**Rice (Oryza) hemoglobins** [v1; ref status: awaiting peer review, http://f1000r.es/4k1]

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**Abstract**

Hemoglobins (Hbs) corresponding to non-symbiotic (nsHb) and truncated (tHb) Hbs have been identified in rice (Oryza). This review discusses the major findings from the current studies on rice Hbs. At the molecular level, a family of the *nshb* genes, consisting of *hb1*, *hb2*, *hb3*, *hb4*, and *hb5*, and a single copy of the *thb* gene exist in *Oryza sativa* var. indica and *O. sativa* var. japonica. Hb transcripts coexist in rice organs and Hb polypeptides exist in rice embryonic and vegetative organs and in the cytoplasm of differentiating cells. At the structural level, the crystal structure of rice Hb1 has been elucidated, and the structures of the other rice Hbs have been modeled. Kinetic analysis indicated that rice Hb1 and 2, and possibly rice Hb3 and 4, exhibit an extremely high affinity for O₂, whereas rice Hb5 and tHb possibly exhibit a low to moderate affinity for O₂. Based on the accumulated information on the properties of rice Hbs and data from the analysis of other plant and non-plant Hbs, it is likely that Hbs play a variety of roles in rice organs, including O₂-transport, O₂-sensing, NO-scavenging and redox-signaling. From an evolutionary perspective, an outline for the evolution of rice Hbs is available. Rice *nshb* and *thb* genes vertically evolved through different lineages, rice nsHbs evolved into clade I and clade II lineages and rice *nshbs* and *thbs* evolved under the effect of neutral selection. This review also reveals lacunae in our ability to completely understand rice Hbs. Primary lacunae are the absence of experimental information about the precise functions of rice Hbs, the properties of modeled rice Hbs and the cis-elements and trans-acting factors that regulate the expression of rice *hb* genes, and the partial understanding of the evolution of rice Hbs.
Introduction

Two decades ago Taylor and co-workers reported the cloning and sequencing of a hemoglobin (Hb) cDNA from barley\(^1\). This was the first report about the existence of Hbs in monocotyledonous plants. Since then Hbs have been identified in a number of monocots, including rice\(^2\), maize\(^3\) and wheat\(^4\). Rice Hbs and genes coding for these proteins are well characterized, thus in many aspects rice Hbs are a model to understand monocot and other land plant Hbs. This review discusses major findings from the study of rice Hbs including a historical perspective, and proposes biochemical and physiological mechanisms for rice Hbs based on information available about rice Hbs and other monocot and land plant Hbs. For general aspects and the biochemistry, physiology and evolution of plant Hbs, we recommend to the reader reviews published elsewhere\(^5\--\(^8\).

Generalities on hemoglobins

Hb is known to the reader because this protein is responsible for the red color of vertebrates\(^9\) blood\(^10\). However, Hbs are widely distributed in living organisms, ranging from bacteria to mammals\(^11\--\(^13\). The tertiary structure of Hbs consists of a specific arrangement of 6 to 8 α-helices (designated with letters A to H) known as the globin-fold. This protein folding forms a hydrophobic pocket where a Fe-heme prosthetic group is located\(^14\--\(^16\). Two structural types of the globin-fold have been identified in Hbs: the 2/2- and 3/3-folding. In the 2/2-Hbs, helices B and E overlap to helices G and H and in the 3/3-Hbs helices A, E and F overlap to helices B, G and H. Likewise, three evolutionary families have been identified in Hbs: the M, S and T Hb families. The M Hbs, which exist in bacteria and eukaryotes, include flavohbs and single domain globins, the S Hbs, which exist in bacteria and yeasts, include globin-coupled sensors, protoglobins and single domain globin sensors, and the T Hbs, which exist in bacteria, unicellular eukaryotes and plants, include truncated Hbs (tHbs). Canonical T Hbs from bacteria and unicellular eukaryotes are ~100 to 120 amino acids in length, however plant T Hbs are longer than canonical T Hbs because of the existence of extra amino acids at the N- and C-terminal. The M and S Hbs fold into the 3/3-folding whereas the T Hbs fold into the 2/2-folding\(^17\--\(^20\).

A variety of ligands bind to the Fe-heme of Hbs, including O\(_2\) and NO. Reversible binding of O\(_2\) is closely associated to the major function of Hbs in organisms, which is the transport of O\(_2\)\(^\rightarrow\). Binding of NO by Hbs is essential to NO-detoxification via a NO-dioxygenase activity\(^21\). Several additional functions have been reported for Hbs, including dehaloperoxidase activity and reaction with free radicals, binding and transport of sulfide and lipids, and O\(_2\)-sensing\(^22\--\(^24\). This indicates that in vivo Hbs might be multifunctional proteins.

