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**The Interplay Between Iron, Haem and Manganese in *Porphyromonas gingivalis***

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## Abstract

*Background:* Transition metals including iron and manganese are necessary for life because of their ability to donate and accept electrons. Approximately one third of all proteins require essential transition metal ions to perform catalytic, structural and regulatory functions. These essential metal ions react differently to the presence of oxygen radicals with iron directly involved in the formation of toxic reactive oxygen species, whilst manganese can protect against oxidative stress.

*Highlight:* Anaerobic bacterial species have been poorly studied with regard to transition metal homeostasis and behave differently in many respects when compared with aerobic or aerotolerant species. To optimize catabolism whilst protecting themselves from unwanted reactions bacterial cells must maintain intracellular metal levels in a very narrow range that varies, dependent on the environment. To maintain metal ion homeostasis, bacteria have evolved complex regulatory mechanisms of metal uptake, secretion and storage. In this review we examine how iron, haem and manganese availability dictate the lifestyle and virulence of the anaerobic Gram-negative, periodontal pathogen *Porphyromonas gingivalis*.

*Conclusion:* *P. gingivalis* has novel haem, iron and manganese transporters and metalloregulatory proteins that enable it to switch rapidly between an energy efficient iron-dependent virulent phase and a protective manganese-dependent survival phase.

**Key words:** *P. gingivalis*; metal ion homeostasis; virulence; survival

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## 1. Introduction

Chronic periodontitis is the most common of the destructive periodontal diseases amongst adults and its prevalence and severity increase with age. The global age-standardised prevalence of severe periodontitis between 1990 and 2010 was 11%, however the exact percentage varies between and within countries [1-3]. In the USA, 38% of the adult population 30 years and older and 65% of adults 65 years and older have either severe or moderate periodontitis [4, 5]. Epidemiological surveys have shown that clinical indicators of chronic periodontal disease are associated with a greater risk of certain cancers such as squamous cell carcinoma of the head, neck, and oesophagus [6], cancer of the tongue [7] and pancreatic cancer [8-10]. There is also a relationship between chronic periodontitis and systemic diseases and disorders such as cardiovascular disease [11], preterm and underweight birth [12], systemic inflammation in solid-organ transplant recipients [13], diabetes and rheumatoid arthritis [11, 14-16].

The bacterial aetiology of chronic periodontitis is acknowledged to be polymicrobial in nature. Whilst the concepts of the roles of particular oral bacterial species in disease have changed over the past two decades, there is consensus that the anaerobic, proteolytic, amino acid fermenting species *Porphyromonas gingivalis* plays a significant role in either initiation or progression of disease [17-20]. Based on animal model data *P. gingivalis* has recently been proposed to be a “keystone pathogen” that manipulates the host response to favour the proliferation of a pathogenic polymicrobial biofilm (dysbiosis) and development of disease [19]. We have previously demonstrated in a longitudinal human study that the imminent progression of chronic periodontitis could be predicted by increases in the relative levels of *P. gingivalis* and/or *Treponema denticola* in subgingival plaque [21], which is consistent with other clinical studies demonstrating that *P. gingivalis* levels in subgingival plaque are

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4 predictive of human disease progression [22-24]. *P. gingivalis* is also capable of causing  
5  
6 periodontitis in animal models of disease [25, 26].  
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9

## 10 11 **2. Divalent metal cations** 12

13 All living cells acquire transition metal ions to meet their basic cellular needs, with  
14 iron, manganese, copper, zinc, nickel and cobalt being of greatest physiological relevance  
15 [27, 28]. It has been estimated that about one third of all proteins require essential transition  
16 metal ions to perform catalytic, structural and regulatory functions [29, 30]. Metals such as  
17 iron, copper, chromium, manganese and cobalt are capable of redox cycling in which a single  
18 electron may be accepted or donated by the metal. These actions catalyse reactions that play  
19 critical roles in the function of many organisms but may also produce reactive radicals and  
20 reactive oxygen species [31-34].  
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31 Iron ( $\text{Fe}^{2+}/\text{Fe}^{3+}$ ) is an obligate requirement for the vast majority of bacteria as it is a  
32 versatile prosthetic component incorporated into many proteins as a biocatalyst or electron  
33 carrier [35, 36]. It has a role as a prosthetic group in many biological enzymatic systems  
34 including cytochromes, RNA polymerase and various amino acid hydrolases [37, 38].  
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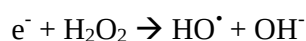
41 Manganese is also essential with greater than 20 identified functions in enzymes and  
42 proteins involved in metabolism, signal transduction and as a stimulus for virulence gene  
43 regulation [36, 39-44]. It is a key cofactor of many metalloenzymes including oxidases and  
44 dehydrogenases, DNA and RNA polymerases, kinases, sugar transferases and decarboxylases  
45 [45].  
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52  $\text{Mn}^{3+} + \text{e}^- \rightleftharpoons \text{Mn}^{2+}$  has a standard reducing potential of +1.51 V, higher than  $\text{Fe}^{3+} + \text{e}^-$   
53  $\rightleftharpoons \text{Fe}^{2+}$  whose standard reducing potential is +0.77 V, thus  $\text{Mn}^{2+}$  has a lower potential to  
54 donate an electron compared with  $\text{Fe}^{2+}$  and thereby a lower potential to reduce other  
55 molecules [41]. Although manganese has similar characteristics to iron being a transition  
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4 metal capable of cycling readily *in vivo* between the +2 and +3 oxidation states [41], instead  
5  
6 of catalyzing oxidative damage like iron, manganese can protect cells against oxidative  
7  
8 damage via enzyme-dependent and protein-independent mechanisms [46, 47]. Manganese  
9  
10 appears to play a significant role in oxidative defence systems in most pathogenic bacteria  
11  
12 [46].  
13  
14

### 15 16 17 18 **3. Oxidative stress**

19  
20 Stepwise reduction of molecular oxygen (O<sub>2</sub>) by high-energy exposure or electron-  
21  
22 transfer reactions leads to production of highly reactive oxygen species (ROS). The  
23  
24 conversion of atmospheric oxygen to ROS occurs inside actively respiring aerobic or  
25  
26 facultative bacterial cells [48]. However, few ROS are generated intracellularly by anaerobic  
27  
28 bacteria due to the absence of molecular oxygen in their environment. Commensal and  
29  
30 pathogenic bacteria can also be exposed to the oxidative burst of macrophages and  
31  
32 neutrophils of the host inflammatory immune response [49]. Transition metal ions can play a  
33  
34 major role in the exacerbation or relief of oxidative stress. Most biological molecules cannot  
35  
36 be damaged at a significant rate by direct reactions with molecular oxygen, superoxide anion  
37  
38 (O<sub>2</sub><sup>-</sup>) [50, 51] or hydrogen peroxide (H<sub>2</sub>O<sub>2</sub>) [52]. However, they can be oxidized by the highly  
39  
40 reactive hydroxyl radical (HO•). This species is formed when a single electron is transferred  
41  
42 to hydrogen peroxide.  
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46  
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48  
49 *In vivo* the most facile donor of single electrons to H<sub>2</sub>O<sub>2</sub> is the transition metal, ferrous  
50  
51 iron (Fe<sup>2+</sup>) via the Fenton reaction [53].  
52



54  
55  
56  
57 This reaction is driven to the right by the subsequent formation of poorly soluble  
58  
59 Fe(OH)<sub>3</sub>. The hydroxyl radicals formed are extremely damaging for cellular components such  
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as nucleic acids (both DNA and RNA), proteins and lipids [35]. The presence of such metals in an uncomplexed form in biological systems can significantly increase the level of oxidative stress.

