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Expression of Odorant Receptor Family, Type 2 OR in the Aquatic Olfactory Cavity of Amphibian Frog *Xenopus tropicalis*

Tosikazu Amano\(^1,2,3\)\(\star\), Jean Gascuel \(^1,2,3\)

\(1\) CNRS, UMR6265 Centre des Sciences du Goût et de l’Alimentation, Dijon, France, \(2\) INRA, UMR1324 Centre des Sciences du Goût et de l’Alimentation, Dijon, France, \(3\) Université de Bourgogne, UMR Centre des Sciences du Goût et de l’Alimentation, Dijon, France

**Abstract**

Recent genome wide *in silico* analyses discovered a new family (type 2 or family H) of odorant receptors (ORs) in teleost fish and frogs. However, since there is no evidence of the expression of these novel ORs in olfactory sensory neurons (OSN), it remains unknown if type 2 ORs (OR2) function as odorant receptors. In this study, we examined expression of OR2 genes in the frog *Xenopus tropicalis*. The overall gene expression pattern is highly complex and differs depending on the gene and developmental stage. RT-PCR analysis in larvae showed that all of the OR2\(\eta\) genes we identified were expressed in the peripheral olfactory system and some were detected in the brain and skin. Whole mount *in situ* hybridization of the larval olfactory cavity confirmed that at least two OR2\(\eta\) genes so far tested are expressed in the OSN. Because tadpoles are aquatic animals, OR2\(\eta\) genes are probably involved in aquatic olfaction. In adults, OR2\(\eta\) genes are expressed in the nose, brain, and testes to different degrees depending on the genes. OR2\(\eta\) expression in the olfactory system is restricted to the medium cavity, which participates in the detection of water-soluble odorants, suggesting that OR2\(\eta\)s function as receptors for water-soluble odorants. Moreover, the fact that several OR2\(\eta\)s are significantly expressed in non-olfactory organs suggests unknown roles in a range of biological processes other than putative odorant receptor functions.

**Introduction**

Olfaction is essential for animal survival to find food and mating partners, and to escape from predators. To recognize the huge variety of odorant molecules in the environment, there are large numbers of odorant receptors (ORs) which often make up the largest gene family in the tetrapod genome [1]. For example, the human and mouse genome contains >800 [2,3] and \(~\)1400 [4,5] OR genes, respectively, including nonfunctional genes. There are 388 intact OR genes in humans [6,7] and 1037 in mice [6], and >800 OR genes are expressed in mouse olfactory epithelium (OE) [8]. In the amphibian frog *Xenopus tropicalis*, more than 1500 OR genes have been identified in the genome [9].

ORs have been classified into two groups [10]. Class I is occasionally referred to as fish-like since this group was initially found in teleost fish. These are thought to function as receptors for water-soluble odorants [10–12]. Tetrapod-specific class II receptors may play a role in the detection of air-borne odorants [10–12]. Phylogenetic analyses showed that class I and II ORs made up one large gene family (type I, (OR1)) that could be divided into several subgroups \(\alpha, \beta, \delta, \epsilon, \zeta\) (class I), and \(\gamma\) (class II) [14]. Bioinformatic studies also revealed that the mammalian genome contained a number of class I ORs [5]. These ORs mainly belong to the \(\alpha\) subgroup, which is not found in the fish genome [14].

Thus, class I ORs are thought to recognize air-borne odorants [15]. Recent genome-wide screening of G-protein coupled receptor genes discovered another type of ORs named type 2 (OR2) in the fish and the frog [14] or family H in the fish, which corresponds to OR2\(\eta\), one of three subgroups of OR2 [16]. OR2s are thought to act as receptors for odorants, even though the function of the OR2 is not clear since no evidence of their expression in olfactory sensory neurons (OSNs) is available. Only one gene OR137-7 (a member of the family H) is known to be expressed in the olfactory epithelium (OE) in zebrafish [9,16].

*Xenopus* adapts to both aquatic and terrestrial life. During the early larval period before metamorphosis, there is a pair of single olfactory cavities (OCs) which specifically recognize water-soluble odorants [17]. The surface of the OE in the PC is covered by mucus containing olfactory binding protein (OBP) [20], which is similar to mammalian OE [21,22]. Although its exact functions are unclear, OBP is thought to be an adaptation of olfaction to odorant detection in the air [23,24]. Thus, it is thought that the PC and the MC participate in the recognition of air-borne odorants and water-soluble odorants, respectively. This unique feature of the *Xenopus* olfactory system gives the opportunity to...
study OR functions. To clarify the chemosensory function of OR2 genes, it is necessary to localize OR2 gene expression in the OSN. Thus, our study aimed to reveal OR2 expression in the frog.

