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Laboratory and metabolomic fingerprint in heart failure with preserved ejection fraction: from clinical classification to biomarker signature

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SUMMARY

Heart failure with preserved ejection fraction (HFpEF) remains a poorly characterized syndrome with many dark aspects related to different patients profile, various associated risk factors and wide aetiologies. It comprises several pathophysiological pathways related to endothelial dysfunction, myocardial fibrosis, extracellular matrix deposition and high inflammatory response. Up to now, it has been described only for clinical appearance and most common associated risk factors without an effective characterization of biological processes responsible for cardiovascular deteriorations. Recent advances in laboratory and metabolomic researches showed that HFpEF appears strictly related to specific cells and molecular mechanisms dysregulation. Some biomarkers are capable to early identify these processes adding new insights into diagnosis and risk stratification. Additionally recent advances on intermediate metabolites reflecting provide relevant information on intrinsic cellular and energetic substrate alterations. The systematic combination of clinical imaging and laboratory data may lead to a precision medicine approach providing prognostic and therapeutic advantages. Current review reports traditional and emerging biomarkers recently investigated in HFpEF setting, and it purpose a new diagnostic approach based on integrative information achieved from risk factors burden, hemodynamic dysfunction and biomarkers signature partnership.

INTRODUCTION

Heart failure with preserved ejection fraction (HFpEF) is an heterogenous syndrome with specific molecular, genetic, metabolomic features reflecting vascular and myocardial cell adaptations. [1] HFpEF encompasses different pathophysiological and cardiac structural profile compared to HF with reduced ejection fraction (HFrEF).[2] It accounts half of whole patients affected by heart failure (HF) but it shows a peculiar clinical profile, cardiac structural and functional alterations. Therefore, the selection criteria are often elusive and mainly based on ejection fraction cut off rather than distinct clinical and laboratory phenotype.[3] Most of inclusion criteria comprise the contemporary presence of left ventricular hypertrophy (LVH), altered diastolic dysfunction and elevation of natriuretic peptide (NP) associated with exertional dyspnea or reduced exercise tolerance. Indeed, recent clinical trials adopted wide inclusion criteria and characteristics of patients enrolled resulted inhomogeneous with various morphological and comorbidities patterns.[4,5] In this framework, an advanced analytic research investigating specific biomarkers in a well phenotyped population, could lead to a better understanding of molecular pathways and biological mechanisms responsible for HFpEF syndrome. The interaction among clinical variables, imaging features and biomarkers could became the model for future researches, and a combined network analysis may change current approach based on traditional knockdown/knockout study. [6]

Conversely from HF with reduced systolic function in which myocyte loss, cellular death and consequent cardiac chamber enlargement, are the main features responsible for disease progression, HFpEF is characterised by collagen overexpression, myocardial fibrosis, extracellular matrix deposition and high inflammatory response.[7] All these mechanisms differently occur according to specific risk factors, comorbidities association, vascular and cardiac remodelling. [8] Thus an analysis starting from detailed phenotyping, cardiac structural alteration and distinctive laboratory investigation may challenge the current scenario going towards a precision medicine model with better targeted therapeutic profiling. [9] This personalized setting begin from machine learning analysis of big data in order to resolve disease heterogeneity by identifying patients within particular subtypes and predicting response to the therapy.

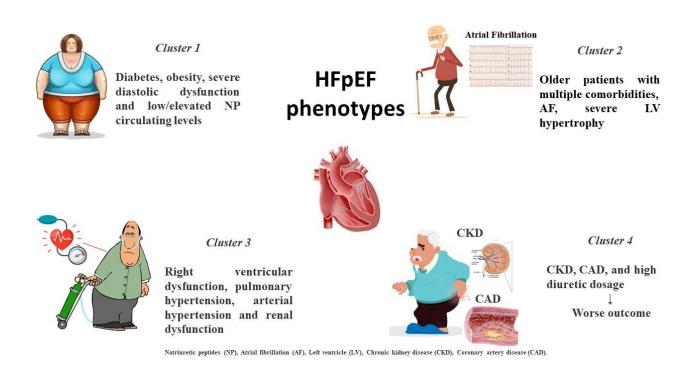
DIFFERENT HFPEF PHENOGROUPS

Despite recent advances in treatment diagnosis and recognition, HFpEF remains a poorly characterized syndrome with many dark aspects related to different patients profile, associated risk factors and pathophysiological pathways. [10] Large trials showed a wide prevalence of LVH left atrial dilatation diastolic dysfunction and pulmonary hypertension. Moreover patients presented various extracardiac comorbidities such as diabetes CKD anemia chronic lung diseases obesity metabolic dysfunction. [5,11-13] Because the interventional Trials did not distinguish among different risk factors and underlying diseases, the one-size-fits-all approach might explain the lack of efficacy and benefit for the tested treatments. Based on the different pathophysiological drivers, some Authors suggested different HFpEF subtypes linked to cardiometabolic alterations, body size conformation or peripheral maladaptation. These appraisals may be related respectively to the presence of systemic disorders leading to skeletal muscle metabolism alterations and vascular rarefaction.[14] Since all these features are widely expressed in HFpEF, the diagnosis based only on cardiac morphology and dysfunction remains difficult to interpret and often misleading. Current pictures may configure a wide HFpEF phenotype that differently interfere on cardiac structure and cardiovascular remodelling related to the underlying biological process and pathophysiological contributor, despite a similar EF.

