFN may render chronic hepatitis C patients, with T1D-susceptible HLA types, more prone to developing T1D than IFN or PEG-IFN alone. To prevent T1D development, we recommend HLA typing prior to initiating RBV plus PEG-IFN administration.

**Key words:** human leukocyte antigen, anti-glutamate acid decarboxylase (GAD) antibody, anti-insulinoma-associated antigen (IA)-2 antibody, autoimmune disease

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## Introduction

Interferon (IFN) is used for chronic hepatitis C and B. Until recently, IFNα was the main option for treating chronic hepatitis C (1). Now, peginterferon (PEG-IFN, polyethylene glycol-binding IFN) combined with ribavirin (RBV), which augments IFN action, is a standard anti-viral therapy for chronic hepatitis C (2). However, IFN therapy can adversely impact the immune system and induce autoimmune diseases including type 1 diabetes (T1D) (3, 4). Not only IFN, but also PEG-IFN (5) and PEG-IFN plus RBV therapy (6, 7), can reportedly induce T1D. We encountered a patient with chronic hepatitis C in whom neither IFN nor PEG-IFN alone induced T1D, while RBV plus PEG-IFN did induce T1D with elevated anti-glutamate acid decarboxylase (GAD) and anti-insulinoma-associated antigen (IA)-2 antibodies. Herein, we emphasize the risk of T1D development with PEG-IFN plus RBV therapy.

## Case Report

A woman was diagnosed as having chronic hepatitis C at the age of 53 and received IFNα 1 million IU/week for 6 months, and subsequently became negative for viral marker (HCV-RNA). At age 60, she was diagnosed as having type 2 diabetes; fasting plasma glucose (FPG) was 199 mg/dL and HbA1c 6.9%. Her HbA1c improved with glimepiride 1 mg/day. Because HCV-RNA was again increased, PEG-IFNα 180 μg/week was started at age 61. Due to a taste disorder, the dose was decreased to 90 μg/week two months later and continued for 9 months. During PEG-IFN administration, blood glucose control worsened, but adding buformin (150 mg/day) to her treatment regimen decreased HbA1c from

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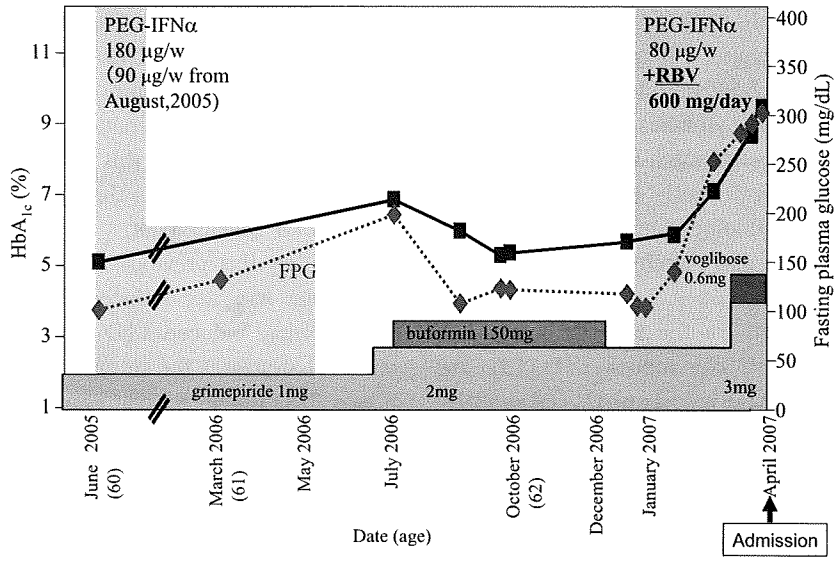


**Figure 1. Clinical course: $HbA_{1c}$ and fasting plasma glucose.**

**Table 1. Data on Admission**

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| WBC | 1600 /μL | T-Bil | 0.9 mg/dL | BUN | 11 mg/dL | Glu | 303 mg/dL |
| Seg | 53 % | AST | 53 IU/L | Cr | 0.4 mg/dL | HbA1c | 9.5 % |
| Eos | 2 % | ALT | 60 IU/L | UA | 2.3 mg/dL | Anti-GAD antibody | 27.0 U/mL (0-1.4) |
| Baso | 0 % | ALP | 213 IU/L | Na | 135 mEq/L | Anti-IA-2 antibody | 3.0 U/mL (0-0.3) |
| Lym | 34 % | γ-GTP | 40 IU/L | K | 4.1 mEq/L | Anti-insulin antibody | 6.5 % (0-10) |
| Mon | 11 % | LDH | 195 IU/L | Cl | 102 mEq/L | Fasting IRI | 4.3 μU/mL(1.84-12.2) |
| RBC | $326 \times 10^4$ /μL | ZTT | 10.2 U | Ca | 8.7 mg/dL | Blood C-peptide | 0.6 ng/mL (1.5-3.5) |
| Hb | 10.7 g/dL | TTT | 6.1 U | TG | 54 mg/dL | Urinary C-peptide | 25.0 μg/day (41-145) |
| Ht | 31.3 % | CHE | 304 IU/L | T-Cho | 78 mg/dL | Free T3 | 2.6 pg/mL (2.5-4.3) |
| Plt | $78 \times 10^4$ /μL | CPK | 25 IU/L | HDL-C | 27 mg/dL | Free T4 | 0.91 ng/mL (1.76-1.65) |
| TP | 6.7 g/dL | | | LDL-C | 39 mg/dL | TSH | 6.72 μIU/mL (0.31-4.69) |
| A/G | 1.48 | | | | | TRAb | 2.1 % (<15%) |
| | | | | | | TgAb | 138.2 IU/mL (0-44) |
| | | | | | | TPOAb | 149.9 IU/mL (<0.72) |