In this paper, we showed that the overall pattern of OR2 gene expression was highly complex and differed according to the gene and the developmental stage. All of the OR2 genes we examined were expressed in the olfactory organ both in the larva and the adult with different expression levels. Moreover, at least two of the OR2 genes so far tested were expressed in the OSNs in the larval OC. Altogether, this is the first evidence of OR2 expression in the OSNs, which support the idea of the putative olfactory function deduced from their predicted protein sequence [16]. In the adult nose, OR2 genes were preferentially expressed in the MC. In addition, because some OR2 genes were also expressed in the brain and skin in the larva, and the brain and testes in the adult, involvement of OR2 genes in non-olfaction processes also has to be considered.

Materials and Methods

Bioinformatics

XtOR2 genes were collected from the latest version of the *X. tropicalis* genome draft [JGI, version 4.1, http://genome.jgi-psf.org/Xenrt4/Xenrt4.home.html], by BLAST using published *X. tropicalis* OR2 gene sequences [14] in the previous version of the genome draft [JGI, version 3.1] as a query. Multiple nucleotide sequence alignments were performed using a web-base program (MAFFT version 6, http://mafft.cbrc.jp/alignment/server/index.html) using default parameters. The phylogenetic tree was constructed using the neighbor-joining method [25]. Three *X. tropicalis* melanocortin receptors were used as an out group. The reliability of each tree node was tested by the bootstrap method with 1000 replications. The amino acid sequence homology analysis was done using MAFFT.

Animals, RNA extraction and PCR

All experimental procedures were submitted to both the French veterinary committee (DSV: Direction des services vétérinaires), and to the local ethics committee of Burgundy University. The experimental procedures were approved by these committees (approval numbers are respectively: DSV accreditation: 21GAE 016, and ethics committee: G04bis, H04bis, I04bis).

*X. tropicalis* tadpoles were staged according to Nieuwkoop and Faber [26]. The olfactory cavities and other organs were dissected from the staged tadpoles and the sexually mature adult frogs. The PC and the MC were separated surgically from the adult frogs. Contamination of the PC tissue in the MC preparation was checked by the detection of OBP RNA, which is specifically digested RNA (0.5 or 1 μg) was used for further experiments. Because of extremely high homology between XoOR2 and 2 and 2, and XoOR2 and 7 and 8, respectively, we used the primer set which amplified both XoOR2 and 2 and 2, and both XoOR2 and 7 and 8, respectively. We confirmed by sequencing that all primer sets we used amplified the given OR2 gene species. To normalize OR expression in the OC in each sample we used olfactory marker protein (OMP) as an internal control since OMP is known to be ubiquitously expressed in mature OSN [28]. Although in *X. laevis* there are two olfactory marker proteins, which show distinct expression pattern in the OC [29], we only found one OMP gene (GenBank accession no NM_203734) in the *X. tropicalis* genome. The primer sequences we used were: XoOR2 and 1(5′-TGTATCTACCTGTGAGCTTCTGATG-3′), XoOR2 and 2(5′-TGTTGAACACCTCGCTTACG-3′), 5′-TTCTTTAGTATGGCCACTAGACC-3′, XoOR2 and 3(5′-TGTTGAACACCTCGCTTACG-3′), 5′-GAACACCTTGAGATCAGGACACAC-3′, XoOR2 and 4(5′-CTCATGCTAGTGTGTGCTGTG-3′), XoOR2 and 5(5′-CTGTTAGTGAGCAGCACC-3′), XoOR2 and 6(5′-GTGATTATAGGCAATGAGCTG-3′), XoOR2 and 7(5′-TATATCAGGATGATGACT-3′), XoOR2 and 8(5′-TGTGATTATAGGCAATGAGCTG-3′), XoOR2 and 9(5′-TATATCAGGATGATGACT-3′), XoOR2 and 10(5′-TATATCAGGATGATGACT-3′).

Whole mount in situ hybridization (WISH) on stage 47 larvae was carried out as described previously [30], and digoxigenin labeled and fluorescein labeled probes were detected by using the TSA plus fluorosence system (PerkinElmer). A cRNA probe was synthesized by T7 RNA polymerase (Promega) from a PCR fragment containing 3′-UTR of XoOR2 and 4 and XoOR2 and 3 ligated to a T7 promoter. Primers used for amplification of XoOR2 and 4 and XoOR2 and 3 3′-UTR were 5′-TACTGCTAGTCTGTTACG-3′ and 5′-ATCTGCTAGTCTGTTACG-3′, respectively.