Living organisms use defence systems to maintain the concentration of O<sub>2</sub>-derived radicals at acceptable levels or repair any damage caused by the toxic ROS [36]. These oxidative stress protection systems also utilise transition metal ions, in particular manganese ions, as co-factors for metalloenzymes that defend against reactive oxygen species.

It is not surprising that some bacteria have evolved metabolic and survival strategies that minimize oxidative damage by acquiring Mn<sup>2+</sup> instead of Fe<sup>2+</sup>/Fe<sup>3+</sup>. *Borrelia burgdorferi*, the etiological agent of Lyme disease and *Lactobacillus plantarum*, a probiotic bacterium were found to be free from Fe<sup>2+</sup> requirements for their growth [42, 44]. Manganese was demonstrated to be the most essential divalent cation for these bacteria instead of iron [42, 44]. The absence of iron in these bacteria may be an advantage, as they are able to overcome the iron limitation found in most hosts and there is no requirement to minimize oxygen free radicals generated from the Fenton reaction [44]. However Mn<sup>2+</sup> has a lower potential to donate an electron compared to Fe<sup>2+</sup>, thus limiting its effectiveness as a metabolic enzyme cofactor.

#### 4. *Porphyromonas gingivalis*

*P. gingivalis* is a Gram-negative, sessile, obligate anaerobe that has an absolute requirement for iron and its growth and virulence are dependent on the availability of iron complexes such as haem [54-57] or ferrous iron [58]. In addition *P. gingivalis* cannot synthesize protoporphyrin IX [59], a porphyrin derivative that combines with ferrous iron to form haem, a cofactor for several enzymes, which can be bound transiently [60], or remain bound to the protein permanently [61].



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4 *P. gingivalis* relies on the anaerobic fermentation of amino acids for energy production,  
5  
6 which requires a number of iron-containing proteins that are involved in redox reactions (Fig.  
7  
8 1). The *P. gingivalis* W83 genome contains at least 20 genes encoding predicted non-haem,  
9  
10 iron-sulphur proteins with similarity to ferredoxins and other iron-containing enzymes. These  
11  
12 include the fumarate reductase iron-sulfur subunit FrdB (PG1614), an iron-containing alcohol  
13  
14 dehydrogenase 4hbD (PG0689), the indolepyruvate ferredoxin oxidoreductase IorA and IorB  
15  
16 (PG0675, PG0674), the pyruvate ferredoxin/flavodoxin oxidoreductase family protein  
17  
18 (PG0548), an iron-dependent fumarate hydratase FumB (PG1417) and a range of putative,  
19  
20 uncharacterised ferredoxins (PG0472, PG1172, PG1421, PG1813). Some of these enzymes  
21  
22 have been demonstrated biochemically to be involved in amino acid fermentation in *P.*  
23  
24 *gingivalis* [62, 63]. The ferredoxins each contain two or more 4Fe-4S clusters.  
25  
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27  
28  
29 Several *P. gingivalis* proteins have been predicted to form complexes as part of the  
30  
31 respiratory chain of this organism for the production of ATP [64]. These include the sodium-  
32  
33 dependent NADH: ubiquinone oxidoreductase ( $\text{Na}^+$ -Nqr) complex composed of NqrA-F  
34  
35 (PG2182-2177) which is the main ion pump and primary entry site for electrons into the  
36  
37 respiratory chain [64, 65]. The Nqr complex mediates electron transfer from NADH to  
38  
39 quinone, and uses iron as a redox cofactor in the 2Fe-2S centre of NqrF [65].  
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41

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43 Although there is little known about the function of the Rnf complex (RnfABCDGE;  
44  
45 PG0303-0308) in *P. gingivalis*, characterisation in other anaerobic bacteria has shown it  
46  
47 mediates electron transfer from ferredoxin to  $\text{NAD}^+$  [66] and utilises six 4Fe-4S clusters and  
48  
49 two 4Fe-4S clusters as cofactors in RnfB and RnfC, respectively [65]. Due to the large  
50  
51 amount of iron required by this complex, genes encoding Rnf proteins are down-regulated  
52  
53 when *P. gingivalis* is grown in iron-limited conditions [67].  
54  
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56  
57 Fumarate reductase, FrdBAC (PG1614-1616), is a trimeric enzyme complex belonging  
58  
59 to the succinate:quinone oxidoreductase (SQOR) family that couples the reduction of  
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61

fumarate to succinate to the oxidation of quinol to quinone during anaerobic respiration [64]. This facilitates the formation of a proton/sodium gradient across the inner membrane coupled to ATP generation [64]. FrdB contains a 2Fe-2S, a 4Fe-4S and a 3Fe-4S cluster, whilst FrdC contains two haem molecules [62] and appears to be the main user of haem as a redox cofactor in the anaerobic respiratory chain of *P. gingivalis* [64]. Inhibition of fumarate reductase activity by oxantel pamoate stopped the growth of the bacterium and strongly inhibited biofilm formation, demonstrating the essential role of this enzyme in *P. gingivalis* metabolism [68, 69].

## 5. Metal acquisition systems of *Porphyromonas gingivalis*

*P. gingivalis* like most anaerobic bacteria does not produce siderophores to scavenge environmental iron or compete with transferrin or lactoferrin for ferric iron binding [70]. *P. gingivalis* utilises human transferrin as a source of iron and peptides via proteolytic cleavage by the cell surface Arg- and Lys-specific cysteine proteinases, RgpA/B and Kgp, collectively known as gingipains [71, 72]. In the absence of gingipains *P. gingivalis* cannot remove the iron from transferrin [71]. The resulting degradation products of transferrin can catalyse the formation of a highly reactive hydroxyl radical (OH<sup>•</sup>), due to the fragments containing iron or due to the release of iron [72].

*P. gingivalis* has been reported to have a high-affinity receptor which binds lactoferrin before complete cleavage by the gingipains [73]. Lactoferrin does have an inhibitory effect on bacterial growth due to its ability to sequester iron [74], and it also has an antimicrobial domain at the N-terminus, which when isolated has potent bactericidal activity [75]. Bovine lactoferrin inhibits *P. gingivalis* planktonic growth and biofilm formation [76] which may in part be due to its sustained inhibition of the gingipains which are required for biofilm formation [77].