Land plant hemoglobins

Land plant Hbs were first identified by Kubo in soybean root nodules\(^25\). Few years after Kubo’s discovery these proteins were named as leghemoglobins (Lbs) by Virtanen and Lane\(^26\) because they were only found in the symbiotic (N\(_2\)-fixing-) nodules of the leguminous plants. Lbs are the most abundant soluble proteins in nodules (e.g. in soybean nodules their concentration is as high as 3 mM)\(^26\)--\(^28\). The x-ray analysis of lupin Lb revealed that the tertiary structure of Lbs was remarkably similar to that of the sperm whale myoglobin\(^29\). This evidence demonstrated that Lbs are plant Hbs and indicated that plant and animal Hbs evolved from a common ancestor more than 600 mya\(^3\). Subsequent work led to the identification of Lb-like (or symbiotic) Hbs in nodules of actinorhizal plants\(^30\--\(^32\), purification of an Hb from the root nodules of the dicotyledonous non-legume Parasponia andersonii\(^33\), cloning and sequencing of an hb gene from the non-nodulating dicot Trema tomentosa\(^34\)--\(^36\), and detection of Hbs in non-symbiotic organs from several land plants, including primitive bryophytes and evolved angiosperms\(^37\--\(^39\). Until now three types of Hbs have been identified in land plants: the symbiotic Hbs, which include Lbs, that are specifically located within nodules of the N\(_2\)-fixing land plants, and the non-symbiotic (nsHbs) and truncated (tHbs) Hbs, that are located within non-symbiotic and symbiotic organs of primitive and evolved land plants\(^40\--\(^42\). Based on sequence similarity the nsHbs are further classified into type 1 and type 2 nsHbs (nsHbs-1 and nsHbs-2, respectively)\(^43\)--\(^45\).

Distribution of hemoglobins in monocotyledonous plants

Monocots are a large family of flowering plants\(^46\)--\(^48\) that includes cereals. Cereals, such as rice, maize and wheat, are the main source of food for humans\(^49\). Because of this, during that last decade the genomes of a number of cereals have been sequenced. This allowed the identification of novel cereal Hbs. The search of hb genes in databases by G. Rodriguez-Alonso and R. Arredondo-Peter\(^50\)--\(^52\) revealed that nsHb and Hb sequences exist in the Brachypodium distachyon, Hordeum vulgare (barley), Oryza glaberrima (rice), O. rufipogon (rice), O. sativa (rice) var. indica, O. sativa (rice) var. japonica, Panicum virgatum (switchgrass), Setaria italica (foxtail millet), Sorghum bicolor (sorghum), Triticum aestivum (wheat) and Zea mays ssp. mays (maize) genomes. The highest number of nsHbs (5) exists in O. sativa var. indica and O. sativa var. japonica, whereas one to three nsHbs exist in barley, Brachypodium, foxtail millet, maize, O. glaberrima, O. rufipogon, sorghum, switchgrass and wheat. Also, with the exception of wheat, which contains two copies of the hb gene, a single copy of hb was identified in the genome of Brachypodium, barley, O. sativa var. indica, O. sativa var. japonica, switchgrass, foxtail millet, sorghum and maize. Little is known about Hbs from non-cultivated monocots. The only Hb reported from a non-cultivated monocot is that of teosinte (Z. mays ssp. parviglumis)\(^53\), which is postulated as the ancestor of maize\(^54\)--\(^56\). Analysis by Southern blot using the teosinte hb gene as probe showed that apparently a single copy of hb exists in teosinte (J. Sáenz-Rivera and R. Arredondo-Peter, unpublished results). Sequence comparison revealed that maize and teosinte Hb polypeptides are identical\(^1\).

Early search and identification of rice hemoglobins

Monocots were a target for searching Hbs after these proteins were detected in non-symbiotic organs of dicotyledonous plants (see subsection above). At that time, monocot genomes had not
been sequenced. Searching approaches consisted in detecting Hb polypeptides and \( h_b \) genes by spectroscopy and molecular biology methods, respectively. Attempts to detect absorption maxima in the Soret (~410 nm) and Q (~500 to 550 nm) regions, which are characteristic of ferric (Fe\(^{3+}\)), ferrous (Fe\(^{2+}\)) and liganded Hbs, were unsuccessful (R. V. Klucars and C. A. Appleby, unpublished results) mostly due to the very low Hb concentration (~50 to 100 nM) in plant non-symbiotic organs. At the molecular level a consensus probe designed from legume and non-legume (\( T. \) tomentosa, \( P. \) andersonii and Casuarina glauca) Hb sequences hybridized with \( h_b \)-like sequences from rice and other monocot total DNAs (Figure 1). This observation suggested that \( h_b \) sequences exist in monocots, however hybridizing fragments were not subsequently cloned and sequenced in order to verify if they actually corresponded to \( h_b \) genes.

Rice Expressed Sequence Tags (ESTs) were first deposited in databases early in the 1990’s. The first rice Hb (\( H_b1 \) and \( H_b2 \)) sequences were detected from ESTs deposited in the DNA Data Bank of Japan (DDBJ) database. Rice \( H_b1 \) and \( H_b2 \) corresponded to clones C741 and C2576 with DDBJ accession number D15507 and D38931, respectively. Rice \( H_b1 \) and \( H_b2 \) genes were subsequently amplified by PCR, cloned and sequenced. Sequence analysis revealed that rice \( h_b1 \) codes for non-symbiotic \( H_b1 \) and that rice \( h_b2 \) codes for non-symbiotic \( H_b2 \). Afterwards, sequencing of the rice (\( O. \) sativa L. ssp. indica) genome more than a decade ago allowed the identification of a family of rice \( nshb \) genes and a single copy of the rice \( thb \) gene (see subsection below).