Results

OR2 genes in the *X. tropicalis* genome

We identified 10 intact XoOR2 genes in the genome by BLAST using published sequences of *X. tropicalis* OR2 (XoOR2) genes [14] as a query, (Table 1). They were clearly separated from the classical OR1 genes (class I and II), and divided into 3 groups (Table 2, Fig. 1) as previously reported [9,14]. We described these genes according to the nomenclature proposed by Ghusman et al. [31] with minor modifications to adapt to the most recent classification of OR genes in the frog and the fish as follows: XoOR2 and 1, *X. tropicalis* OR2 | Odorant Receptor | type 2 | group A |
individual gene number 1 in the group. Both group η and θ contained a single copy gene and were located on scaffold 55 (JGI ver.4.1), but were separated by many non-OR genes. The largest group, η, consisted of 8 genes. Seven genes of group η (OR2η1-7) were mapped on a single scaffold, 982, making a gene cluster (Table 1) and one (OR2η8) was on another scaffold, 1014. Both were surrounded by different sets of non-OR genes indicating that XtOR2η8 was located outside the XtOR2η cluster in the genome. Very recently, basically similar results were obtained by Niimura [9]. This study identified 14 OR2 genes (1κ, 4h, 1η including two pseudogenes and one truncated gene) in the X. tropicalis genome. All the OR2 genes we identified were included in this group. This small difference in the number of genes might have been due to a different parameter setting for the BLAST search.

Overall pattern of expression of XtOR in the tadpole and adult
To understand the putative function of OR2 receptors, we first examined the expression of all of the XtOR2 genes we identified in various organs in the larval and adult animals by RT-PCR. The expression of XtOR2κ1 and XtOR2θ1 was hardly detected in the olfactory system in both the larval and the adult animals (Data not shown). We therefore focused on XtOR2η expression. The RT-PCR analysis in the organs of XtOR2η genes demonstrated a variety of expression patterns (Fig. 2). In the larva (Fig. 2, left panel), two, out of six, XtOR2η genes were expressed only in the nose, one at a high expression level (OR2η5) and the other at a low level (OR2η6). XtOR2η1, 2/3 and 4 RNAs were detected, not only in the nose, but also at various levels in the brain. OR2η4 was also expressed in the skin and the tail. Since the tail contained

### Table 1. X. tropicalis OR Type 2 genes.

| Gene name | Scaffold | Position | + or −* | size** | Gene ID | Protein ID | Another name*** |
|-----------|----------|----------|---------|--------|---------|------------|----------------|
| XtOR2κ1   | 55       | 340794–341681 | −       | 295    | e_gw1.55.204.1 | 320008    | Xetr-κ1         |
| XtOR2θ1   | 55       | 2538054–253991   | +       | 344    | gw1.55.343.1 (part) | 143443   | Xetr-θ1.1       |
| XtOR2η1   | 982      | 80133–81065     | −       | 310    | fgensh1_pg.C_scaffold_982000006 | 188437   | Ors982.1        |
| XtOR2η2   | 982      | 93665–94591     | −       | 308    | none    | none       | Ors982.3        |
| XtOR2η3   | 982      | 117240–118166   | −       | 308    | fgensh1_pg.C_scaffold_982000010 | 188441   | Ors982.5        |
| XtOR2η4   | 982      | 124362–125276   | −       | 304    | fgensh1_pg.C_scaffold_982000012 | 188443   | Ors982.6        |
| XtOR2η5   | 982      | 134704–135672   | −       | 322    | fgensh1_pg.C_scaffold_982000013 | 188444   | Ors982.7        |
| XtOR2η6   | 982      | 150541–153538   | −       | 319    | fgensh1_pg.C_scaffold_982000014 (cDNA) | 188445   | Ors982.8        |
| XtOR2η7   | 982      | 166466–167351   | −       | 295    | fgensh1_pg.C_scaffold_982000015 | 188446   | Ors982.9        |
| XtOR2η8   | 1014     | 161856–162743   | −       | 295    | fgensh1_pg.C_scaffold_1014000016 | 188695   | Ors1014.2       |

*orientation.
**amino acid length.
***annotated by Niimura (9).

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### Table 2. Amino acid sequence identity (%) of X. tropicalis type 2 ORs and class I Ors.

|          | XtOR2κ1 | XtOR2θ1 | XtOR2η1 | XtOR2η2 | XtOR2η3 | XtOR2η4 | XtOR2η5 | XtOR2η6 | XtOR2η7 | XtOR2η8 | MCR | XtOR1(I)a1 | XtOR1(I)b1 |
|----------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|-----|------------|------------|
| XtOR2κ1  | 20      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15  | 12         | 18         |
| XtOR2θ1  | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15  | 18         | 18         |
| XtOR2η1  | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15  | 18         | 18         |
| XtOR2η2  | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15  | 18         | 18         |
| XtOR2η3  | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15  | 18         | 18         |
| XtOR2η4  | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15  | 18         | 18         |
| XtOR2η5  | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15  | 18         | 18         |
| XtOR2η6  | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15  | 18         | 18         |
| XtOR2η7  | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15  | 18         | 18         |
| XtOR2η8  | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15  | 18         | 18         |
| MCR      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15  | 18         | 18         |
| XtOR1(I)a1 | 15    | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15  | 18         | 18         |
| XtOR1(I)b1 | 15    | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15      | 15  | 18         | 18         |

*XtOR1(I)a1: estEXT_fgenesh1.pg.C_5720016.
**XtOR1(I)b1: e_gw1.799.21.1.

