



Saliva Proteomics as Non-Invasive Application for Biomarker Studies

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Abstract

Nowadays, saliva being a source of broad-spectrum biomolecules (mainly proteins, lipids, hormones, and nucleic acids that originated from various local/systemic sources) holds a promising future among diagnostic samples. Compared to blood, the use of saliva is advantageous because sample collection and processing are easy, minimally invasive, low cost, and better tolerated by individuals. Saliva proteome analysis can therefore give valuable contributions in understanding the pathophysiology of diseases and provide a foundation for the recognition of potential protein markers. A pathophysiological condition caused by an ascent to a high altitude named hypobaric hypoxia occurs due to deficiency of oxygen at the tissue level caused by lower atmospheric pressure of oxygen. Although few reports have documented the effect of exposure to hypobaric hypoxia on plasma and tissue proteome, salivary proteome-based studies remain uninvestigated. Therefore, identification of molecular signatures having key roles in hypobaric hypoxia by analyzing the salivary proteome finds promising. Through salivary proteome, a few proteins such as alpha-enolase, cystatins, apoptosis inducible factor 2, prolactin inducible protein, carbonic anhydrase 6, phospholipid transfer protein (PLTP), interleukin 1 receptor antagonist (IL1R1), albumin, alpha-1 acid glycoprotein, and alpha-1 antitrypsin were found to be evolved as biomarkers for hypobaric hypoxia. In conclusion, these studies provided the proofs of concept for translating salivary proteins into a non-invasive putative diagnostic panel for assessing hypobaric hypoxia.

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10.1 Saliva: A Novel Informative Sample

Saliva is an oral fluid that originates from major salivary glands such as parotid, sublingual, and submandibular and minor salivary glands such as labial, buccal, lingual, and palatal glands (Fig. 10.1) (Carranza et al. 2005; Forde et al. 2006; Yoshizawa et al. 2013).

Some of the salivary components may not have originated from salivary glands as saliva also contains fluids from oral mucosal cells, upper respiratory secretions, and gastro-intestinal reflux (Mager et al. 2005; Zhang et al. 2010). Salivary glands are enveloped by capillaries and highly permeable for exchanging blood based molecules into saliva freely (Fig. 10.2) (Haeckel and Hanecke 1996). Also, blood based compounds move from plasma to saliva involving several processes (Yoshizawa et al. 2013; Yamaguchi et al. 2005). These processes include a) ultra-filtration of molecules such as water, ions, catecholamines, and steroids through gap junctions between secretory cells; b) selective transport (actively or passively)

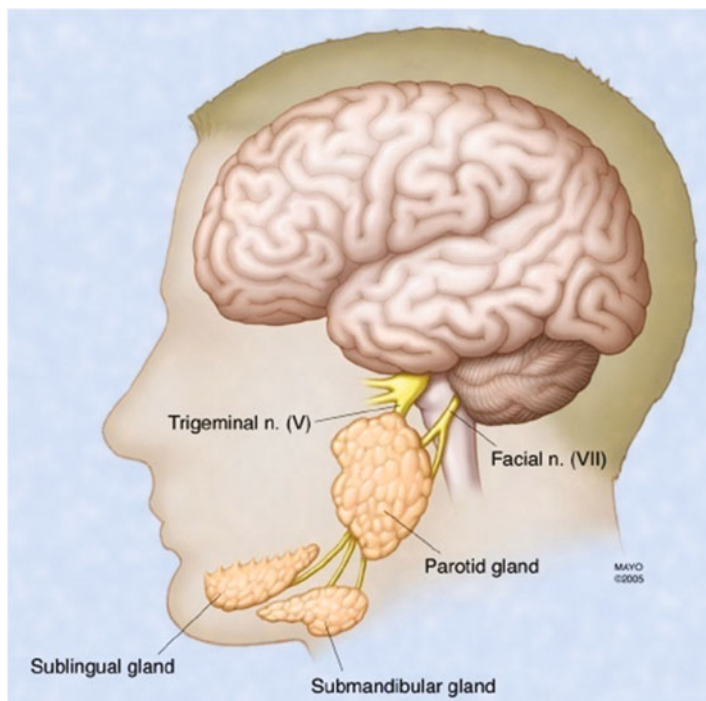
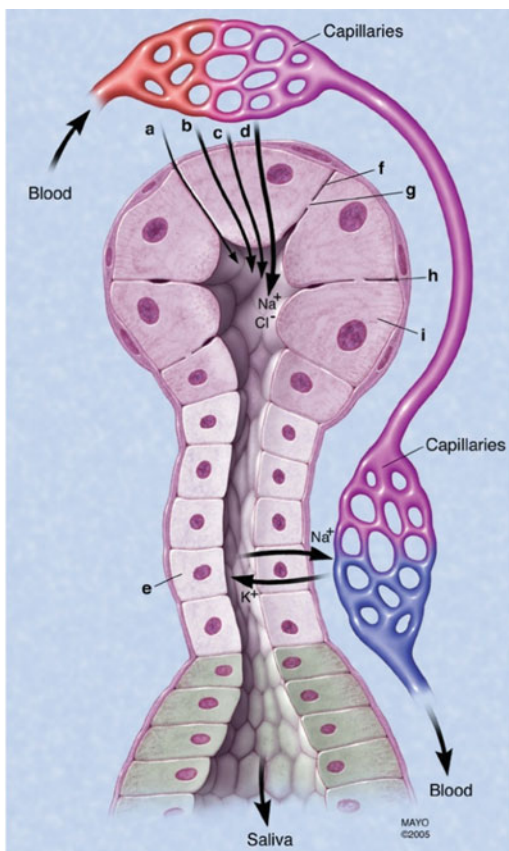