### Molecular biology of rice hemoglobins

#### Rice hemoglobin genes

The \( O. \) sativa var. indica and \( O. \) sativa var. japonica genomes are fully sequenced, and the \( O. \) glaberrima and \( O. \) rufipogon genomes are partially sequenced. Rice genome sequences are mainly available from the GenBank (http://www.ncbi.nlm.nih.gov) and Phytozome (http://www.phytozome.org) databases. Search of Hb sequences in the above databases showed that a family of the \( nshb \) genes, consisting of \( h_b1, h_b2, h_b3, h_b4 \) and \( h_b5 \), and a single copy of the \( thb \) gene exist in the \( O. \) sativa var. indica and \( O. \) sativa var. japonica genomes. A single copy of the \( nshb \) gene was detected in the \( O. \) glaberrima and \( O. \) rufipogon genomes, however \( h_b \) genes have not yet been detected in these plants. Given that the sequencing of the \( O. \) glaberrima and \( O. \) rufipogon genomes is in progress the identification of \( h_b \) genes in these genomes is incomplete. Thus, the following discussion will focus on the \( O. \) sativa var. indica and \( O. \) sativa var. japonica \( h_b \) genes.

The structure of known rice \( h_b \) genes corresponds to four exons and three introns, with introns located at similar position as all of the known plant \( h_b \) genes. Canonical TATA boxes and a variety of potential promoters exist upstream of the rice \( h_b \) genes which suggests that rice \( h_b \)s are functional and that the regulation of the \( h_b \) genes in this plant is complex. Figure 2 shows the localization of \( h_b \)s in the \( O. \) sativa chromosomes and mapping of \( h_b \)s in the \( O. \) sativa genome. Rice \( h_b1, h_b3 \) and \( h_b4 \) cluster forming the \( h_b1-h_b4 \) cluster which is localized in chromosome 3. Rice \( h_b2 \) is also

**Figure 1.** Early (1991) detection of rice, maize, sorghum and wheat \( h_b \)-like sequences by dot-blot hybridization (R. Arredondo-Peter, unpublished results). Approximately 20 μg of undigested total DNA was used as template and a consensus oligonucleotide for legume and non-legume plant Hbs was used as probe. Sequence of the consensus probe was 5’-GTA GCC TAT GAT GAA TTG GCA GCT GCA-3’. The probe was labeled by nick translation with Biotin-dATP using a Bionick labeling system (Gibco BRL). The membrane was prehybridized with SSC 2x for 4h at 42°C, hybridized overnight at the same temperature. washed at high stringency (SSC 2x/SDS 0.1% for 3 min at room temperature, SSC 0.2x/SDS 0.1% for 15 min at room temperature and SSC 0.16x/SDS 0.1% for 15 min at 65°C) and incubated with the streptavidin-alkaline phosphatase conjugate and the BCIP/NBT mix to develop color. Animal (salmon sperm and calf thymus) and legume DNAs were included as negative and positive controls, respectively.
Figure 2. Localization of hbs in the O. sativa chromosomes (A) and mapping of hb genes into the O. sativa genome (B). The hb genes were localized in the rice chromosomes by BlastN analysis using the rice (O. sativa) genome resource from the GenBank database as template and the sequence for the rice hb1, 3 and 4 (GenBank accession number AF335500,hb2 and 5 (GenBank accession numbers AF335503 and EF061459, respectively) and thb (GenBank accession number NM_001064507) genes as probes. The hb (black boxes) and flanking (gray boxes) genes were mapped into 50 kb fragments of the O. sativa genome by BlastN2.2.26+ analysis using the Phytozome V9.1 server (www.phytozome.org) and the above hb sequences as probes. Arrows indicate the transcription orientation. Information for each gene corresponds to predicted protein (following the Phytozome nomenclature), locus name in the O. sativa genome and position at the O. sativa chromosome. Gene sizes and distance between genes are not shown at scale. Pltd, chloroplast chromosome; MT, mitochondrial chromosome.
localized in chromosome 3 but 467 kb upstream of the *hb1-hb4* cluster. In contrast, rice *hb5* and *hb* genes are localized in chromosomes 5 and 6, respectively (Figure 2A). Rice *hbs* are flanked by a variety of genes with known and unidentified functions (Figure 2B). However, with the exception of genes coding for a ternary complex factor macrophage inflammatory protein MIP1 and an ubiquitin fusion protein which are located 239 and 411 nucleotides up- and downstream of the *hb1-hb4* cluster, respectively, distance of flanking genes to *hbs* is >1 kb. This suggests that co-expression of *hb* and flanking genes is unlikely.