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Figure 1. Phylogenetic tree of *X. tropicalis* OR1 and OR2 genes. Amino acid sequences of all XtOR2 and all XtOR1 class I (OR(I)), four XtOR1 class II ORs (OR(II)γ), and three melanocortin receptors (MCRs), were used for the phylogenetic analysis.

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Figure 2. XtOR2 gene expression in various organs in stage 55 larvae and full-grown adults. The primer set for class II OR amplified multiple class II OR genes. PCR cycles were adjusted to obtain adequate amounts of the products (35 cycles for OR2 and class I ORs, and 30 cycles for rpL8 and class II ORs).

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the skin, the signal in the tail might be due to the skin of the tail. Besides the strong expression of XtOR2g7/8 in the nose, these two genes were also expressed at a low level in all of the organs tested.

The expression pattern of these genes in the adult frog, was different from that in the tadpole (Fig. 2, right panel). Expression in the nose and the brain of the adult was much lower than in the larva. Interestingly, all XtOR2g genes except for XtOR2g6 were expressed at various levels in the tests.

Like for the class I OR that we examined here, the expression of XtOR2g in the nose was stronger in the larva than in the adult whereas class II OR expression was strongly up-regulated in the adult nose.

Respective expression between the PC and MC in adult

The adult frog has two distinct OCs, the PC and the MC (Fig. 3A), which are involved in the detection of air-borne and water-soluble odorants, respectively [19]. It has been shown that the surface of the sensory epithelium in the PC of the adult frog is covered with OBP which could be considered a marker for the aerial olfactory system [20]. Our results confirmed that the OBP gene was exclusively detected in the PC [20] at an extremely high level (approximately 15,000 times higher than the OMP, Fig. 3B), OBP RNA was hardly detected in the MC (Fig. 3B), indicating that the MC preparation did not contain a significant amount of PC tissue contamination. In contrast, most class I OR genes (we examined more than 30 class I OR genes from all 4 subgroups, Fig. 3B and data not shown), including tetrapod-specific class I subgroup α, were preferentially expressed in the MC (aquatic olfactory system) whereas the class II ORs were exclusively expressed in the PC as reported by Freitag et al. [10] (Fig. 3B). One significant exception was the OR1g5 gene [JGI; e_gw1.2098.6.1] which belongs to the tetrapod-specific subgroup of class I OR, was equally expressed in both the MC and the PC. Our results showed that XtOR2g genes were differentially expressed in the adult olfactory system (Fig. 3B). These genes were preferentially expressed in the MC. No or very low expression was detected in the PC; levels were comparable to levels of expression of each single class I OR (Fig. 3B).

WISH analysis of OR2g expression in the OSN

If OR2g are involved in odorant detection they should be expressed in the OSN. Thus, we performed WISH of the OC of the tadpole to determine whether OR2 gene expression was limited to the OSN. The small size (1070+/−183 cells (n = 10) in the OE) of the OC of stage 47 tadpoles enabled us to analyze gene expression in the entire organ with a confocal microscope. At this stage there is only one pair of aquatic OC in the tadpole [17]. We chose two OR2g genes for this experiment because of their distinct expression profile in the tadpole. OR2g5 was exclusively expressed in the olfactory organ and OR2g4, which, besides being expressed in the nose, was expressed in other organs such as the brain and the skin. Confocal microscopic analysis clearly demonstrated colocalization of these two OR2g genes and the OMP gene which is regarded as a good molecular marker of mature OSN [28] (Fig. 4A–C). OMP expression was hardly detected in the vomeronasal organ in this stage tadpole (Fig. 4A). Thus, at least two OR2g genes, so far tested, XtOR2g4 and XtOR2g5 were specifically expressed in the OSN in the larval OC. Each OC contained on average 8.9±2.3 (s.d., n = 24) XtOR2g4-positive and 6.0±3.6 (n = 22) XtOR2g5-positive OSN cells (Fig. 4D). The expression was hardly detected in the vomeronasal organ (Fig. 4B). The XtOR2g4- and XtOR2g5-expressing cells were randomly distributed in the OC (data not shown).