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4 Haem is preferentially obtained by *P. gingivalis* from haemoglobin and is acquired  
5  
6 through the activity of the gingipains [78-80] and other haem-binding proteins that some  
7  
8 researchers have proposed act as haemophores [81]. Haemophores are specialized bacterial  
9  
10 proteins that are secreted from the cell and released into the environment which then acquire  
11  
12 haem and facilitate uptake through a specific cell surface transporter [82]. Although the  
13  
14 gingipains have been shown to cleave haemoglobin and the HA2 domain of the gingipains  
15  
16 Kgp and RgpA and the haemagglutinin HagA binds haemoglobin or haem via an iron-  
17  
18 independent mechanism that recognises the porphyrin ring [81, 83, 84], these proteins are  
19  
20 covalently attached at the cell surface but are released by *P. gingivalis* on outer membrane  
21  
22 vesicles (*vide infra*) [85].  
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26  
27 In fact, *P. gingivalis* produces a range of haem-binding lipoproteins anchored to the  
28  
29 outer membrane (Fig. 2). The best studied example is HmuY, which uses two His residues to  
30  
31 bind haem or haemin in a 1:1 molar ratio [86, 87] and is part of a haem acquisition  
32  
33 mechanism with HmuR, a TonB-linked outer-membrane receptor involved in haem transport  
34  
35 through the outer membrane [84, 88]. The proposed mechanism of action of the  
36  
37 HmuY/HmuR acquisition system is that HmuY scavenges haem liberated by the cleavage of  
38  
39 host haem-carrier proteins by the gingipains [87, 89]. Binding of haem leads to  
40  
41 tetramerisation of HmuY, protecting the haem from host scavengers [87]. HmuR then induces  
42  
43 disruption of the HmuY tetramer via its His axial ligands to enable haem transfer [87]. Haem  
44  
45 is then passed through the outer membrane HmuR to the periplasm where it is transported  
46  
47 from the periplasm to cytoplasm, presumably by the other *hmu* operon proteins HmuSTUV  
48  
49 (Fig 2.) [90]. Expression of the entire *hmu* locus is upregulated under haemin-limited growth  
50  
51 [62].  
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57 More recently, the novel haem binding protein HusA has been identified in *P.*  
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59 *gingivalis* and was found to have more than 1,000-fold greater affinity for haem than HmuY.  
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4 With this high haem binding affinity and a fast haem association rate HusA could compete  
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6 directly with host haemoproteins such as serum albumin [91]. HusA has a preference for  
7  
8 dimeric haem and may serve as the predominant bishaem chelating protein under low haem  
9  
10 growth conditions [91]. Like HmuY, HusA is bound to the cell surface and once dimeric  
11  
12 haem is bound, is proposed to deliver haem to HusB, an integral outer membrane protein for  
13  
14 transport to the periplasm (Fig. 2) [91].  
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17  
18 Several other haemin binding outer membrane proteins in *P. gingivalis* have been  
19  
20 described including OMP26, OMP32, HBP35, HtrE (Tlr) and IhtB, many of which are  
21  
22 expressed under low haemin growth conditions (Fig. 2) [62, 92-96]. The lipoprotein IhtB is  
23  
24 an outer membrane haemin-binding ferrochelatase [93] homologous to a precorrin-2 cobalt  
25  
26 chelatase [59]. The close proximity of the *ihtB* gene to a gene encoding a predicted TonB-  
27  
28 linked outer membrane protein (IhtA) led to the proposal that IhtB removes iron from haem  
29  
30 prior to IhtA-mediated iron transport through the outer membrane [93].  
31  
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33  
34 HtrE (Tlr) is a TonB-linked outer membrane transporter that is essential for growth at  
35  
36 low concentrations of haemin [95]. The gene encoding HtrE is located adjacent to an operon  
37  
38 encoding a putative ATP binding cassette transport system with sequence similarity to haem  
39  
40 transport systems of other bacteria, thus together, these genes may encode a haem transport  
41  
42 system [95]. The PG1019-1020 locus of *P. gingivalis* encodes a predicted outer membrane  
43  
44 lipoprotein and an outer membrane TonB-linked receptor respectively that are greatly  
45  
46 increased in abundance during haem-limitation [62] and iron-limitation [67], also suggesting  
47  
48 a role in haem/iron transporter (Fig. 2).  
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51  
52 Strikingly, many of the outer membrane components of these putative iron-complex  
53  
54 transport systems are composed of a haem-binding lipoprotein coupled with a TonB-linked  
55  
56 transmembrane transporter (Fig. 2). A proteomics-based study of the outer membrane  
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58 vesicles (OMVs) produced by *P. gingivalis* indicated that the lipoproteins HmuY and IhtB  
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4 were preferentially packaged onto the vesicle surface whilst their cognate TonB-linked  
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6 receptor proteins HmuR and IhtA remained on the cell surface [85]. The increased abundance  
7  
8 of these haem binding lipoproteins and the gingipains on OMVs suggests that OMVs may  
9  
10 extend the functionality of these proteins and that *P. gingivalis* OMVs may be important for  
11  
12 haem acquisition by acting as haemophores [85]. For example, the release of OMVs  
13  
14 containing the gingipains from the biofilm on the tooth root into the gingival tissue has been  
15  
16 suggested to play a role in vascular disruption and immune dysregulation [85, 97, 98].  
17  
18 Through the concerted action of the gingipains and haem-binding proteins in the tissue the  
19  
20 OMVs may become loaded with haem. The resulting inflammation and gingival exudate  
21  
22 could then return the loaded vesicles back to the biofilm allowing haem transfer to the  
23  
24  
25  
26  
27 biofilm cells.

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29 *P. gingivalis* like many other Gram-negative bacteria transports ferrous ion across the  
30  
31 cytoplasmic membrane using the transmembrane FeoB protein, FB1 [58, 99]. FeoB proteins  
32  
33 are 700-800 amino acids in length and have a cytoplasmic G protein domain directly tethered  
34  
35 to a polytopic membrane domain [100]. GTP binding to the G protein domain initiates the  
36  
37 transport of  $\text{Fe}^{2+}$  across the membrane, which is completed by the hydrolysis of GTP to GDP.  
38  
39 The GTPase activity of FeoB is activated by  $\text{K}^{+}$  which leads to a 20-fold acceleration in its  
40  
41 hydrolysis rate, bringing it close to the active transport rate of hydrolysis of the ATP-binding  
42  
43 cassette transporters [101]. FB1 is the only ferrous ion transporter in *P. gingivalis* as  
44  
45 inactivation of this transporter abolished ferrous ion transport and the iron content of the  
46  
47 mutant was half that of the wild-type (Fig. 2) [58]. The FB1 mutant was avirulent in a mouse  
48  
49 model of disease indicating the importance of this transporter to the *in vivo* survival of *P.*  
50  
51 *gingivalis* [58].