**Gene expression and localization of hemoglobins in rice organs**

The expression of *hb* genes and localization of Hb polypeptides have been analyzed in rice growing under normal and stressed conditions. Under normal conditions the expression level of rice *nshb* was low. However, analysis by RT-PCR revealed that *hb1, hb2* and *hb5* genes were expressed in embryonic and vegetative organs obtained from rice plants grown under a normal environment. Specifically, transcripts for rice *Hb1* were detected in embryos, seminal roots, leaves and roots, transcripts for rice *Hb2* were detected in embryos, coleoptiles, seminal roots and leaves, and transcripts for rice *Hb5* were detected in embryos, coleoptiles, seminal roots, leaves and roots. Likewise, evaluation of the β-glucuronidase (GUS) activity from a construct containing the rice *nshb2* gene promoter that is responsive to the cytokinin-regulated ARR1 trans-acting factor showed that this promoter is activated in roots, the vasculature of young leaves, flowers and the pedicel/stem junction of transgenic *Arabidopsis* in a variety of potential promoters was identified upstream of the rice *nshb* genes, such as those involved in the ethylene synthesis, photoregulation, heat shock response and plant defense signaling. However the activities of these promoters have not been determined.

Transcriptomic analyses revealed that *nsHb* and *tHb* transcripts coexist in rice embryonic and vegetative organs (Table 1). This evidence suggests that *nsHb* (i.e. *Hb1, Hb2, Hb3, Hb4* and *Hb5*) and *tHb* polypeptides coexist and probably function in rice organs. Immunoanalysis by Western blot and confocal microscopy using a polyclonal anti-rice *Hb1* antibody revealed that Hb polypeptides exist in rice seeds and in rice leaves and roots from 2 to 14 weeks after seed germination. These analyses also revealed that Hb polypeptides exist in the cytoplasm of differentiating cells of the root cap, schlerenchyma, aleurone, and in the vasculature, principally in the differentiating xylem. However, the anti-rice *Hb1* antibodies cross-react with different rice Hbs (G. Sarath and E. J. H. Ross, unpublished results) and thus it is not known which Hb polypeptides were detected in the above analyses by the anti-rice *Hb1* antibodies.

It is well documented that land plant *hb* genes are either up- or down-regulated by stress conditions. Table 1 shows that Hb transcripts coexist in rice growing under cold, drought and salt stress conditions. Also, Ohwaki and co-workers reported that *nshb1* and *nshb2* are induced by nitrate, nitrite and NO in cultured rice cells. These observations indicate that rice *hb* genes response to a variety of stress conditions. However, the detection of Hb polypeptides by Western blot using the anti-rice *Hb1* antibodies showed that level of Hbs increased in rice etiolated leaves and flooded roots, but not in rice plants subjected to oxidative (H₂O₂), nitrosative (SNP) and hormonal (2,4-D) stresses. These observations suggest that rice Hbs do not appear to be part of a generalized stress response, but may be functional in plant organs subjected to specific stress conditions.

**Structure and biophysical properties of rice hemoglobins**

**Structure of rice hemoglobins**

Rice *hb* genes are functional and code for Hb polypeptides with a predicted molecular mass of ~16 to 19 kDa. Rice *Hb1* was the first monocot *nsHb* whose crystal structure was elucidated. This protein crystallizes as a dimer, thus it is possible that in *vivo* rice *Hb1* forms dimers when its concentration is ≥1 mM. After the elucidation of the rice *Hb1* structure the tertiary structure of rice *Hb2*, *Hb3, Hb4* and *Hb5* (CASPUR PMDB ID PM0075009, PM0075873, PM0076005 and PM0075011, respectively) was predicted using computational methods and rice Hb1 (PDB ID 1D8U) as the structural homolog. The crystal structure of rice *Hb1* and that of predicted rice *Hb2, Hb3* and *Hb4* is highly similar. The tertiary structure of these proteins consists of six helices that fold into the 3/3-folding (see subsection on *Generalities on hemoglobins*). However, the
The structure of rice Hb1 to 4 is characterized by the existence of a short pre-helix A located at the N-terminal and an extended and poorly ordered CD-loop. The heme pocket in these proteins differs from that in "traditional" Hbs because the proximal and distal His side chains coordinate the Fe-heme forming a hemichrome (Figure 3), resulting in that Fe-heme from rice Hb1 to 4 is hexacoordinate. Also, the amino acid residues (V50, S53, E123, V124, F127 and A128) located at the monomer-monomer interface of dimeric rice Hb1 are highly conserved in rice Hb2 to 4. This suggests that rice Hb1 to 4 can potentially form homo- or hetero-dimers if the hbs1 to 4 genes coexpress in rice organs. The tertiary structure of rice Hb5 also consists of six helices that fold into the 3/3-folding. However, rice Hb5 differs from rice Hb1 to 4 in missing 11 amino acids in helix E which results in that the length of the CD-loop and helix E in the predicted Hb5 structure are unusually long and short, respectively. An apparent consequence from this characteristic is that distal His is located far away (13.92 Å, compared to 2.11 Å in rice Hb1) from the Fe-heme within the predicted Hb5 structure, resulting in that Fe-heme from rice Hb5 could be pentacoordinate. The amino acid residues located at the monomer-monomer interface of dimeric rice Hb1 are poorly conserved in rice Hb5 which suggests that rice Hb5 exists in vivo as a monomer.