Discussion

The OR2 family was recently identified by in silico genome research in the teleost fish and the frog as a close but distinct group of the OR gene super family [14,16]. Overall sequence homology between OR2 and OR1 (class I and class II ORs), which have 7 transmembrane domains [16], suggests that OR2 is also involved in odorant reception. However, because of the lack of expression

Figure 3. OR gene expression in adult olfactory cavities. A: Schematic illustration of the nasal cavities of the adult frog. The MC is filled in water and the PC is open to air. The air flow goes through the PC to the lung. B: The expression of OR2g5g and some OR1s (class I and II) in adult nasal cavities. Quantitative PCR was done for each OR gene and normalized by using the OMP gene, which is expressed in every mature OSN. Most class I ORs were preferentially expressed in the MC. Class I ORs5 was exceptionally expressed at a significant level in the PC as well as the MC. Bars represent standard deviation (n = 22). Note that the expression level of OBP and class II (mix) OR was much higher than each single OR2g and class I OR gene (different scale). Gene ID: OR1s2: ENSXETG00000024801.1, OR1s4: fgenes1_pg_C_scaffold_107800009, OR1s5: e_gw1.2098.6.1, OR1s3: fgenes1_pg_C_scaffold_97600003, OR1s15: e_gw1.976.19.1, OR1s2: e_gw1.799.9.1, OR1s4: e_gw1.799.69.1. doi:10.1371/journal.pone.0033922.g003
data in OSN, the odorant receptor function of OR2 remains unclear. The scope of this paper was to investigate expression patterns of these genes. Our results did not demonstrate direct evidence of the involvement of these receptors in odorant detection. However, we have provided pertinent data to support this hypothesis for OR2\eta.

OR2 genes in the X. tropicalis genome

The XtOR2\eta genes were closely related (39–100% identity in amino acid sequences) and made a gene cluster with one exception. XtOR2\eta8 was located outside the OR2\eta cluster. This exceptional XtOR2\eta8 had a 98% nucleotide identity in the cDNA coding region to that of XtOR2\eta7 located in the cluster, suggesting that the XtOR2\eta8 gene duplicated from the XtOR2\eta7 gene and translocated. OR genes are thought to have increased in number from a small number of ancestor genes by duplication and translocation in the evolution process [32]. Thus, XtOR2\eta8 is probably one example of the evolution process. We also identified two OR2 genes of two distinct subgroups (k and \theta) outside the OR2\eta cluster in the genome. However, we found no significant expression of these two genes in the nasal cavities. Thus, OR2k and \theta genes are probably not odorant receptors. The non-OR function of OR2k and \theta was also suggested by Nimura [9] based upon their expression in only non-olfactory tissues [33] and their distinct evolutionarily dynamics from the OR genes [9]. In fact, Alioto and Ngai [16] did not identify these highly divergent groups as odorant receptors in the fish genome.

OR2\eta genes were preferentially expressed in the olfactory system and some other organs (see below) with one exception. Non-specific weak expression of the XtOR2\eta7 and/or 2\eta8 gene was detected in all organs tested. Such expression of the OR genes in a broad range of organs has been reported [34], and is thought to be a result of neutral or nearly neutral mechanisms such as small DNA sequence changes in regulatory regions [35,36]. The OR2\eta8 gene might have lost its regulatory region by translocation, resulting in the ectopic expression.

Expression in the olfactory system

Present data showed the co-localization of the expression of two XtOR2\eta genes so far tested (XtOR2\eta4 and XtOR2\eta5) with the OMP gene in the OE in the tadpole. Because the OMP is a marker of mature OSN, this is the first demonstration of the cellular level of the expression of representatives of the XtOR2\eta gene family by OSN. Because the tadpole is an aquatic animal it is reasonable to suppose that these receptors are involved in aquatic olfaction in the tadpole. We found no particular spatial concentration of the OR2\eta4 and 5-expressing cells. The distribution of tested OR2\eta-expressing OSN in the larval OC is probably random. This suggests that OR2\eta-expression is possibly regulated in a stochastic manner similar to that in other OR genes [37,38].

In the adult, the MC is known to express class I ORs which detect water-soluble odorants [10,12]. Our qPCR analysis also showed that most class I OR genes are preferentially expressed in the MC. In this context, preferential expression of OR2\eta in the MC suggests that like class I ORs they have a water-soluble odorant receptor function similar to the class I ORs. This hypothesis is well supported by the fact that the OR2 family is solely found in aquatic animals such as fish and amphibian frogs. In contrast to this, class II ORs are exclusively expressed in the PC ([10,18], this paper) and thought to recognize volatile ligands [12]. In the mammalian genome the receptors for water-borne odorants such as OR2\eta and most class I ORs were selectively lost during tetrapod evolution [14–16]. Surprisingly, our data showed that like other class I ORs the mammalian group of class I OR (\zeta and \beta) was preferentially expressed in the adult MC with one exception: class I ORz5 which is expressed in both the MC and the PC. These results are inconsistent with the hypothesis according to which the mammalian class I ORz and probably \beta function as receptors for air-borne odorants [9,14,15]. One alternative hypothesis could be that during tetrapod evolution, some class I receptors acquired the ability to bind to volatile ligands and subsequently they expanded the number of genes in the genome for adaptation to terrestrial life.