Notably, recent machine learning analysis attempt to cluster specific phenotype by latent class study. In a post hoc analysis of TOPCAT patients were classified into three categories according to vascular and cardiac remodelling: patients with mild LV hypertrophy and chronic pulmonary disease with normal vascular stiffness characterized for increased expression of metalloproteinase; older patients with multiple comorbidities LV hypertrophy and reduced vascular compliance, characterized for elevated tissue calcification biomarker; obese subgroup with several metabolic

alterations increased levels of renin angiotensin system activity, lipidic profile derangement and increased inflammatory pattern. [15] Similarly, another study identified a group including youngest with increased body mass index, typical abnormalities in cardiac structure and function and low natriuretic peptide levels; a pattern with high prevalence of diabetes and obesity characterized for severe diastolic dysfunction and elevated NP circulating levels; a cluster characterized by RV dysfunction, pulmonary hypertension, and renal dysfunction, experiencing the worst outcomes.[16]

Finally a combined analysis of SwedeHF and CHECK HF registries distinguished among 5 different phenogroups accordingly to a combined approach including risk factors and associated comorbidities confirming that cluster with CKD, coronary artery disease (CAD) and high diuretic amount revealed the worst outcome. [17] FIGURE 1



Taken together these data reveal some common features but also some discrepancies underlying the needing of a more homogenous classification. Of note a detailed laboratory screening capable to identify specific cluster by the combination of structural cardiac abnormalities with underlying molecular mechanisms responsible for disease progression may open the way for a better HFpEF understanding opening targeted therapeutic opportunities. [18]

CURRENT BIOMARKERS IN HFpEF

Several risk prediction scores have been produced including biomarkers, (mainly natriuretic peptides NP) ,but important gaps exists regarding the knowledge of underlying pathophysiological

mechanisms, biological process And disease evolution. Circulating biomarkers should reflect cardiac and extra cardiac disorders responsible for HFpEF development and related pathological pathways. [19,20] Since HFpEF is characterized by LVH with increased parietal stress, systemic vascular damage and stiffness, increased inflammation, and enhanced fibrosis, we recognize four main biomarkers targets: Myocardial injury, extracellular fibrosis, inflammation and endothelial dysfunction. TABLE 1

	Name of Biomarker	Mechanism of action
Markers of myocardial injury	↑↑ High sensivity troponin	the final results of microvascular dysfunction, and subendocardial layer damage due to systemic oxygen reduction.
	Natriuretic peptides	related to diuresis and natriureis that fovour the congestion reduction and euvolemia
	↑↑ Adrenomedullin	regulatory peptide produced by endothelial and smooth muscle cells with antiproliferative vasodilatatory and antiapoptotic effects.
Markers of extracellular fibrosis	↑↑ Galectin -3	inflammatory and pro fibrotic processes and it is synthetized by macrophage
	↑↑ Soluble ST2	roduced by myocardial cells, but also smooth muscle cells and endothelium are capable to synthetize the peptide in relation to congestion
	↑↑ Matrix Metalloproteinases	involved in collagen synthesis and collagen degradation
	↑↑ Pro collagen type I (PIP) and procollagen type III N-terminal peptide (PIINP),	reflect collagen increases deposition and turnover.
Markers of inflammation	↑↑ CRP and pentraxin	inducing complement and cytokine stimulation causing myocyte loss and endothelial dysfunction by NO production decrease.
	↑↑ Grow differentiation factor 15	expressed in inflammatory chronuic diseases, lung, kidney, and cardiovascular diseases and providing additional informations on LV

		remodeling and function.
	↑↑ Intereleukin-6	contributes by direct myocites damage and indirect inflammatory burden elevation.
	↑ Tumor necrosis factor α	correlates with atrial dimension and diastolic dysfunction degree
Markers of endothelial dysfunction	↑↑ vascular cel adhesion molecules (VCAM) and E selectin	activates von villerbrand and other pro thrombotic factor
	↑ endothelin 1	secreted by the endothelial cells in response to renin angiotensin system activation.
	↑↑ Plasminogen activator inhibitor	in association with D-dimer levels suggesting an association with pro thrombotic and procoagulant state
	↑↑ Insulin grow factor binding	left atrial dysfunction and dilatation reflecting diastolic dysfunction in HFpEF.