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57 The major manganese transporter in *P. gingivalis* has been identified as a FeoB  
58  
59 transport protein homologue called FB2 that had likely arisen by gene duplication [58]. FB2  
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4 was found to contribute to the survival of *P. gingivalis* in human umbilical vein endothelial  
5  
6 cells (HUVECs) [102]. Although the full mechanism has not been elucidated, it is the  
7  
8 acquisition of manganese that is required for intracellular survival of *P. gingivalis* in host  
9  
10 cells [102].  
11  
12

13 Little is known about the translocation of manganese and other divalent cations across  
14  
15 the outer membrane and into the periplasm; it was generally thought that they would diffuse  
16  
17 through porins in the outer membrane [103, 104]. However, it was recently demonstrated in  
18  
19 *Bradyrhizobium japonicum* that  $Mn^{2+}$  does not diffuse through the outer membrane but is  
20  
21 transported through a selective outer membrane channel that is expressed specifically under  
22  
23 manganese limitation [105]. The gene encoding this outer membrane channel was in the same  
24  
25 operon as the gene encoding the inner membrane  $Mn^{2+}$  transporter in this organism, MntH,  
26  
27 ensuring co-ordinated expression of the whole transport system [105]. Such an outer  
28  
29 membrane channel has not been identified in *P. gingivalis*, nor is there an outer membrane  
30  
31 protein predicted to be encoded in the same operon as the  $Mn^{2+}$  transporter FB2.  
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36 Whilst examining the *P. gingivalis* W50 global pattern of protein and transcript  
37  
38 abundances in response to haem-limitation in continuous culture, 160 genes and 70 proteins  
39  
40 were found differentially regulated by haem availability, with broad agreement between the  
41  
42 transcriptomic and proteomic data (Fig. 1) [62]. Haem-limitation caused upregulation of a  
43  
44 number of gene products in *P. gingivalis* that are linked to metabolism, oxidative stress  
45  
46 response, virulence and invasion of host cells [62]. A change in abundance of the iron and  
47  
48 haem containing enzymes of the aspartate and glutamate catabolic pathways was observed  
49  
50 during haem-limitation which was reflected in organic acid end products. This included  
51  
52 down-regulation of the fumarate reductase which is essential for energy production [62, 64].  
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57 There was a notable increase in expression of two haem transport systems encoded by  
58  
59 the *hmu* and *htr* operons, as well as a large increase in the abundance of alkyl hydroperoxide  
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4 reductase subunits (AhpC, PG0618; AhpF, PG0619), a peroxide scavenging enzyme shown  
5  
6 to play an important role in peroxide resistance in *P. gingivalis*. Haem-limitation also reduced  
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8 *P. gingivalis* biofilm development with a 56% decrease in biomass and a 78% decrease in  
9  
10 biofilm depth [77].  
11

12  
13 Vascular disruption and bleeding are characteristics of periodontitis, providing a  
14  
15 protein/peptide and iron/haem rich environment for bacterial growth during disease  
16  
17 progression. However, inflamed gingival tissues contain considerable numbers of  
18  
19 polymorphonuclear leucocytes (PMNs) that produce  $O_2^-$  and  $H_2O_2$  as part of their bactericidal  
20  
21 armoury. As a consequence of this the bacterium must have a defence system against  
22  
23 oxidative stress. Under conditions of haem excess the bacterium forms an oxidative shield by  
24  
25 accumulating haem from haemoglobin on the cell surface as  $\mu$ -oxo bishaem which binds  
26  
27 reactive oxygen intermediates, hence maintaining a locally reduced environment [106]. This  
28  
29 haem layer protects the bacterium from direct contact with reactive oxidants generated by  
30  
31 neutrophils in periodontal lesions [106]. This is also a novel way to store reactive iron outside  
32  
33 the cell where it can't cause damage to intracellular components.  
34  
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38 *P. gingivalis* has developed various intracellular oxidative stress defence systems,  
39  
40 including superoxide dismutase (SOD) which can utilise either iron or manganese as co-  
41  
42 factor, [107], the DNA-binding protein from starved cells (Dps) [108, 109], alkyl  
43  
44 hydroperoxide peroxidase subunit C (AhpC) [110] and rubrerythrin (Rbr) [111]. Superoxide  
45  
46 dismutase (SOD) is the only known *P. gingivalis* oxidative defence system which requires  
47  
48 manganese as a cofactor, however, the intracellular accumulation of manganese itself has  
49  
50 been shown to have anti-oxidative properties, protecting *P. gingivalis* from atmospheric  
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52 oxygen and hydrogen peroxide [102].  
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## 59 **6. The polymicrobial biofilm nature of health and disease**

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4 *P. gingivalis* is a normal component of the human oral microbiota and is a late  
5  
6 colonizer of polymicrobial oral biofilms, relying on complex interactions with a range of  
7  
8 other oral bacteria including *Streptococcus gordonii*, *Fusobacterium nucleatum*, *Tannerella*  
9  
10 *forsythia* and *T. denticola* [112-114]. Therefore although much has been learnt by studying *P.*  
11  
12 *gingivalis* in isolation, its interactions with other bacterial species in the biofilm will have a  
13  
14 considerable influence on its role as an opportunistic pathogen in inducing dysbiosis and  
15  
16 disease. For example results from a polymicrobial biofilm analysis showed a decrease in  
17  
18 abundance of HtrE (Tlr), IhtB, HmuY and fumarate reductase which could possibly be due to  
19  
20 the cross feeding of succinate from *T. denticola* to *P. gingivalis* thereby reducing the need for  
21  
22 haem (Fig. 1), or due to reduced growth rates in the biofilm [115]. This is in contrast to  
23  
24 findings in a monospecies biofilm, which would have a similar growth rate to a polymicrobial  
25  
26 biofilm, where HmuY was more abundant than in planktonic cells [116]. Commensurate with  
27  
28 this polymicrobial approach Mashburn *et al.* [117] have shown that *Pseudomonas aeruginosa*  
29  
30 relies on *Staphylococcus aureus* as an iron source *in vivo*. It has also been shown that the  
31  
32 presence of *T. denticola* reduces energy consuming processes of *P. gingivalis* such as fatty  
33  
34 acid synthesis, which would reduce the need for cellular iron [114]. The expression of 134 *P.*  
35  
36 *gingivalis* genes was modulated by the presence of *T. denticola* and the two species showed a  
37  
38 range of symbioses and syntrophy that resulted in higher biomass when grown in coculture  
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45 [114, 118].  
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47  
48 When in association with *S. gordonii* 10 of the 33 genes that altered in expression in *P.*  
49  
50 *gingivalis* were classified as encoding proteins involved in metabolic pathways whilst a  
51  
52 further 4 encoded transport and binding proteins, including HmuY that was down-regulated  
53  
54 [119]. These results suggested that the initial adaptation of *P. gingivalis* to a polymicrobial  
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56 biofilm with *S. gordonii* involved a shift in metabolic and physiologic status, and that the  
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4 cells were stressed, as both superoxide dismutase and excinuclease were also upregulated  
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6 [119].  
7