Expression in other organs

The expression of OR in organs other than olfactory organs is not exceptional and has been reported in other vertebrates. In mammals and birds, OR genes are expressed in the telencephalon [39] and the olfactory bulb [40,41] during early development. OR proteins are expressed on the axon termini in the olfactory bulb [42,43], where OR is thought to be involved in axonal guidance of the OSNs to their glomerular targets [44–46]. It is also well known that ORs are expressed on the surface of sperm cells and play a role in chemotactic behavior of spermatozoa by the reception of sperm attractant molecules coming from the oviduct [47–50]. In this respect it is not surprising that in this study, we found expression of XtOR2\eta1, 2/3, 4 (and may be 7/8) genes in the brain or all XtOR2\eta genes except for XtOR2\eta8 in the testes. As for mammals, such expression in the brain may possibly be involved in development and axonal guidance. The testicular...
expression could be related to chemotactic behavior of spermatozoa to eggs. If this is true, one of the putative ligands for OR2\eta on the sperm surface could be allurin protein which is related to mammalian sperm binding proteins [51] and recently identified as a sperm chemoattractant in X. laevis and P. tropicus [52,53]. More puzzling is the expression of XlioR2\eta in the skin. It is known that chemosensory cells, the so-called solitary chemosensory cells, are distributed in the epidermis over the body surface in fish [54–56] and in frog tadpoles [57]. OR expression in these cells is not yet clear. However, it may be possible to hypothesize that OR has a chemoreceptor function in these cells. In future studies, it is necessary to identify XlioR2\eta-expressing cells in tadpole skin to examine this hypothesis.

Our results demonstrate that OR2\eta genes in Xenopus display different expression patterns. At least two OR\eta genes (XlioR2\eta and 5) are expressed in OSN in the larval olfactory system, suggesting involvement in aquatic olfaction at this stage. In the adult, OR2\eta are preferentially expressed in the MC (qPCR experiments), which responds to water-soluble odors. Thus, the hypothesis of involvement of OR2\eta in aquatic olfaction is strong enough to suggest that the physiology should be investigated in future work. Several OR2\eta genes are expressed in non-olfactory tissues such as the brain and the skin in the larva, besides being expressed in the olfactory organ. In the adult, most OR2\eta are expressed in the testes and some in the brain. Therefore, these OR2\eta may also have other functions, in addition to olfaction in the nose, such as developmental functions in the brain, chemosensory functions in the skin, and chemotaxis of sperm. In this respect, they share this peculiar feature with mammalian ORs. Further studies of OR2\eta will provide important insights into various OR functions as well as the evolution of chemosensory receptors. Moreover, the study of receptors for water-soluble odors may important for fishery production.

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Author Contributions
Conceived and designed the experiments: JA TA. Performed the experiments: TA. Analyzed the data: TA. Contributed reagents/materials/analysis tools: JG. Wrote the paper: TA JG.