Fig. 10.1 Major salivary glands. (Adapted from Forde et al. 2006)

Fig. 10.2 Mechanism of molecular transport from blood to saliva through capillaries. (Adapted from Haeckel and Hanecke 1996)



through cellular membranes; and c) transudation of albumin directly from cervical fluid into oral cavity (Chiappin et al. 2007).

Healthy individuals produce 500–1500 mL of saliva (slightly acidic clear fluid having pH = 6.0–7.0) per day (Chicharro et al. 1998; Edgar 1990; Humphrey and Williamson 2001; Van Nieuw Amerongen et al. 2004; Zalewska et al. 2000). Several pathophysiological conditions can modify the amount of saliva (Chicharro et al. 1998; Aps and Martens 2005; Walsh et al. 2004). Saliva contains a variety of compounds such as inorganic (water, ions); organic (non-proteins such as uric acid, bilirubin, creatine, glucose, lipids, amines, and lactate); proteins and hormones (catecholamines and steroids) (Chicharro et al. 1998; Actis et al. 2005; Agha-Hosseini et al. 2006; Cooke et al. 2003; Coufal et al. 2003; Diab-Ladki et al. 2003; Guan et al. 2004; Larsson et al. 1996; Lloyd et al. 1996; Nagler et al. 2002; Rehak et al. 2000; Zelles et al. 1995). These biomolecules being present in the saliva provide information from several organs and systems and raise the possibility of their use as disease biomarkers.

A huge number of protein components are present in saliva (Hu et al. 2005; Huang 2004). These proteins have been identified using proteomics tools such as 2-DE coupled with MALDI-TOF/TOF followed by shotgun proteomics and LC-MS/MS (Castagnola et al. 2017). By using these techniques, most of the salivary proteins secreted in saliva from salivary glands were found to be proline-rich proteins (PRPs), mucins, cysteine-rich proteins (cystatins), and histidine-rich proteins (histatins). PRPs are highly polymorphic in nature with 50 different proteins encoded by different gene arrangements and post-secretory processing of only six genes (Carpenter 2013).

Secretion from each salivary gland differs in concentration of proteins and salts/ions (Hu et al. 2004; Kalk et al. 2002). For example, sublingual gland secretes mucin MUC5B and calgranulin, whereas submandibular gland secretes cystatin C. Human salivary proteins have functions related to immune defense in which a variety of proteins such as lactoferrin, lysozyme, immunoglobulins, agglutinins, and mucins participate in the protection of oral tissues and proteins like histatins and defensins possess bactericidal properties (Chiappin et al. 2007). Other functions of salivary proteins include inhibition of calcium precipitation by PRPs and statherins; taste perception by carbonic anhydrase; digestion of starch by amylase; endonuclease activity by Von Ebner minor gland proteins; and proteinase inhibition by cystatins (Amerongen and Veerman 2002).

