Membrane topology of the Drosophila OR83b odorant receptor

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Received 10 October 2007; revised 2 November 2007; accepted 2 November 2007

Available online 20 November 2007

Edited by Maurice Montal

Abstract By analogy to mammals, odorant receptors (ORs) in insects, such as Drosophila melanogaster, have long been thought to belong to the G-protein coupled receptor (GPCR) superfamily. However, recent work has cast doubt on this assumption and has tentatively suggested an inverted topology compared to the canonical N\textsubscript{in} → C\textsubscript{out} 7 transmembrane (TM) GPCR topology, at least for some Drosophila ORs. Here, we report a detailed topology mapping of the Drosophila OR83b receptor using engineered glycosylation sites as topology markers. Our results are inconsistent with a classical GPCR topology and show that OR83b has an intracellular N-terminus, an extracellular C-terminus, and 7 TM helices.

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Keywords: Odorant receptor; Membrane protein; Topology; Drosophila melanogaster

1. Introduction

In mammals, odorant receptors (ORs) belong to the large superfamily of G-protein coupled receptors (GPCRs) and have a typical 7 transmembrane (TM) topology with an extracellular (EC) N-terminus and an intracellular (IC) C-terminus [1]. Because insects also have an expanded repertoire of GPCRs it has long been assumed that their ORs have the same canonical 7TM topology, yet recent work on the Drosophila OR83b OR tentatively placed its N-terminus intracellularly rather than extracellularly [2,3]. This unexpected result is in accordance with theoretical topology predictions [1]. OR83b is a ubiquitously expressed and highly conserved member of the insect OR family and heteromerizes with other ORs, forming active receptor complexes [2].

Here, we report a detailed study of the membrane topology of OR83b inserted into Drosophila rough microsomes (DRMs), using both an endogenous and engineered acceptor sites for N-linked glycosylation as topological markers. Our results support a 7TM N\textsubscript{in} → C\textsubscript{out} topology for OR83b.

2. Materials and methods

2.1. Enzymes and chemicals

Unless otherwise stated, all enzymes, plasmid pGEM1, and the TNT\textsuperscript{TM} Quick transcription/translation system were from Promega (Madison, WI). [\textsuperscript{35S}]Methionine, [\textsuperscript{14C}]methylated marker proteins and deoxynucleotides were from GE Healthcare (Uppsala, Sweden). BigDye Terminator v1.1 Cycle Sequencing Kit was from AB Applied Biosystems (Foster City, CA) and oligonucleotides were from Cybergene AB (Stockholm, Sweden).

2.2. Plasmid construction

Fragments from full-length Or83b cDNA prepared Drosophila heads was modified in two ways during PCR amplification: (i) by the introduction of a 5’ XbaI site, and (ii) by changing the context of the region immediately upstream of the initiator ATG codon to a Kozak consensus ribosome binding sequence, GCCACCATGG [4]; both changes were encoded within the 5’PCR primer. The reverse primer encoded the 3’-end of the selected OR gene, two stop codons, and a Smal site for cloning. The Or83b gene was amplified by PCR using the Expand High Fidelity PCR system from Roche Diagnostics GmbH (Mannheim, FRG) and cloned into pGEM1 downstream of the SP6 promoter as an XbaI-Smal fragment. The amplified DNA products were purified using the QiAquick PCR Purification kit from QIAGEN (Hilden, FRG).

2.3. DNA manipulations

Glycosylation acceptor sites were designed as described previously [5], i.e. by replacing or insertion of one or more appropriately positioned codons for the acceptor tripeptide Asn-Ser-Thr (NST). To destroy the endogenous glycosylation acceptor site (Asn\textsuperscript{169}Ser-Ser (N169)), it was mutated to Gln-Ser-Ser (QSS). To create glycosylation acceptor sites the sequence was changed to N\textsuperscript{20}NST (N20), V\textsuperscript{112}NST (N112), E\textsuperscript{175}NST (N175), A\textsuperscript{265}NST (N265), and K\textsuperscript{440}NST (N440). To introduce the C-terminal glycosylation acceptor site, the C-terminal end of OR83b was extended with the sequence K\textsuperscript{439}PSYKRTMSFDK-LIENSTOKT (C-term NST).