References
1. Rouquier S, Georgi D (2007) Olfactory receptor gene repertoires in mammals. Mutation Res 616: 95–102.
2. Glusman G, Yanai I, Rubin I, Lancel D (2001) The complete human olfactory subgenome. Genome Res 11: 685–702.
3. Olender T, Feldmesser E, Aparat T, Eisenstein M, Lancel D (2004) The olfactory receptor universe—from whole genome analysis to structure and evolution. Genet Mol Res 3: 545–553.
4. Young JM, Friedman C, Williams EM, Ross JA, Tonts-Priddy L, et al. (2002) Different evolutionary processes shaped the mouse and human olfactory receptor gene families. Hum Mol Genet 11: 535–546.
5. Zhang X, Firestein S (2002) The olfactory receptor gene superfamily of the mouse. Nat Neurosci 5: 124–133.
6. Niimura Y, Nei M (2005) Evolutionary changes of the number of olfactory receptor genes in the human and mouse lineages. Gene 346: 23–28.
7. Niimura Y, Nei M (2005) Evolution of olfactory receptor genes in the human genome. Proc Natl Acad Sci USA 100: 12235–12240.
8. Zhang X, Rogers M, Tian H, Zhang X, Zou DJ, et al. (2004) High-throughput microarray detection of olfactory receptor gene expression in the mouse. Proc Natl Acad Sci USA 101: 14160–14173.
9. Niimura Y (2009) On the origin and evolution of vertebrate olfactory receptor genes: comparative genome analysis among 23 chordate species. Genome Biol Evol 2009: 34–44.
10. Freitag J, Krueger J, Strommann J, Breer H (1995) Two classes of olfactory receptor genes in Xenopus laevis. Neuron 15: 1303–1392.
11. Freitag J, Ludvig G, Andreini I, Rossler P, Breer H (1998) Olfactory receptors in aquatic and terrestrial vertebrates. J Comp Physiol A 180: 635–650.
12. Medel M, Fielescher J, Breer H (2003) Characteristic features and ligand specificity of the two olfactory receptor classes from Xenopus laevis. J Exp Biol, pp 2987–2997.
13. Alito TS, Ngai J (2006) The repertoire of olfactory G family G protein-coupled receptors in zebrafish: candidate chemosensory receptors for amino acids. BMC Genomics 7: 309–326.
14. Niimura Y, Nei M (2005) Evolutionally dynamics of olfactory receptor genes in fishes and tetrapods. Proc Natl Acad Sci USA 102: 6039–6044.
15. Nei M, Niimura Y, Nozawa M (2008) The evolution of animal chemosensory receptor gene repertoires: roles of chance and necessity. Nature Rev 9: 501–502.
16. Alito TS, Ngai J (2005) The odorant receptor repertoire of teleost fish. BMC Genomics 6: 175–186.
17. Ahner H (1962) Untersuchungen über Leistungen und Bau der Nase des Süßwasser- und Meeressäugers, der Krait und des Raubfisches Xenopus laevis (Daudin, 1803). Z Vergl Physiol 45: 272–306.
18. Medel M, Konzelmann S, Freitag J, Rossler P, Breer H (1999) Expression of olfactory receptors during development in Xenopus laevis. J Exp Biol 202: 365–376.
19. Reiss JO, Eisthen HL (2008) Comparative anatomy and physiology of chemical senses in amphibians. In Thewissen JGM, Nummela S, eds. Sensory evolution in aquatic and terrestrial vertebrates. J Comp Physiol A 183: 635–650.
20. Millery J, Briand L, Bezirard V, Blon F, Fenech C, et al. (2005) Specific expression of olfactory binding protein in the aerial (PC) olfactory cavity of adult and developing Xenopus. Eur J Neurosci 22: 1309–1399.
21. Pes D, Mameli M, Andreini I, Krueger J, Weber M, et al. (1998) Cloning and expression of odorant-binding protein 1a and lb from mouse nasal tissue. Gene 212: 49–55.
22. Pelosi P (2001) The role of perireceptor events in vertebrate olfaction. Cell Mol Life Sci 58: 503–509.
23. Briand L, Eliot C, Nespoulous C, Bezirard V, Huard JC, et al. (2002) Evidence of an odorant-binding protein in the human olfactory mucus: location, structural characterization, and odorant-binding properties. Biochemistry 41: 7241–7252.
24. Tsuchioki L, Nespoulous C, Perrelet JC, Briand L (2006) A single lysyl residue defines the binding specificity of a human odorant-binding protein for aldehydes. FEBS Lett 580: 2102–2108.
25. Saitou N, Nei M (1987) The neighbor-joining method: a new method for constructing phylogenetic trees. Mol Biol Evol 4: 406–425.
26. Newdoope AA, Faber J (1994) Normal time table of Xenopus laevis (Daudin). New York: Garland Publishing Inc.
27. Shi Y-B, Liang VC-T (1994) Cloning and characterization of the ribosomal protein L3 gene from Xenopus laevis. Biochem Biophys Acta 1217: 227–230.
28. Rogers KE, Dasgupta P, Grillo M, Khos-Goodall YS, Margolis FL (1987) Molecular cloning and sequencing of a cDNA for olfactory marker protein. Proc Natl Acad Sci USA 84: 1704–1708.
29. Rossler P, Medel M, Breer H (1998) Two olfactory marker proteins in Xenopus laevis. J Comp Neurol 395: 273–280.