8 *F. nucleatum* is capable of generating a CO<sub>2</sub>-enriched environment [120] that enables it  
9  
10 to support the growth of *P. gingivalis* in aerated and CO<sub>2</sub>-depleted environments in which *P.*  
11  
12 *gingivalis* would not survive on its own [120]. When *P. gingivalis* was grown in a three  
13  
14 species community with *F. nucleatum* and *S. gordonii*, proteomic differences were again  
15  
16 noted that implied extensive interactions between the three organisms and suggested a  
17  
18 favourable environment, which resulted in increased *P. gingivalis* protein expression and  
19  
20 decreased stress [113].  
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23  
24 *P. gingivalis* cells use LuxS-dependent signalling to communicate with each other in  
25  
26 the biofilm [121, 122] and to mediate interspecies communication in mixed-species biofilms  
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28 [123, 124]. Thus *P. gingivalis* interacts with other members of the polymicrobial biofilm that  
29  
30 will modify its iron complex acquisition and use.  
31  
32

33  
34 In the healthy oral cavity *P. gingivalis* is exposed to low iron/haem environments that  
35  
36 are also likely to have a higher oxygen exposure. In response to this dynamic environment, *P.*  
37  
38 *gingivalis* must regulate gene expression to survive.  
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## 41 42 43 **7. Metalloregulatory Proteins** 44

45 To protect against the toxic effect of the Fenton reaction, cells must utilize, store and  
46  
47 maintain iron concentrations with careful management of cellular free iron sequestered in  
48  
49 high affinity protein-bound forms [125]. Intracellular concentrations of metal ions in living  
50  
51 cells are maintained and co-ordinated through a system known as metal ion homeostasis that  
52  
53 involves metal ion influx across the cell membrane depending on the intracellular metal ion  
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55 concentration, availability and demand. Excess metal uptake may lead to toxic effects and  
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57 cell death. In order to maintain and balance intracellular metal ion concentration, metal  
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homeostasis needs to be regulated at the level of transcription [30]. Proteins that are responsible for regulation are known as metalloregulatory or ‘metal sensor’ proteins, in which metal ions bind directly to the protein which in turn can then either repress, derepress or activate gene transcription depending on its mode of action [126]. To date, ten major families of metalloregulatory proteins in prokaryotic organisms have been identified and characterized as the ArsR (or ArsR/SmtB), MerR, DtxR, Fur, NikR, CopY, TetR, MarR, LysR and CsoR/RcnR families (Table 1.0) [27, 30]. These metalloregulatory proteins have been divided into two groups in relation to their functions: protein families that control gene expression linked to metal efflux / sequestration (ArsR, MerR, CopY, CsoR, TetR) and protein families that control the expression of genes for metal ion uptake (DtxR, Fur, NikR, MarR, LysR) (Table 1.0). Of these ten structural superfamilies of metalloregulatory proteins, only two are known to contain members that sense manganese and are thus required for manganese homeostasis (Table 1.0). These are MurR from the Fur superfamily and MntR from the DtxR superfamily. *P. gingivalis* encodes one homologue from each of the Fur and DtxR superfamilies of metalloregulators.

In Gram-negative bacteria, gene regulation in response to intracellular iron availability is usually mediated by the ferric uptake regulatory (Fur) protein [127]. Fur is a small, approximately 17 kDa, global transcriptional regulator that in the presence of iron regulates the expression of genes involved in iron acquisition, transport, storage, oxidative stress and virulence [128]. The Fur protein of the facultative generalist bacterium, *Escherichia coli* (EC-Fur) is the best characterised representative of this family of metalloregulatory repressor proteins. Fur acts as a transcriptional repressor due to its Fe<sup>2+</sup>-dependent DNA binding activity [129]. Fur binds free intracellular Fe<sup>2+</sup> as its co-repressor, acquiring a conformation able to bind specific DNA sequences known as Fur boxes which overlap gene promoters, thus preventing transcription of these genes. When iron is scarce, Fur no longer binds Fe<sup>2+</sup> or