The folding pathway and kinetics of rice nsHbs were predicted using the Average Distance Map (ADM) method. This analysis indicated that rice Hb1 and Hb2 could fold in the C→N direction at a moderate rate, that rice Hb3 could fold in the N→C direction at a fast rate, and that rice Hb4 and Hb5 could fold in the N→C direction at a moderate rate. Thus, it appears that the predicted folding pathway and kinetics among rice nsHbs are diverse. Also, the ADM analysis showed that pre-helix A and CD-loop apparently do not play a role during the folding of rice nsHbs. The ADM analysis has not been performed on rice tHb, thus the predicted folding pathway and kinetics for this protein are not known.

Rice (O. sativa) tHb (GenBank accession number NP_001057972) is 172 amino acids in length, which corresponds to a globin domain (position 26 to 147) flanked by N- and C-terminal extensions. No monocot tHb has been analyzed by x-ray crystallography, however the tertiary structure of a rice tHb was predicted using computational methods (Figure 3). The predicted structure of rice tHb is highly similar to the crystal structure of an Arabidopsis thaliana tHb. The globin domain from rice and A. thaliana tHbs folds into the 2/2-folding (see subsection on Generalities on hemoglobins). Similarly to the A. thaliana tHb structure, flanking regions to the globin domain of predicted rice tHb correspond to an N-terminal helical extension and a C-terminal unfolded extension (Figure 3). The high similarity between the crystal structure of A. thaliana tHb and the predicted structure of rice tHb suggests that the biochemical properties and function of dicot and monocot tHbs are similar.

Spectroscopic characteristics of rice hemoglobins

Visible spectroscopy is a tool to analyze the redox state of and ligand-binding to the Fe-heme of Hbs. Rice Hb1 is the only rice nsHb that has been spectroscopically characterized. This protein exhibits spectral characteristics that are similar to other Hbs. However, rice Hb1 exhibits distinctive absorption maxima in the deoxygenferrous form: the unligated ferrous state exhibits maxima at 526 and 556 nm which are characteristic of hexacoordinate...
Fe-heme$^{94}$. This is in contrast to pentacoordinate Hbs which display a broad peak centered at 556 nm in their deoxyferrous form$^{95,96}$. The distal ligand that coordinates the Fe-heme in rice Hb1 was identified as His74 by site directed mutagenesis. Absorbance spectra of the ferric and deoxyferrous forms of an H74L mutant of rice Hb1 showed no evidence of His coordination. Also, the addition of exogenous imidazole to ferric and deoxyferrous H74L mutant resulted in a spectrum identical to that of the wild-type rice Hb1$^{7}$. This evidence indicated that in rice Hb1 the distal ligand to Fe-heme is His74. A similar case can be predicted for rice Hb2 to 4. In contrast, distal His appears to be located far away from the Fe-heme in the predicted structure of deoxyferrous rice Hb5, resulting in that Fe-heme in rice Hb5 could be pentacoordinate$^{75}$.

Rice tHb has not been subjected to spectral analysis, however the predicted structure of this protein (Figure 3) is highly similar to the crystal structure of an *A. thaliana* tHb$^{74}$ (see subsection on Structure of rice hemoglobins). The absorption spectra of an *A. thaliana* tHb showed that Fe-heme is pentacoordinate$^{92,98}$. Thus, it is likely that Fe-heme in rice tHb is pentacoordinate and that the O$_2$-binding properties of rice tHb are similar to those of pentacoordinate Hbs, *i.e.* the O$_2$-association and -dissociation rate constants are high.

**Kinetic properties of rice hemoglobins**

Analysis of ligand-association and -dissociation rate constants of pentatomic and hexacoordinate Hbs using stopped-flow methods indicated that these proteins exhibit low to moderate and high affinity for O$_2$, respectively. Rice Hb1 to 4 are hexacoordinate and apparently rice Hb5 and tHb are pentacoordinate. The O$_2$-association rate constants for hexacoordinate rice Hb1 and 2, and possibly for rice Hb3 and 4, are similar to those of other O$_2$-transport and -storage proteins, such as the spermwhale myoglobin and soybean Lhbs$^{4,16,75,97}$. However, in rice Hb1$^1$ and 2$^{18}$, and possibly in rice Hb3 and 4, the bound O$_2$ is stabilized by distal His after binding to the Fe-heme, which results in very low O$_2$-dissociation rate constants. The O$_2$-association and -dissociation rate constants of hexacoordinate rice Hb1 and 2, and possibly of rice Hb3 and 4, result in that the affinity of these proteins for O$_2$ is extremely high (*e.g.* $K_{O_2} = 1.800$ and 1,316 μM$^{-1}$ for rice Hb1 and 2, respectively$^{16,18}$). In contrast, the O$_2$-association and -dissociation rate constants of pentacoordinate rice Hb5 and tHb could be moderate to high, which could result in a low to moderate affinity for O$_2$.