Previously, blood/serum/plasma was frequently used as the source of biomarker but in many conditions, the blood sample collection could be problematic, expensive, and invasive. Comparatively, saliva offers various advantages over blood such as: (a) quick and easy method of sample collection: non-requirement of a trained professional and self-collection; (b) non-invasive: painless collection; (c) safe handling: diseases such as HIV cannot be transmitted through saliva samples; (d) easy storage and shipping as saliva does not clot like blood; and (e) cost-effective (Yoshizawa et al. 2013; Chiappin et al. 2007; Schafer et al. 2014; Kaczor-Urbanowicz et al. 2017; Lee and Wong 2009; Pfaffe et al. 2011; Campo et al. 2006). Recently, it gained attention as an effective strategy for screening, diagnosis, prognosis, and monitoring post-therapy status. And, it is imperative to explore potential of saliva based diagnostics as discussed in the following section.

10.2 Hypobaric Hypoxia: A Pathophysiological Condition

Ascent of an individual to high altitude, the parallel low atmospheric pressure of oxygen leads to decreased body's partial pressure of oxygen, thereby causing a pathophysiological condition named hypobaric hypoxia (HH) (Fig. 10.3). HH affects the ability of body to exchange oxygen between the lungs and the bloodstream, thereby disrupting the oxygen availability to the tissues. A significant population of world resides at an elevation of 10,000 ft. above sea level. This population consists of people who have lived there for generations and travelers who travel to high altitude intermittently (soldiers) or for short to moderate periods

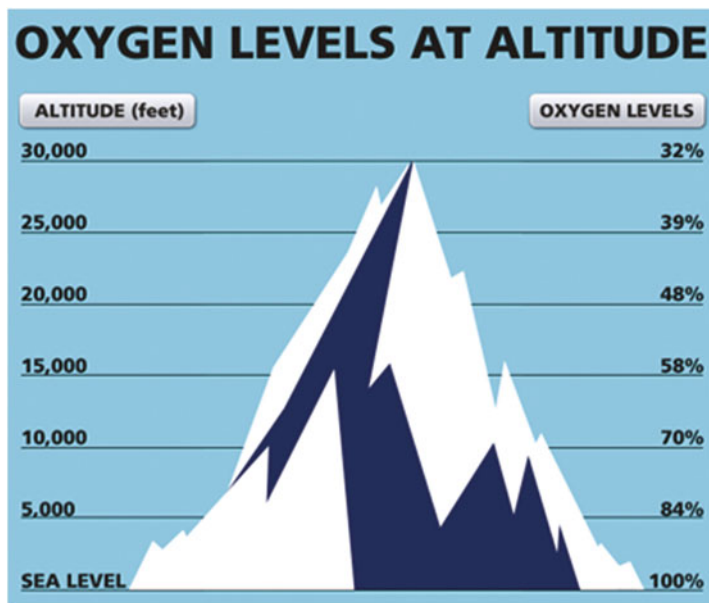


Fig. 10.3 Oxygen levels at different altitude elevations. (Adapted from <http://www.altitude.org>)

of time (e.g. mountain climbers) (Askew 2002). The people residing at high altitude for generations have already evolved various mechanisms to generate energy at high altitude (Hoppeler and Vogt 2001). Whereas travelers may experience AMS or potentially more serious impairments such as HACE and HAPE (Hackett and Roach 2001, 2004; San et al. 2013; Sharp and Benaudin 2004; Wilson et al. 2009). These maladies develop over hours to days at high altitude and are known to be preventable but still remain common consequences of rapid ascent to high altitude.

10.3 Redox Stress: Molecular Responses in Hypobaric Hypoxia

The main consequence of hypobaric hypoxia is generation of reactive oxygen and nitrogen species (RONS). RONS, physiological modulators of cellular redox mechanism control wide range of physiological and pathophysiological processes (Bakonyi and Radak 2004). Hypoxia is caused by the limited availability of oxygen in mitochondria for reduction to H_2O at cytochrome oxidase and leads to generation of RONS. In order to produce energy (ATP), auto-oxidation of one or more mitochondrial complexes, such as the ubiquinone–ubiquinol redox couple results in accumulation of reducing equivalents (RONS) (Fig. 10.4). Despite the presence of antioxidant system, the levels of RONS generation can lead to oxidative stress (Askew 2002). These accumulated oxidants such as RONS cause imbalance between oxidative stressors and antioxidant capacity. Oxidants and antioxidants