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4 DNA, thus the RNA polymerase can access the promoters and the genes are expressed [127].  
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6 Structural and functional studies of EC-Fur revealed that Fur exists as a dimer, with each  
7  
8 monomer containing two metal-binding sites [130]. The N-terminal domains are involved in  
9  
10 DNA binding, whilst the C-termini are involved in dimerisation [130]. Although the EC-Fur  
11  
12 crystal structure has not been solved, the crystal structure derived from the *Pseudomonas*  
13  
14 *aeruginosa* Fur (PA-Fur; Fig. 3) protein has provided a model for the EC-Fur structure. These  
15  
16 structural studies predict that both the EC-Fur and PA-Fur share similar domain structures,  
17  
18 they both exist as dimers and contain one  $Zn^{2+}$  and one  $Fe^{2+}$  binding site per monomer [130,  
19  
20 131]. Later structural and biochemical studies of Fur orthologues HpFur and BsFur from  
21  
22 *Helicobacter pylori* and *Bacillus subtilis* respectively showed three functional metal binding  
23  
24 sites in each protein [132, 133]. Disruption of Site 3 in HpFur significantly reduced DNA  
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26 binding affinity [132].  
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32 *P. gingivalis* W83 has one Fur orthologue (PG0465) encoded in its genome, but the  
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34 molecular mechanisms of iron-dependent regulation appear to be novel in *P. gingivalis* as the  
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36 deletion of the Fur protein had no effect on the expression of iron-regulated genes or  
37  
38 manganese-regulated genes [67, 134]. Instead, this Fur orthologue, called Har for haem  
39  
40 associated regulator, was demonstrated to regulate haem-responsive biofilm formation [134].  
41  
42 Har dimerises in the presence of  $Zn^{2+}$  and binds one haemin molecule per monomer with high  
43  
44 affinity via the haem regulatory motif Cys97-Pro98 [134]. The binding affinity of Har for  
45  
46 haemin ( $K_d$  of 0.23  $\mu M$ ) [134] was comparable to the affinity for haemin for the *Anabaena*  
47  
48 FurA (0.35  $\mu M$ ) [135] and *E. coli* Fur (<1  $\mu M$ ) [136]. When Har was inactivated, there was  
49  
50 no significant change in metal content of *P. gingivalis*, suggesting that *P. gingivalis* does not  
51  
52 use its only Fur orthologue to regulate metal homeostasis [134]. Instead Har conferred the  
53  
54 ability to respond to environmental haem and develop biofilms, both of which are key  
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56 attributes for the *in vivo* survival and pathogenicity of *P. gingivalis*.  
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4 *P. gingivalis* is an iron-dependent Gram-negative bacterium that has a distinct iron-  
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6 responsive regulon [67] but does not utilize a member of the Fur superfamily to regulate iron  
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8 homeostasis, instead linking the transport of haem and ferrous iron from exogenous sources  
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10 with quorum sensing via LuxS. James *et al.* [137] have shown that LuxS was required for a  
11  
12 1.5-fold increase in transcript levels of the ferrous ion transport system but negative  
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14 regulators of this system have not yet been identified.  
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17  
18 The DtxR family of transcriptional regulators was characterized after being discovered  
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20 as the first iron metalloregulator in *Corynebacterium diphtheriae* (CdDtxR) [138]. CdDtxR is  
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22 a 226 amino acid polypeptide, which functions as a homodimer [139, 140]. Each CdDtxR  
23  
24 monomer consists of 3 domains. Domain 1 (residues 1-73) is the DNA binding domain,  
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26 which contains the helix-turn-helix (HTH) motif. Domain 2 (residues 74-140) is the  
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28 dimerisation domain and has two iron binding sites. The ancillary site has a higher iron-  
29  
30 binding affinity than the primary site and binds iron prior to the primary site [140]. Domain 3  
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32 (residues 145-226) provides two amino acids to the ancillary iron-binding site and has  
33  
34 structural similarity to an SH3 domain, an important domain in signal transduction in  
35  
36 eukaryotes [141]. Between Domain 2 and 3 is a flexible poly-proline rich linker sequence.  
37  
38 SH3 domains recognize poly-proline-rich sequences and are involved in protein-protein  
39  
40 interactions [142]. The C-terminal domain of DtxR shares function and structural similarity  
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42 with its SH3 counterpart but without sequence similarity [142]. The SH3 tail of DtxR plays  
43  
44 two roles, providing amino acids Glu<sup>170</sup> and Gln<sup>173</sup> for iron-binding as part of the ancillary  
45  
46 iron binding site of the dimeric DtxR holorepressor and binding the poly-proline linker found  
47  
48 between domain 2 and domain 3 in a deep crevice of the monomeric DtxR aporepressor, thus  
49  
50 acting as a regulatory switch that modulates the activation of repressor activity [143-146].  
51  
52 Domain 3 of DtxR is now known as a FeoA domain, due to a common-fold in bacterial FeoA  
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4 proteins and eukaryotic SH3 domains as revealed by crystal structures [99], suggesting a  
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6 similar role in mediating protein-protein interactions [147].  
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8  
9 A homologue of CdDtxR, IdeR (MtIdeR) [148] and orthologues of DtxR, MntR  
10 (BsMntR) [149] and TroR (TpTroR) [43] were first discovered in *Mycobacterium*  
11  
12 *tuberculosis*, *Bacillus subtilis* and *Treponema pallidum* respectively. Although MtIdeR  
13  
14 responds to iron, BsMntR and TpTroR were found to respond to manganese [43, 149]. Other  
15  
16 experimentally characterized DtxR-related manganese-responsive homologues identified are  
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18 SirR (*Staphylococcus epidermis*; SeSirR) [150], ScaR (*Streptococcus gordonii*, SgScaR)  
19  
20 [151], EfaR (*Enterococcus faecalis*; EfEfaR) [152] and SloR (*Streptococcus mutans*;  
21  
22 SmSloR) [153]. Work by Guedon *et al* showed that specificity for  $Mn^{2+}$  originates from the  
23  
24 primary metal binding site [154].  
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29 The DtxR homologue of *P. gingivalis* W83 (PG1044; PgMntR) is encoded in the same  
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31 operon as the FB2 manganese transporter and based on its predicted amino acid sequence,  
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33 has aspects of both an iron-binding and a manganese-binding primary metal binding site [58].  
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35 Recombinant PgMntR was used to probe the specificity of metal binding and its impact on  
36  
37 PgMntR structure and DNA binding (unpublished). PgMntR dimerised in the absence of a  
38  
39 structural divalent transition metal cation and unusually bound three Mn(II) or two Fe(II) per  
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41 monomer. *In vitro*,  $Mn^{2+}$  increased the DNA binding affinity of PgMntR to the promoter  
42  
43 region of the gene encoding the FB2 manganese transporter whilst  $Fe^{2+}$  destabilised the  
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45 protein-DNA complex which would result in the derepression of the transcription of  $Mn^{2+}$   
46  
47 transport genes (unpublished). This may suggest a novel regulatory mechanism of the  
48  
49 interplay between iron and manganese in bacterial pathogenesis.  
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54 Although not a metalloregulatory protein, OxyR activity is significantly upregulated  
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56 when *P. gingivalis* is grown in a haem-limited environment, indicating that *P. gingivalis*  
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58 coordinately regulates expression of oxidative-stress-related genes by a haemin  
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4 concentration-dependent pathway [155]. The OxyR regulatory protein of *P. gingivalis*  
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6 functions differently compared to the OxyR of facultative anaerobes and aerobic  
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8 microorganisms where this regulator co-ordinates the response of these microorganisms to  
9  
10 H<sub>2</sub>O<sub>2</sub> [156]. Instead, OxyR does not act as a sensor of H<sub>2</sub>O<sub>2</sub> in *P. gingivalis* but constitutively  
11  
12 activates transcription of oxidative-stress-related genes under anaerobic growth. Common  
13  
14 OxyR-regulated genes such as *dps* and *ahpFC* were not positively regulated in *P. gingivalis*  
15  
16 in response to H<sub>2</sub>O<sub>2</sub> [156], instead expression of *sod*, *dps*, and *ahpC* were upregulated when  
17  
18 OxyR activity was increased in low-haemin growth conditions [155]. Phenotypic  
19  
20 characterisation of an *oxyR* mutant showed that OxyR plays a role in both the resistance to  
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22 H<sub>2</sub>O<sub>2</sub> and the aerotolerance of *P. gingivalis*.  
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## 29 **8. Walking the tightrope: The nexus between haem, iron, manganese and oxygen**

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31 There is interplay between iron and manganese homeostasis in *P. gingivalis* as in a  
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33 FeoB mutant, which had half the cellular iron of wild-type, there was a concomitant three-  
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35 fold increase in cellular manganese [58]. This increase in cellular manganese content in the *P.*  
36  
37 *gingivalis* mutant was attributed to manganous ions binding to vacant sites of ferrous ion  
38  
39 binding proteins thus lowering the free manganous ion concentration within the cell. Given  
40  
41 the link between increased OxyR expression under haem-limitation resulting in increased  
42  
43 oxidative stress protection, this increase in Mn<sup>2+</sup> could also be *P. gingivalis* using the  
44  
45 antioxidative properties of Mn<sup>2+</sup> itself [102, 125] or replacing iron in key enzymes  
46  
47 susceptible to oxidative attack. *E. coli* cells shift from an iron to manganese central  
48  
49 metabolism during oxidative stress and mononuclear enzymes such as ribulose-5-phosphate  
50  
51 epimerase switch to using Mn<sup>2+</sup> as a cofactor [157]. The shift to the use of manganese in *P.*  
52  
53 *gingivalis* highlights the interdependence of these two ions and their critical role in virulence  
54  
55 and survival. The close linkage between iron and manganese accumulation in *P. gingivalis* is  
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also reflected in the cambialistic nature of its superoxide dismutase (SOD, PG1545), which can utilise either manganese or iron to give maximum specific activity for the disproportionation of superoxide radicals into hydrogen peroxide and molecular oxygen [158-161]. This flexibility in superoxide dismutase metal ion specificity may have evolved to aid *P. gingivalis* exploit habitats where iron is not freely available and may have resulted in a more coordinated balance between iron and manganese cellular content.

The combination of a cambialistic SOD that is able to utilize  $Mn^{2+}$  or  $Fe^{2+}$  as well as the ability to use  $Mn^{2+}$  for oxidative stress protection, an OxyR-dependent peroxidase activity catalysed by Dps and a surface layer of  $\mu$ -oxo-bishaem endows *P. gingivalis* with a high degree of aerotolerance to survive in the oral cavity.