Site-specific mutagenesis was performed using the QuickChange™ Site-Directed Mutagenesis kit from Stratagene (La Jolla, USA). All mutants were confirmed by sequencing of plasmid DNA at BM labbet AB (Furulund, Sweden). All cloning steps were done according to standard procedures using restriction enzymes from Promega (Madison, USA).

2.4. Preparation of Drosophila rough microsomes

Drosophila S2 cells (ATCC: CRL-1963) from cultures growing in logarithmic phase were washed twice with PBS and once with buffer H (50 mM HEPES-KOH pH 7.4, 165 mM KOAc, 2 mM Mg(OAc)\textsubscript{2}) with centrifugation steps for 3 min at 200 × g, 20 °C. Cells were...
resuspended in 3 volumes buffer H containing 0.01% saponin (Sigma) and incubated 10 min at 20 °C. Buffer H was added to decrease the saponin concentration to 0.002%, and the DRMs were pelleted for 1 min at 2500 g, 4 °C. Buffer H was added to decrease the saponin concentration to 0.002%, and the DRMs were pelleted for 1 min at 2500 g, 4 °C. DRMs were adjusted to 20 A280/ml with RM buffer (50 mM HEPES-KOH pH 7.6, 50 mM KOAc, 2 mM Mg(OAc)2, 250 mM sucrose, 1 mM DTT), CaCl2 and PMSF were added to a final concentration of 1 mM and 0.2 mg/ml, respectively. DRMs were incubated with 150 U/ml micrococcal nuclease (Nuclease S7 from Staphylococcus aureus, Roche) for 10 min at 25 °C, and the reaction was stopped by the addition of EGTA to a final concentration of 2 mM. DRMs were layered on a sucrose cushion (50 mM HEPES-KOH pH 7.6, 50 mM KOAc, 2 mM Mg(OAc)2, 500 mM sucrose, 1 mM DTT) and separated by centrifugation for 30 min at 35,000 × g, 4 °C. The pellet was resuspended in RM buffer and DRMs adjusted to 100 A280/ml (i.e. 2 equiv./μl).

2.5. Expression in vitro

Constructs in pGEM1 were transcribed and translated in the TnT Quick systems from Promega. 1 μg DNA template, 1 μl [35S]-Met (15 Ci) and 1 equiv. of DRM or 2 equiv. of dog pancreas rough microsomes (CRM) [6] were added at the start of the reaction, and samples were incubated for 90 min at 30 °C [7]. Samples were analyzed by SDS–PAGE, and proteins were visualized in a Fuji FLA-3000 phosphorimager using the Image Reader V1.8J/Image Gauge V 3.45 software.

3. Results

3.1. Prediction models and topology assay

The Phobius [8], TMHMM [9], HMMTOP [10], Memsat 2.0 [11] and Toppred [12] algorithms all predict the same 7TM N-in C-out topology for OR83b, Fig. 1A. In an attempt to experimentally map the topology of OR83b, we took advantage of a potential acceptor site for N-linked glycosylation (N169SS) present in the second predicted EC loop (EC2). N-linked glycosylation is a reliable topology marker, as the endoplasmic reticulum (ER)-resident oligosaccharide transferase enzyme can only transfer glycans to lumenally exposed parts of membrane proteins inserted into the ER [13]. OR83b was cloned behind the SP6 promoter in the pGEM1 vector and transcribed and translated in vitro in the absence or presence of DRMs. In the presence of DRMs, a more slowly migrating form of the protein was observed (Fig. 1B, compare lanes 1 and 2), which disappeared when the glycosylation site was mutated from N169SS (N169) to Q169SS (QSS) (lanes 3 and 4). We conclude that the EC2 loop is located in the lumen of the microsomes. This result also shows that the other two potential glycosylation sites (N33FT (N33) and N188AS (N188)) in OR83b are not utilized, possibly because they are located in a cytoplasmic part of the protein (N33FT) or too close to a TM segment (N188AS) [14].