**Postulated migration routes for gaseous ligands to the Fe-heme in rice Hb1**

The bis-histidyl hexacoordinated form of rice Hb1 displays a hydrophobic distal cavity which appears to be connected with the external solvent through the position of Phe44 (also known as FB10 because it occupies the tenth position in helix B). It was suggested that this amino acid regulates the migration of small ligands in rice Hb1, for example in ligand binding to the Fe-heme, ligand migration through internal docking sites and ligand release into the external solvent$^{99,100}$. Kinetic analysis after laser flash photolysis of rice Hb1 encapsulated in silica gel combined with computational analysis revealed the existence of two channels in the rice Hb1 CO-bound species. The first channel is located in the distal region of the heme pocket and is connected with a secondary channel that is directly connected with the external solvent. Apparently, the position of FB10 in hexacoordinated rice Hb1 leaves the distal heme pocket accessible to the external solvent, however after the ligand entrance the phenyl ring rotates closing the cavity and thus hindering the exit of the bound ligand$^{100}$. Thus, together with distal (H74) His (see subsection Spectroscopic characteristics of rice hemoglobins) and aromatic (F40, F41, F55, F57, Y145 and L126) amino acids that are located in the distal region of the heme pocket, FB10 appears to regulate hexacoordination and functioning of rice Hb1.

**Postulated functions for rice hemoglobins**

While data on the localization, kinetics, regulation and structure of rice Hbs have accumulated, little work has been performed to fully understand the function of these proteins in rice organs. However, previous work from other plant and non-plant Hbs provides data that enable us to propose potential functions for rice Hbs. Rice Hbs could potentially function within cells through O$_2$-transport and -signaling, binding to small molecules (most notably NO) and other as yet undetermined mechanisms. Here we evaluate the evidence for and against these modes of action.

Oxygen transport is a major function of many Hbs. This process requires that the kinetics of O$_2$-binding do not limit the O$_2$-diffusion process$^{200,204}$. Based on the concentration of Hb polypeptides in rice organs (~50 to 100 nM)$^{93}$, the O$_2$-association rate constant of rice Hb1 and 2 (68 and 50 μM$^{-1}$ s$^{-1}$, respectively$^{207,208}$) and possibly that of rice Hb3 to 5 and tHb (see subsection Kinetic properties of rice hemoglobins), and the free O$_2$ concentration in aerated rice roots (<1.4 μM)$^{107}$, it is likely that Hbs would be substantially oxygenated in rice organs. However, the O$_2$-dissociation rate constants of rice Hb1 and 2 ($k_{O_2} = 0.038$ s$^{-1}$, 18), and possibly that of rice Hb3 and 4, are extremely low. These data do not support the O$_2$-transport function for rice Hb1 to 4 because these proteins would not release O$_2$ after oxygenation. In contrast, the predicted kinetic constants for rice Hb5 and tHb suggest that these proteins bind and release O$_2$ easily and thus that they function by transporting O$_2$.

It was reported that hexacoordinate Hbs interact with either organic molecules or protein partners$^{31,38}$ and thus a possibility is that such interactions could impact the kinetic constants, particularly the O$_2$-dissociation rate constants, of hexacoordinate nHbs$^{106}$. There have been no direct biochemical evaluations of this hypothesis in rice or in other plants, precluding definitive answers. However, their unique structural features could result in as yet undiscovered interactions.

Rice Hbs may function in O$_2$-signaling if they easily bind and release O$_2$. Appleby and co-workers’ proposed that under normal conditions Hbs would be oxygenated and under O$_2$-limiting conditions the concentration of deoxyHb would increase triggering an anaerobic response. It was reported that levels of Hbs increase in rice roots from flooded plants indicating that the synthesis of rice Hbs increases under O$_2$-limiting conditions$^{35}$. Rice is a flooding resistant crop, thus under flooding (*i.e.* hypoxia) conditions rice Hbs could sense low O$_2$-concentrations and trigger an anaerobic metabolism for rice growth. To act as a signaling molecule, rice Hbs will need to bind directly to the DNA, to additional proteins, such as transcription factors, or catalyze some unique reactions that
can influence key downstream events. To date there are no reports of immunoprecipitation experiments specially targeting rice Hbs coupled to further proteomic analysis. It is thus uncertain if rice Hbs bind to other partners. There is also no structural evidence that indicates that rice Hbs can bind directly to DNA. In planta, they appear to be soluble and essentially contained within the cytoplasm\(^\text{100}\). There are reports of nuclear-localized Hbs\(^\text{107}\), but no direct evidence for a function arising from translocation of Hbs from the cytoplasm to the nucleus currently exist.