Normal ranges are in parenthesis

7.0% to 5.0%. At age 62, because HCV-RNA levels had not decreased, PEG-IFN (80 μg/week) plus RBV (600 mg/day) combination therapy was started. Glycemic control rapidly deteriorated; FPG and HbA1c were increased to 280 mg/dL and 8.8%, respectively, two months after the initiation of RBV therapy (Fig. 1). One month later, the patient was admitted to our hospital for blood glucose control. On admission, her body mass index was 20.8 $kg/m^2$, with no remarkable physical findings. Laboratory data included high blood glucose (FPG 303 mg/dL, HbA1c 9.5%) with slightly elevated hepatic transaminases (AST/ALT 53/60 IU/L). It was noteworthy that she was positive for both anti-GAD and anti-IA2 antibodies. Thyroid hormone levels were normal with slightly elevated TSH. Anti-thyroglobulin antibody (TbAb) and anti-thyroid peroxidase antibody (TPOAb) were positive (Table 1), suggesting autoimmune thyroiditis with subclinical hypothyroidism. Her HLA types included A24, DRB1*0405/0901, DQA1*0302 and DQB1*0401/0303, which confer high susceptibility to T1D. Based on positive autoantibodies against pancreatic islets, T1D was diagnosed. The PEG-IFN and RBV combination therapy was stopped and intensive insulin therapy was started, resulting in gradual improvement of blood glucose control with 35 units/day of insulin. Five months later, anti-GAD antibody remained positive (31.7 U/mL) with fair blood glucose control (HbA1c 5.5%) using 27 units/day of insulin.

## Discussion

Since IFN was first reported to be effective for HCV infection in 1986 (8), IFN has been widely used for patients with chronic hepatitis C. However, autoimmune diseases, such as autoimmune thyroiditis (9), rheumatoid arthritis (10), autoimmune hepatitis (11), systemic lupus erythematosus (12) and T1D (13), reportedly develop with IFN therapy. In particular, several reports have documented the development of thyroid autoimmune disorders in cases receiving IFN plus RBV combination therapy (14, 15) and the present patient is likely such a case.

T1D is at least in part an autoimmune disease character-

ized by loss of pancreatic β cells with T lymphocyte infiltration of islets (16). IFNα activates T-helper (Th)1 lymphocytes which are $CD4^+$ and secrete interleukin-2, IFNγ and tumor necrosis factor β. These cytokines facilitate the generation of $CD8^+$ cytotoxic T cells which injure pancreatic β cells (17). In fact, IFNα is significantly up-regulated in patients with T1D (18). These findings suggest that IFNα is involved in β cell destruction and thereby in T1D development.

In 1992, it was documented for the first time that IFN therapy for chronic hepatitis C can induce T1D (13), and this was followed by similar case reports (reviewed in (19)). Subsequently, PEG-IFN therapy was also reported to induce T1D (5). Therefore, IFN administration is likely to affect Th1 immune reactions, leading to the development of T1D, as discussed above.

The present case was first diagnosed as having type 2 diabetes 7 years after IFN therapy. IFN therapy reportedly worsens insulin resistance, resulting in deterioration of glucose tolerance (20). In our case as well, blood glucose control deteriorated slightly during PEG-IFN therapy, though fair control of blood glucose was achieved with biguanide treatment but no insulin, indicating that the diabetes in this case was not clinically insulin-dependent T1D during this period. In contrast, after RBV was added to PEG-IFN, glucose control rapidly worsened with positive autoantibodies, i.e. anti-GAD and anti-IA2 antibodies, suggesting T1D onset. Although the possibility that IFN or PEG-IFN alone had induced T1D several years or months earlier can not be completely excluded in this patient, her clinical course (see Fig. 1) strongly suggests that the RBV addition was a trigger for T1D development.

It is likely that previous administrations of IFN and PEG-IFN alone had not induced T1D, while adding RBV to PEG-IFN had induced T1D in the same patient. These three anti-viral strategies for chronic hepatitis C can all reportedly induce T1D (3-7). To our knowledge, however, no studies have compared these three therapies in terms of the likelihood of T1D induction. The clinical course of our case strongly suggests that adding RBV renders patients, who have T1D-susceptible HLA, more prone to T1D development than either IFN or PEG-IFN alone. RBV is a guanosine analog which exerts immunological effects on Th1-like activation (21). Therefore, adding RBV to IFN therapy might augment the autoimmune response to IFN. We emphasize the importance of HLA typing, particularly prior to RBV addition, since the combination of PEG-IFN with RBV is now established as the first line therapy for chronic hepatitis C (22, 23). RBV administration should be avoided in patients with T1D-susceptible HLA.

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