The tight interplay between iron and manganese in *P. gingivalis* has also extended to metal transport with the discovery of a ferrous ion transport system, Feo that has evolved to transport manganese; the first report of a FeoB orthologue used to transport a metal other than iron [58]. Thus *P. gingivalis* has two FeoB transporters, FB1 which transports ferrous iron and FB2 which transports manganese. Both FeoB transporters are required for *P. gingivalis* to colonise and cause disease in the oral cavity. When the FB1 transporter is inactivated *P. gingivalis* is avirulent in a murine abscess model of disease whereas when the FB2 transporter is inactivated *P. gingivalis* is not able to survive intracellularly [58, 102].

The interplay between  $Mn^{2+}$  and  $Fe^{2+}$  in *P. gingivalis* is also apparent in the PgMntR metalloregulatory protein which has a primary metal binding site capable of binding Mn(II) or Fe(II) [58](unpublished).

## 9. Conclusion

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4 The clear interplay between iron, manganese, haem and oxidative stress protection may  
5  
6 enable the anaerobic *P. gingivalis* to maintain a high level of intracellular ferrous iron to  
7  
8 maximise growth and virulence using energy efficient iron-dependent metabolism, but to  
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10 rapidly replace this potentially deadly metal with manganese for survival during oxidative  
11  
12 stress by switching to a more protective, but much more restrictive, manganese-based  
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15 physiology.  
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## 21 **Ethical Approval**

22  
23  
24  
25 Ethical approval was not required.  
26  
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## 31 **Conflict of Interest**

32  
33  
34 There are no potential conflicts of interest to be disclosed.  
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**Table 1.0. Superfamilies of bacterial metalloregulatory proteins.**

| Super-family <sup>a</sup> | Mode of action | Metallo-regulator | Metal Effector               |
|---------------------------|----------------|-------------------|------------------------------|
| ArsR <sup>b</sup>         | Derepression   | ArsR              | As(III), Sb(III)             |
|                           |                | AztR              | Zn(II), Cd(II), Pb(II)       |
|                           |                | BxmR              | Cu(I), Ag(I), Zn(II), Cd(II) |
|                           |                | CadC              | Cd(II), Pb(II), Zn(II)       |
|                           |                | CmtR              | Cd(II), Pb(II)               |
|                           |                | CzrA              | Zn(II), Co(II)               |
|                           |                | SmtB              | Zn(II), Co(II), Cd(II)       |
| MerR <sup>c</sup>         | Activation     | CadR              | Cd(II)                       |
|                           |                | CueR              | Cu(I), Ag(I), Au(I)          |
|                           |                | HmrR              | Cu(I)                        |
|                           |                | MerR              | Hg(II)                       |
|                           |                | PbrR              | Pb(II)                       |
|                           |                | ZntR              | Zn(II), Cd(II), Pb(II)       |
| CsoR                      | Derepression   | CsoR              | Cu(I)                        |
|                           |                | RcnR              | Ni(II), Co(II)               |
| CopY                      | Derepression   | CopR              | Cu(II)                       |
| TetR <sup>d</sup>         | Derepression   | SczA              | Zn(II)                       |
|                           |                | ComR              | Cu(II)                       |
| Fur                       | Corepression   | Fur               | Fe(II)                       |
|                           |                | Har <sup>e</sup>  | Fe(II) of Haem               |
|                           |                | Irr               | Haem                         |
|                           |                | Mur               | Mn(II)                       |
|                           |                | Nur               | Ni(II)                       |
|                           |                | Zur               | Zn(II)                       |
| DtxR                      | Corepression   | DtxR              | Fe(II)                       |
|                           |                | IdeR              | Fe(II)                       |
|                           |                | MntR              | Mn(II)                       |
| NikR                      | Corepression   | NikR              | Ni(II)                       |
| MarR                      | Corepression   | AdcR              | Zn(II)                       |
| LysR                      | Corepression   | ModE              | Mo(II)                       |

**Metals up regulate metal efflux / sequestration systems**

**Metals down regulate metal uptake systems**

<sup>a</sup> [162] ([http://regprecise.lbl.gov/RegPrecise/collections\\_tffam.jsp](http://regprecise.lbl.gov/RegPrecise/collections_tffam.jsp))

<sup>b</sup> [163]

<sup>c</sup> [164]

<sup>d</sup> [165]

<sup>e</sup> [134]

## Figure Captions

### Figure 1. Major *P. gingivalis* metabolic pathways, highlighting the dependence on iron.

Enzymes are shown that were identified in a proteomic analysis of *P. gingivalis* W50 grown in haem limitation and were found to be increased (▲), decreased (▼) or unchanged (—) in abundance relative to growth in haem excess. Enzymes identified in the transcriptomic analysis are underlined. Enzymes that have iron as a cofactor are shaded. Figure modified from [62].

### Figure 2. Characterised and proposed iron (complex) and manganese acquisition

**systems of *P. gingivalis*.** Sources of haem and iron such as haemoglobin and transferrin are proteolytically cleaved by the surface associated gingipains Kgp and RgpA. The released haem is actively transported across the outer membrane (OM) via TonB-linked outer membrane proteins either with or without an associated lipoprotein; this transport is energized by TonB/ExbBD complexes. Once in the periplasm, haem is transported through the cell wall (CW) and across the inner membrane (IM) via ABC transporters where A is a periplasmic binding protein, B is an inner membrane permease and C is an ATPase. ABC transporters have been predicted as part of the Htr and Hmu transport systems. An ABC transporter system was also predicted for the transport of  $\text{Fe}^{2+}$  through the inner membrane following the removal of  $\text{Fe}^{2+}$  from haem by the ferrochelatase IhtB and transport through IhtA into the periplasm.  $\text{Fe}^{2+}$  and  $\text{Mn}^{2+}$  are also predicted to enter the periplasm via specific outer membrane channels prior to active transport across the inner membrane by FB1 and FB2, respectively.

**Figure 3.** Ribbon diagram of the crystal structure of the *P. aeruginosa* ferric uptake regulator (PA-Fur) dimer [131]. Each monomer consists of an N-terminal DNA-binding domain, a C-terminal dimerisation domain and two metal binding sites represented by spheres. One monomer is boxed.