The NO dioxygenase activity exhibited by Hbs is well documented\(^\text{108-110}\). NO is a hormone-like radical that modulates several aspects of the plant physiology, including plant immunity, seed germination, de-etiolation, apoptosis, stomata guard cells opening/ closure and the rhizobia-legume symbiosis\(^\text{111-112}\). Scavenging of NO is considered a function of plant Hbs\(^\text{113,123-126}\). During this process, oxygenated plant Hbs react with NO producing nitrate and oxidizing ferrous Hb to the ferric form. Ferric plant Hbs are subsequently reduced to ferrous Hb by enzymatic\(^\text{127,128}\) and non-enzymatic\(^\text{129-133}\) mechanisms. This process regenerates ferrous Hb which is able to bind NO in a cyclic pathway referred to as the Hb/NO cycle\(^\text{126,134}\). The operation of this cycle appears to be involved in maintaining an active metabolism in the plant cells\(^\text{135}\). Rice Hb1 exhibits NO dioxygenase activity\((k_{\text{cat, SOD}} = 90\ \text{s}^{-1})\)\(^\text{136}\) thus a possible function of Hbs into the rice physiology is modulating levels of reactive oxygen species by scavenging NO. However, the inability of rice Hb1 to substitute the NO scavenger activity in a flavohb knockout Escherichia coli\(^\text{137}\) and the observation that levels of Hbs did not change in rice seeds germinated under nitrosative stress\(^\text{138}\) suggest that the NO dioxygenase activity of rice Hbs is limited in vivo.

A consequence of the operation of the Hbs/NO cycle could be the maintenance of cell respiration and energy status. Based on the studies on over- and under-expressing barley nsHb in maize cells, it was proposed that under hypoxic conditions barley nsHb is involved in the ATP metabolism, particularly in maintaining the energy status under O\(_2\)-limiting conditions\(^\text{139}\). Immuno localization data showed that rice Hbs are localized in differentiating cells (see subsection on Gene expression and localization of hemoglobins in rice organs\(^\text{140}\)). The metabolism of these cells is redirected in response to differentiation signals, such as a change in the cell redox state. Rice Hbs could be involved in redox signaling if the redox state of the heme is functional\(^\text{141}\). Thus, under these conditions rice Hbs may function by sensing or maintaining redox environments that promote specific cell metabolisms\(^\text{142}\).

It was proposed that one of the functions of plant Hbs could be related to the peroxidase activity\(^\text{143,146}\). This is of interest because peroxidase activity modulates the levels of reactive oxygen species and a variety of cellular processes\(^\text{147-149}\). In plants, evaluation of the peroxidase activities of Arabidopsis Hbs (AtGLB1, AtGLB2 and AtGLB3) revealed that these proteins oxidize Amplex Red, DHR123 and guaiacol substrates\(^\text{144}\) and overexpression of AtGLB1 increased tolerance of Arabidopsis to H\(_2\)O\(_2\) stress\(^\text{145}\). These observations suggested that Arabidopsis Hbs function as antioxidants. However, levels of Hb polypeptides did not change in rice seeds germinated under H\(_2\)O\(_2\) stress\(^\text{146}\). Also, the analysis of the peroxidase activity of rice Hb1 compared to that from horseradish peroxidase (HRP) showed that the catalytic efficiency of rice Hb1 for the oxidation of guaiacol using H\(_2\)O\(_2\) as electron donor is several orders of magnitude lower than that of HRP\((k_{\text{cat}}/K_m = 15.8 \text{ and } 44,833\ \text{mM}^{-1}\text{min}^{-1}\))\(^\text{147}\). Additionally, it was observed that recombinant rice Hb1 poorly protects E. coli from H\(_2\)O\(_2\) stress\(^\text{148}\). This evidence indicates that it is unlikely that rice Hbs function in vivo as peroxidases.

Based on gene expression (Table 1), protein localization and structural and kinetic properties of rice Hbs and data from the analysis of other plant and non-plant Hbs it is likely that Hbs play a variety of roles in rice plants growing under normal and stressed conditions. These functions may include O\(_2\)-transport, O\(_2\)-sensing, NO-scavenging and redox-signaling. Future work on rice Hbs should focus on testing the above potential functions as well as newly proposed functions that emerge from novel observations.

### Evolution of rice hemoglobins

Hbs are widely distributed in land plants, ranging from primitive bryophytes to evolved angiosperms\(^\text{6}\). The outline of plant Hb evolution subsequent to land colonization was clarified\(^\text{15}\). Briefly, a phylogenetic analysis showed that plant and animal hb genes diverged 900-1,400 mya, that land plant nshb and hb genes vertically evolved through different lineages from algal ancestors, that nsHbs-1 and nsHbs-2 are monophyletic and evolved via a gene duplication event prior to the divergence of monocots and dicots at ca. 140 mya, and that symbiotic hbs originated from nshb genes at ca. 94 mya. Likewise, the structural analysis of primitive nsHbs and Lbs revealed that changes during the evolution of nsHbs to Lbs were a hexacoordinate to pentacoordinate transition at the heme prosthetic group, a length decrease at the CD-loop and N- and C-terminal regions, and a compaction of the protein into a globular structure\(^\text{11,14}\).