3.2. Topology mapping Or83b

Additional acceptor sites for N-linked glycosylation were engineered into the N-terminal tail of OR83b, as well as into loops IC1, IC2, IC3, and EC2. A 22-residue peptide (PQSIYQKTMSFDKLIENSTQKT) containing a glycosylation acceptor site (underlined) was also fused to the C-terminus. The EC1 and EC3 loops were not targeted, as they are

![Fig. 1](image-url). The topology of the Or83b protein. (A) Predicted topology of OR83b. Phobius [8] predicts an N-in C-out topology with the following 7TM helices: 50–68, 80–98, 137–158, 194–213, 350–371, 391–413, 462–483. Engineered and endogenous (N33FT, N169SS and N188AS encircled) putative glycosylation sites are indicated; sites that become modified upon insertion into DRMs are in black, non-modified sites are in gray. (B) Glycosylation mapping of OR83b. In vitro translation of OR83b wild-type and variants with engineered glycosylation sites in the absence (−DRM) and presence (+DRM) of Drosophila rough microsomes. Molecules glycosylated only on the endogenous N169SS site are indicated by * and molecules glycosylated on an additional engineered site are indicated by arrows.
too short to be modified by the oligosaccharyl transferase [14,15]. The engineered glycosylation site (N175) in loop EC2 was efficiently modified in the presence of DRMs, resulting in a protein carrying two N-linked glycans (Fig. 1B, lanes 11 and 12). When the natural glycosylation site N169SS was mutated to N169QSS in this construct (N175QSS), only the N175 site was modified (lanes 13 and 14). The extended C-terminal tail (C-term NST) was also modified in the presence of DRMs (lanes 19 and 20); the somewhat lower modification efficiency of this site is probably caused by its location very close to the C-terminus of the protein [16]. In contrast, none of the acceptor sites in loops IC1 (N112), IC2 (N265), or IC3 (N440) were modified. The engineered site (N21) in the N-terminal tail was mostly non-glycosylated, although a faint doubly glycosylated product (modified on both N21 and N169) was also seen for this construct (lanes 5 and 6). Since no faint doubly glycosylated bands were seen for the N112 and N112+N120 constructs (lanes 7–10), loop IC1 faces the cytosol in all molecules. Molecules glycosylated on N21 thus represent a minor, probably misfolded, fraction of the protein in which the first or second TM segment does not span the membrane. Earlier work using GFP and YFP fusions and epitope staining is consistent with a cytosolic location of the N-terminus and a lumenal location of the EC2 loop [2].

4. Discussion

The Drosophila OR83b protein is an ubiquitously expressed member of the insect OR family, and it forms functional heteromers with other OR proteins [2]. Mammalian ORs are 7TM GPCRs with an EC N-terminus, but there is no detectable sequence similarity between mammalian and insect ORs [2]. Recent work has tentatively located the N terminus of OR83b to the cytosol [2], arguing that this protein is not a classical GPCR. Given this rather surprising conclusion, we decided to perform a detailed study on the topology of OR83b using glycosylation mapping, an approach that has been widely applied to eukaryotic membrane proteins [17].

In short, our results confirm the suggested IC location of the N-terminal tail of OR83b and in addition show that the EC2 loop and the C-terminal tail are EC. We also find that glycosylation acceptor sites engineered into loops IC1, IC2, and IC3 are not modified by the lumenally disposed oligosacchide transferase, in accordance with the proposed 7TM N\text{in}/C\text{out} topology [2].

When the available experimental data is used to constrain [18] the Phobius predictor, the predicted topology for OR83b is as shown in Fig. 2, i.e., essentially the same as predicted by the unconstrained Phobius, TMHMM, HMMTOP, PHDhtm, Memsat 2.0, and Toppred algorithms (cf., Fig. 1). We conclude that OR83b has 7TM helices, an IC N-terminus and EC C-terminus, and is thus inverted compared to the canonical 7TM topology of the GPCR family of mammalian ORs.

Acknowledgements: We thank Prof. Bernard Dobberstein for advice concerning Drosophila microsomes and Prof. Arthur E. Johnson for providing dog pancreas microsomes. This work was supported by grants from the Swedish Cancer Foundation to IN and GvH, from the Swedish Research Council to GvH, from the Swedish Foundation for International Cooperation in Research and Higher Education (STINT) to IN, from Magnus Bergvalls Stiftelse, Henrik Granholms Stiftelse, and Carl Tryggers Stiftelse to IN, and from the NIH to JC.

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.febslet.2007.11.007.
References