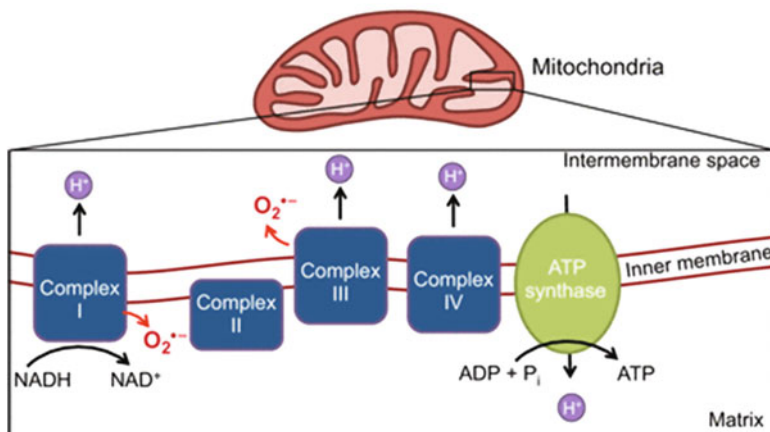


Fig. 10.4 Oxidants generation in mitochondria. (Adapted from Bigarella et al. 2014)

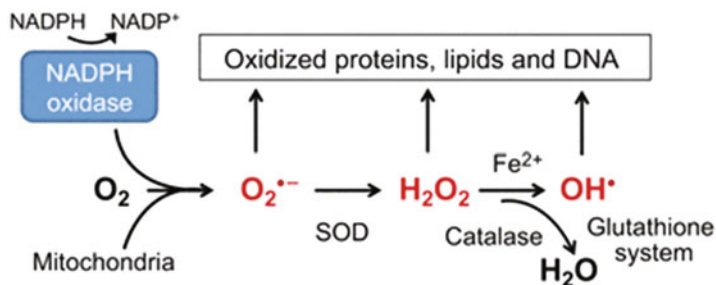


Fig. 10.5 Oxidative stress to biomolecules. (Adapted from Bigarella et al. 2014)

imbalance leads to damage in biomolecules such as lipids, proteins, and DNA (Fig. 10.5) (Dosek et al. 2007; Jefferson et al. 2004; Strapazzon et al. 2016).

This oxidative damage to biomolecules is nearly similar to the stress associated with cancer, neurological, pulmonary, and cardiovascular diseases (Reuter et al. 2010).

In literature, the increased production of oxidants has been documented in blood, tissue, urine, and breath samples of rats and humans in response to hypoxia (Strapazzon et al. 2016; Chang et al. 1989; Irrarazaval et al. 2017; Magalhaes et al. 1985; Maiti et al. 2006; Radak et al. 1994; Ribon et al. 2016; Siervo et al. 2014; Singh et al. 2013; Yoshikawa et al. 1982).

In vivo, aerobic cells develop antioxidant system to regulate the effects of RONS. This system contains mitochondrial, cytosolic, and extra-cellular superoxide dismutase (SOD). SOD converts reactive superoxide ions to H_2O_2 which is then decomposed into water by the action of glutathione system and catalase. Previously, high altitude related studies measured the content of glutathione, SOD, and GPX (Askew 2002; Bakonyi and Radak 2004; Radak et al. 1994, 1997; Nakanishi et al.

1995; Imai et al. 1995; Ilavazhagan et al. 2001; Joanny et al. 2001). And, it appeared that the capacity of antioxidant system was found to be decreasing at high altitude. These changes in redox parameters are responsible behind physiological and pathophysiological changes in the body.

10.4 Use of Biological Fluids Such as Plasma/Serum in Search of Potential Protein Markers

In hypobaric hypoxia related molecular studies, particularly proteomics, biological fluids such as blood/plasma/serum have been used among clinicians and biological scientists in search of potential protein markers for hypobaric hypoxia and acclimatization. Multiple scattered plasma proteins have been identified in samples from patients suffering from high altitude illnesses such as AMS, HAPE, and HACE (Lu et al. 2018; van Patot et al. 2005; Droma et al. 1996; Sartori et al. 1999; Charu et al. 2006; Berger et al. 2009; Barker et al. 2016; Ahmad et al. 2011, 2015; Zhang et al. 2013; Sikri and Bhattachar 2017).

Another important aspect is that the redox imbalance could also trigger healthy cellular processes that aid in acclimatization to hypobaric hypoxia. Protein markers have been studied in rats and humans to understand such cellular processes in acclimatized state (Ahmad et al. 2013, 2014, 2015; Siervo et al. 2014; Luks et al. 2017; Levett et al. 2011; Hartmann et al. 2000).

Newer strategies that are completely non-invasive in nature such as study of saliva have been implicated for diagnostics purposes. Thus, we move on to newer studies for exploration and improvement.