**Figure 1**  
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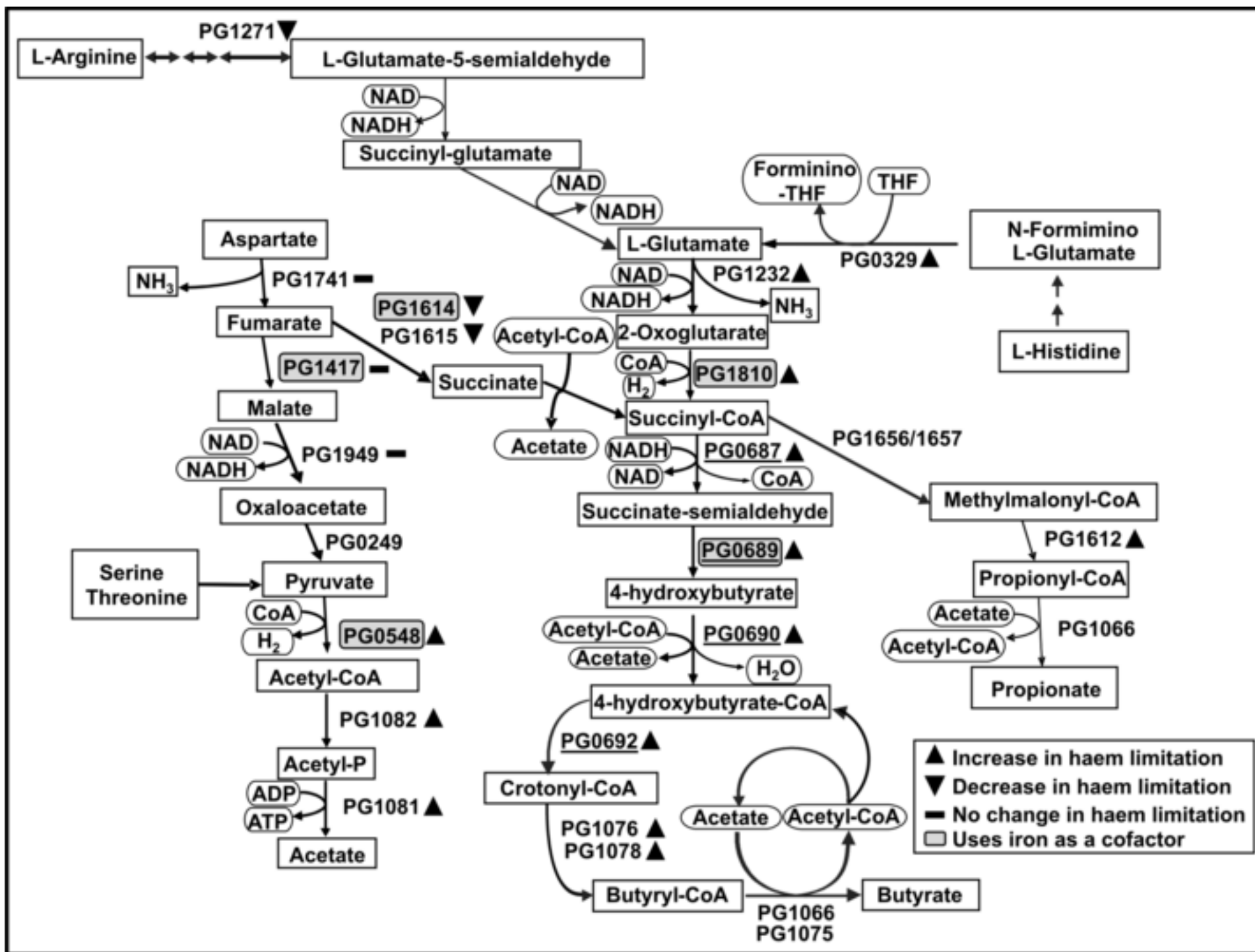


Figure 2  
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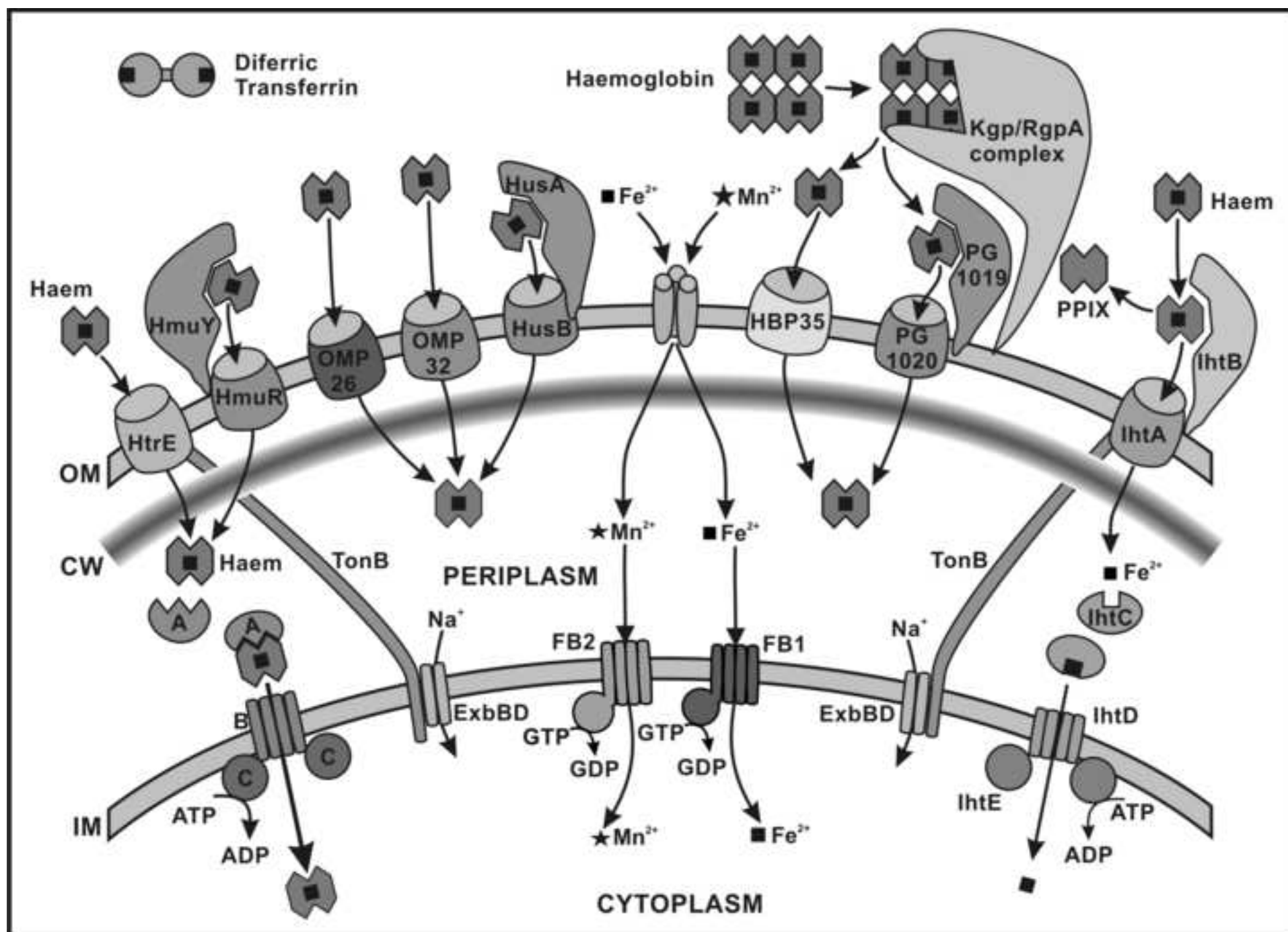


Figure 3  
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