30. Harland RM (1991) In situ hybridization: an improved whole-mount method for Xenopus embryos. Methods Cell Biol 36: 605–609.
31. Glusman G, Buhar A, Sharon D, Filipc V, White J, et al. (2000) The olfactory receptor gene superfamily: data mining, classification, and nomenclature. Mammalian Genome 11: 1016–1023.
32. Soinski A, Glusman G, Lancel D (2000) The genomic structure of human olfactory receptor genes. Genomics 70: 49–61.
33. Parmigiani RB, Magalhães GS, Galante PA, Manzini CV, Camargo AA, et al. (2004) A novel human G protein-coupled receptor is over-expressed in prostate cancer. Genet Mol Res 3: 521–531.
34. Feldmesser E, Olender T, Klein M, Yanai I, Ophir R, et al. (2006) Widespread ectopic expression of olfactory receptor genes. BMC Genomics 7: 121–138.
35. Khaitovich P, Weiss G, Lachmann M, Hellmann I, Enard W, et al. (2004) A neutral model of transcriptome evolution. Plos Biol 3: e42.
36. Yanai I, Graur D, Ophir R (2004) Incongruent expression profiles between human and mouse orthologous genes suggest widespread neutral evolution of transcription control. Oncies 8: 15–24.
37. Serizawa S, Ishii T, Nakatani H, Tsuobi A, Nagawa F, et al. (2000) Mutually exclusive expression of odorant receptor transgenes. Nat Neurosci 3: 607–603.
38. Shykoff BM (2005) Regulation of odorant receptors: one allele at a time. Hum Mol Genet 14: R35–R39.
39. Nef P, Hermans-Borgmeyer I, Arriez-Pin H, Bealey L, Dionne VE, et al. (1992) Spatial pattern of receptor expression in the olfactory epithelium. Proc Natl Acad Sci USA 89: 8948–8952.
40. Reissler J, Sullivan SL, Buck LB (1994) Information coding in the olfactory system: evidence for a stereotyped and highly organized epitope map in the olfactory bulb. Cell 79: 1245–1253.
41. Vassar R, Chao SK, Sitcheran R, Nunez JM, Vosshall LB, et al. (1994) Topographic organization of sensory projections to the olfactory bulb. Cell 79: 981–991.
42. Barnea G, O’Donnel S, Mancia F, Sun X, Nemes A, et al. (2004) Odorant receptors on axon termini in the brain. Science 304: 1468.
43. Strotmann J, Levai O, Fischer J, Schwarzenbacher K, Beer H (2004) Olfactory receptor protein in axonal processes of chemosensory neurons. J Neurosci 24: 7754–7761.
44. Feinstein P, Mombaerts P (2004) A contextual model for axonal sorting into glomeruli in the mouse olfactory system. Cell 117: 817–831.
45. Imai T, Suzuki M, Sakano H (2006) Odorant receptor-derived cAMP signals direct axonal targeting. Science 314: 657–661.
46. Serizawa S, Miyamichi K, Takeuchi H, Yamagishi Y, Suzuki M, et al. (2006) A neuronal identity code for the odorant receptor-specific and activity-dependent axon sorting. Cell 127: 1057–1069.
47. Vanderhaeghen P, Schurmans S, Vassart G, Parmentier M (1997) Specific repertoire of olfactory receptor genes in the male germ cells of several mammalian species. Genomics 39: 239–246.
48. Spehr M, Gisselmann G, Poplawski A, Riffell JA, Wetzel CH, et al. (2003) Identification of a testicular odorant receptor mediating human sperm chemotaxis. Science 299: 2054–2058.
49. Spehr M, Schweik K, Riffell JA, Zimmer RR, Hatt H (2006) Odorant receptors and olfactory-like signaling mechanisms in mammalian sperm. Mol Cell Endocrinol 25: 128–136.
50. Vosshall LB (2004) Olfaction: Attracting both sperm and the nose. Current Biol 14: R918–R920.
51. Olson JH, Xiang X, Ziegert T, Kittelson A, Rawls A, et al. (2001) Allurin, a 21-kDa sperm chemoattractant from Xenopus egg jelly, is related to mammalian sperm-binding proteins. Proc Natl Acad Sci USA 98: 11205–11210.
52. Xiang X, Burnett L, Rawls A, Bieber A, Chandler D (2004) The sperm chemoattractant “allurin” is expressed and secreted from the Xenopus oviduct in a hormone-regulated manner. Dev Biol 275: 343–355.
53. Burnett LA, Boyes S, Spencer C, Bieber AL, Chandler DE (2008) Xenopus tropicalis allurin: expression, purification, and characterization of a sperm chemoattractant that exhibits cross-species activity. Dev Biol 316: 408–416.
54. Kotrschal K (1991) Solitary chemosensory cells—taste, common chemical sense or what? Rev Fish Biol Fish 1: 3–22.
55. Kotrschal K (1996) Solitary chemosensory cells: why do primary aquatic vertebrates need another taste system? Trends Ecol Evol 11: 110–114.
56. Whitear M (1992) Solitary chemoreceptor cells. In: Hara TJ, ed. Chemoreception in fishes Chapman & Hall, London. pp 103–152.
57. Whitear M (1976) Identification of the epidermal “Stifchenzellen” of frog tadpoles by electron microscopy. Cell Tissue Res 175: 391–402.