10.5 Saliva as a Diagnostic Fluid in Translational Studies

Previous findings have described that chronic diseases such as cancer, cardiovascular, diabetes, pulmonary, and neurological diseases are associated with continued oxidative stress (Reuter et al. 2010). In translational research, saliva has been explored for the detection of oral cancer (de Jong et al. 2010; Hu et al. 2007a; Gallo et al. 2016), Sjogren's syndrome (Giusti et al. 2007; Hu et al. 2007b; Peluso et al. 2007), breast cancer (Streckfus et al. 2008), lung cancer (Xiao et al. 2012), and systemic disorders such as hepatitis, HIV, and HCV (Elsana et al. 1998; Yaari et al. 2006; Hodinka et al. 1998). A previous study by Shen Hu et al. provided a proof for exploring salivary proteins in oral cancer and revealed thioredoxin as a salivary biomarker for human oral cancer (Hu et al. 2007a). Other researchers, Ebbing P. de Jong et al. reported myosin and actin as promising salivary biomarkers for distinguishing between pre-malignant and malignant oral lesions (de Jong et al. 2010). Another recent study done by Eva Csoz et al. highlighted the importance of identification of population tailored biomarkers and reported oral squamous cell carcinoma (OSCC) biomarkers in a Hungarian population. And, S100A9 and IL-6 were shown to be candidate biomarkers for OSCC (Csoz et al. 2017). In a study

performed by G. Peluso et al. in Sjogren's syndrome (SS), saliva collected from patients with primary SS revealed higher levels of alpha-defensin 1 and the presence of beta-defensin 2 which could be potential markers of oral inflammation in SS patients group (Peluso et al. 2007). Omer Deutsch et al. observed profilin and CA-I as biomarker candidates for Sjögren's syndrome following high-abundance protein depletion (Deutsch et al. 2015). In HIV and HCV, rapid point-of-care HIV tests utilize oral fluids to rapidly provide test results to patients (Hodinka et al. 1998; Fernandez Rodriguez et al. 1994). In cases of non-oral cancers such as lung and breast cancers, various researchers suggested modifications in the salivary proteome and provided proof for candidate biomarkers (Streckfus et al. 2008; Xiao et al. 2012; Bigler et al. 2009; Streckfus and Bigler 2016). Another example of its use for determining hormone levels, including estradiol, progesterone and testosterone, DHEA, and cortisol (Groschl 2008).

10.6 Saliva in Response to Hypobaric Hypoxia

In the context of events related to hypobaric hypoxia, studies on saliva have been performed due to its diagnostic potential. An initial study, observed in 1990s, suggested an increase in salivary flow rate and low concentration of potassium in response to acute hypobaric hypoxia exposure (Pilardeau et al. 1990). Another researcher, McLean reported decreased levels of aldosterone in response to both ACTH and renin-angiotensin stimulation at high altitude (McLean et al. 1989). Additionally, a rise in the salivary activities of aminotransferases was observed while HH exposure (Mominzadeh et al. 2014). A recent study by Woods DR et al. reported an alteration in the levels of salivary cortisol and suggested that an elevated cortisol levels may contribute to fluid retention associated with acute mountain sickness (Woods et al. 2012).

In molecular omics-based studies, preferably proteomics, only limited studies have been performed so far. Jain et al. have reported significantly altered proteins such as alpha-enolase, cystatin SN, apoptosis inducing factor 2 (AIF-2), cystatin S, carbonic anhydrase 6 (CA6), and prolactin inducible protein (PIP) and plausible pathways involving these proteins such as inflammation, impaired glycolysis, and respiratory alkalosis during HH exposure (Jain et al. 2018). Another study by Jain et al. suggested proteins such as albumin, carbonic anhydrase 6, prolactin inducible protein, alpha-enolase, phospholipid transfer protein (PLTP), alpha-1 acid glycoprotein, interleukin 1 receptor antagonist (IL1RA), and alpha-1 antitrypsin as protein candidates for assessing hypobaric hypoxia (Jain et al. 2020).

10.7 Proteins Evolved as Biomarkers for Hypobaric Hypoxia

10.7.1 Alpha-Enolase

Alpha-enolase is a multifunctional enzyme known to be involved in various processes such as allergic responses, growth control as well as glycolysis other than inflammatory hypoxic tolerance. Earlier studies suggested in hypoxic situations, expression of alpha-enolase got differentially modulated and provides protection to cells so as to acclimatize to low oxygen levels through increased anaerobic metabolism (Aaronson et al. 1995; Sedoris et al. 2010). Alpha-enolase has several interacting partners such as glyceraldehyde 3-phosphate dehydrogenase, phosphoglycerate kinase, and pyruvate kinase. Alpha-enolase has earlier been observed in various studies and well-established with hypoxia induced physiological changes (Kim et al. 2006; Semenza et al. 1996), suggesting its role as potential protein marker if carefully evaluated and utilized (Mikuriya et al. 2007; Xu et al. 2005).