In contrast, the evolution of rice Hbs is partially understood owing to the limited availability of Hb sequences from a wide variety of wild and cultivated rice. However, the outline of monocot Hb evolution is rather well understood. Thus, in this section we will discuss the evolution of rice Hbs within the context of major events that occurred during the evolution of monocot Hbs. A major event during the evolution of land plant nsHbs was the duplication of an ancestral nshb into nshb-I and nshb-2 prior to the monocot-dicot divergence\(^\text{14,146}\). Sequence analysis revealed that nshb-I and nshb-2 genes exist in dicots and that apparently only nshb-I genes exist in monocots\(^\text{9,34,14}\). Earlier Garrocho-Villegas and co-workers\(^\text{75}\) reported the existence of a nshb (Hb5) divergent from rice (Hb1 to 4) nsHbs-1 and suggested that nsHbs divergent from nsHbs-1 evolved within monocots. Subsequent phylogenetic analysis of monocot nshb sequences revealed that apparently only nshb-I evolved within monocots, that nshb-I duplicated early in the evolution of monocots originating clade I and clade II nshbs (nshbs-I and nshbs-II, respectively), that nsHbs-I correspond to dicot nsHbs-1, and that nsHbs-II diversified into regular nsHbs-II, post-helix H-containing nsHbs-II and 11 amino acids deletion-containing nsHbs-II\(^\text{10}\). This analysis also showed that O. sativa var. indica and O. sativa var. japonica Hb1 to 4 and Hb5 cluster within clade I and clade II, respectively, and that O. glaberrima and O. rufipogon (whose all nshb copies remain unidentified because their genome sequencing is in progress) nsHbs cluster within clade I. Thus, apparently clade I and clade II lineages remain conserved during the evolution of rice nsHbs\(^\text{10}\).

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Evaluation of the rate of divergence of selected land plant Hbs revealed that evolutionary rates slowed down previous to the origin of magnoliophyta and that the rate of divergence was slower in rice Hb1 than in rice Hb5 [10]. This observation suggested that rice Hb1 (and conceivably other rice nsHbs) evolved under the effect of the stabilizing selection. However, the estimation of the variability of the O. sativa var. indica, O. sativa var. japonica, O. glaberrima and O. rufipogon nsHb and thb genes revealed that in these plants variability is higher in nsHbs than in thbs and that these genes evolved under the effect of neutral selection[61]. Currently the effect of rates of divergence and gene variability on the Hbs function during the rice evolution is not known.

Concluding remarks and future directions
In the preceding sections of this review we summarized major findings from the study of rice Hbs. This review also reveals some major lacunae in our ability to completely understand rice Hbs, more specifically the lack of information about the precise functions of Hbs in rice organs. The proposed functions for rice Hbs are mostly based on the analysis of other plant and non-plant Hbs. Thus, future work should evaluate the Hb activities (e.g. the NO-binding and -detoxifying activities) in either rice organs or rice cell cultures under a variety of growing conditions. Elucidating the functions of rice Hbs also requires the identification of either homo- or heterodimeric rice Hbs and possible organic molecules and protein partners that interact with rice Hbs. Other lacunae are the absence of biochemical, biophysical and cellular data on the properties of rice Hb2 to 5 and Hb. Generating recombinant rice Hb2 to 5 and Hb should provide Hb polypeptides for a variety of analyses that reveal the biochemical and biophysical properties of these proteins.

With the exception of rice hb2, a lacuna is the absence of experimental information about the cis-elements and trans-acting factors that regulate the expression of rice hbs. This information may help to integrate the hb gene expression into the rice metabolisms, including those that are modulated by plant hormones.

A final lacuna is the incomplete understanding of the evolution of rice Hbs. Sequencing of the O. glaberrima and O. rufipogon genomes will be completed soon and most likely a number of rice genomes (including that of O. barthii, which is postulated as the ancestor of O. glaberrima [92,151,152]) will be sequenced within the near future. This will provide new Hb sequences for phylogenetic analysis and the understanding of the evolution of rice Hbs, including the identification of ancestral rice Hbs and the evaluation of the effect of rice domestication and breeding during the evolution of rice Hbs.

Author contributions
RAP conceived the review and prepared the first draft of the manuscript. RAP, JFM and GS were involved in the revision of the draft manuscript and prepared the final version.

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References

method. Of residue contacts. (computer) methods to predict and analyze the tertiary structure of plant symbiotic hemoglobin genes by nitrate, nitrite and nitric oxide in cultured rice

PubMed Abstract

98 to truncated hemoglobins of microorganisms. hemoglobin. PubMed Abstract

2001; Oryza sativa

Integr Biol. PubMed Abstract

symbiotic haemoglobin-2 promoter by the cytokinin-regulated transcription structural analysis of a rice (Oryza sativa) hemoglobin 5. PubMed Abstract


60. Wittenberg JB: Nitric oxide in plants: To NO or not to NO. F1000Research 2014, 3:253 Last updated: 27 OCT 2014