10.7.2 Cystatins

Salivary cystatins such as cystatin S and SN were observed in whole human saliva. Cystatin S was known to be present in three forms: mono-phosphorylated, di-phosphorylated, and non-phosphorylated (Isemura et al. 1991) and involved in the mineral balance of the tooth. And cystatin-SN was found to inhibit the human lysosomal cathepsins B, H, and L in vitro (Baron et al. 1999). Recent studies reported salivary cystatins as prospective biomarkers of oral diseases and diabetes (Rudney et al. 2009; Bencharit et al. 2013). Cystatins are not elevated in normal conditions.

10.7.3 Apoptosis Inducing Factor 2 (AIF2)

AIF 2, an oxidoreductase acts as a caspase-independent mitochondrial effector of apoptotic cell death and plays a role in mediating apoptosis response. AIF 2 was over-expressed in response to hypobaric hypoxia, thereby confirming its induction by hypoxia (Greijer and van der Wall 2004).

10.7.4 Prolactin Inducible Protein (PIP)

PIP, an extra-parotid glycoprotein associated with secretory cell differentiation was found to be decreased in hypobaric hypoxia. Earlier, it was observed that decreased levels of salivary PIP were found in patients with bleeding oral cavities (Huang 2004).

10.7.5 Carbonic Anhydrase 6 (CA6)

CA6, an enzyme involved in respiratory alkalosis, could be considered as potential marker (Taylor 2011). As per earlier reports, buffering capacity of saliva plays an important role in oral homeostasis and the bicarbonate buffer is the main buffer that contributes to the salivary buffering capacity (Bardow et al. 2000; Peres et al. 2010). Other findings suggested an ascent to high altitude was known to be associated with decreased concentration of bicarbonate and hydrogen ions, increased pH and thus, resulting in respiratory alkalosis (Goldfarb-Rumyantzev and Alper 2014). The increased expression of carbonic anhydrase 6 in this study suggested its probable role in conferring acclimatization to hypobaric hypoxia by neutralizing pH through bicarbonate balance.

10.7.6 Phospholipid Transfer Protein (PLTP)

PLTP, a regulator of lipid metabolism is known to play an important role in oxidative stress. Recent research suggested that PLTP modulates BBB integrity, possibly through its ability to transfer vitamin E, and modulate cerebro-vascular oxidative stress (Zhou et al. 2014). Another study suggested regulation of vitamin E bioavailability in lipoproteins through PLTP in order to protect circulating lipoproteins from oxidative stress (Jiang et al. 2002). Also, a finding suggested that this protein showed enhanced expression in hypoxia stimulus in case of emphysema (Jiang et al. 1998).

10.7.7 Interleukin 1 Receptor Antagonist (IL1R1)

Interleukin 1 receptor antagonist (IL1R1) is an upstream regulator of the pathway and a cytokine widely known to be associated with inflammation and expressed by activated mononuclear cells. The levels of circulating IL1RA in the plasma were increased in response to hypoxia suggesting the reason for its decreased level in salivary secretions and as a potential target for anti-inflammatory therapy (Fritzsching et al. 2015).

10.7.8 Albumin, Alpha-1 Acid Glycoprotein, and Alpha-1 Antitrypsin

These downstream regulators of acute phase response signaling also showed similar patterns as IL1R1. According to previous research, albumin was observed to suppress VEGF via alteration of HIF/HRE pathway (Katavetin et al. 2008). Albumin also provides protection against hypoxia induced injuries (Strubelt et al. 1994). Another protein, alpha-1 acid glycoprotein is known to provide protection against hypoxia by inhibiting inflammation and apoptosis, thereby could be given exogenously as therapeutics (de Vries et al. 2004; Hochepped et al. 2003; Van Molle et al.

1997). Similar to other downstream regulators of the pathway, alpha-1 antitrypsin also has anti-inflammatory properties (Ahmad et al. 2013).

10.8 Concluding Remarks

In conclusion, these studies provided the proof of concept for translating salivary proteins into a non-invasive putative diagnostic panel for assessing hypobaric hypoxia. This panel has the potential to be used in future to diagnose individuals affected by hypobaric hypoxia.

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