Myocardial Injury-High sensivity troponin (HsTn) is universally considered a markers of myocardial damage in acute coronary syndrome, however it has a prognostic significance in HF and it implies myocardial damage apoptosis and progressive fibers loss independently on coronary vessel diseases. It could be the final results of microvascular dysfunction, and subendocardial layer damage due to systemic oxygen reduction configuring an altered supply-demand mismatch. Other features such as increased wall tension, high LV filling pressure and right ventricular dysfunction are related with increased HsTn levels.[21] In patients with HFpEF increased HsTn level correspond to more severe diastolic degree and higher pulmonary pressure. Elevated levels are also associated with increased wall stress and much more pronounced LV hypertrophy subtending and increased workload. [22] Many reports showed that HsTn predict poor outcome in HFpEF, with better prediction in men than in women. In hospitalized patients with acute HFpEF the persistence of increased HsTn levels at both admission and discharge is related with increased events rate in terms of rehospitalization and death.[23,24] Similarly in TOPCAT trial, elevation of HsTn was independently associated with increased risk of hospitalization and cardiovascular events. [25]Current findings were confirmed in the PARAGON study in which even a mild HsTn elevation was associated with worse outcome across 3 years follow-up, and patients taking salcubitril valsartan showed a significative reduction compared to placebo. [26]

Natriuretic peptides (NPs) are the hallmark biomarkers in HF and its measurement is accounted in HF guidelines across the spectrum of the whole EF.[27] The biologically active NP form and its precursor amino-termianl portion pro B type natriuretic peptide is cleaved into NT-pro BNP and BNP are released in response to enhanced cardiac wall tension and increased filling pressure, their levels increase proportionally to the degree of systolic dysfunction. The two peptides are released in response to sympatethic activity systemic vasoconstriction and and fluid retention as opposite response to the increased neuro hormonal overdrive.[28] NP activity counteract sympathetic activity promoting cardiac afterload reduction and myocardial relaxation by direct vasodilatation and myocardial relaxation effects. The main mechanism of action is related to diuresis and natriureis that fovour the congestion reduction and euvolemia. [29] The Levels of NPs are directly related to intracardiac pressure values including LV end diastolic pressure, wedge pressure, and pulmonary systolic pressure. Both peptides are largely analyzed in patients with reduced systolic function as valuable diagnostic and prognostic features, in HFpEF they are generally less increased but they keep their diagnostic relevance.[30] Some authors believe that this appaeranace is due to the reduced wall stress in this setting together with extracardiac conditions such as metabolic syndrome chronic lung disease and obesity in which adipocyte cells favor a reduced receptor expression. [31] These comorbidities are often associated in HFpEF causing a relevant NPs levels variations. Despite some studies reveals that some HFpEF cluster experienced low NPs below 100 pg/ml, recent metanalysis showed an optimal diagnostic accuracy in this setting (AUC 0.80 CI 0.73-0.87). [32] Moreover, a combined analysis of NPs and Tn showed that patients with higher plasma level have the increased risk for death and hospitalization. Finally in acute patients, NP assay reveals similar prognostic informations in HFpEF as In HFrEF, and the related changes during hospitalization. confer equal risk assessment adjusted for potential confounding factors.[34]

Adrenomedullin is a regulatory peptide produced by endothelial and smooth muscle cells with antiproliferative vasodilatatory and antiapoptotic effects. It is synthetized mainly by adrenal medulla but its receptors are expressed in many tissues such as lung heart and kidney. [35] It is an important biomarker of pulmonary and systemic congestion and its is produced in relation to sympathetic activity. [36] It counteracts systemic vasoconstriction induced by renin angiotensin system activation facilitating vascular permeability and elastance. Due to its instability with plasma protein and short half life, a reliable quantification of ADM is difficult to achieve and its precursor mid regional pro- hormone (MRpro-ADM) is usually measured. [37] A large study conformaed the close relationship between ADM and congestion in patients with worseining heart failure, therefore high plasma level appears related to increased risk and recurrent hospitalization for HF. [38]MRpro-

ADM measured at admission is also related to all cause of cardiovascular mortality, sudden death and cardiac arrest. In patients with acute coronary syndrome (ACS) elevated MRpro-ADM levels predict the risk for HF occurrence. Finally in the PROTECT trial the MRproADM was related to longer hospitalization increased congestion signs and elevated NP levels, the assessment before discharge confers relevant prognostic information related to incomplete decongestion statuis and early rehospitalization risk.[40]

Extracellular Fibrosis-Collagen deposition and increased myocardial fibrosis are two relevant features in HFpEF. The more extensively analyzed biomarkers of this process are Galectin 3 and soluble ST2- Galectin -3 is a glycoprotein involved in many inflammatory and pro fibrotic processes as galactosidases family member, and it is synthetized by macrophage . [41] It directly increases fibroblast proliferation and fibrogenesis in animal models inducing myocardial and vascular stiffness. Its is also associated with renal dysfunction and LV remodelling.[42] Galectin-3 Inhibition attenuated myocardial fibrosis and induce a reverse remodelling by reduction of systemic overaload. [44] High Galectin 3 levels are associated with poor outcome in both patients with HFrEF and HFpEF. In patients with elevated levels, galectin is associated with other comorbidities such as hypertension and CKD and it is an useful markers for target therapy and risk stratification. [45] Therefore, changes in galectin 3 over time provide prognostic insights in patients with HFpEF.[46]

Soluble ST2 is another markers reflection myocardial fibrosis and it is overexpressed in HFrEF and HFpEF patients. It is primarily produced by myocardial cells, but also smooth muscle cells and endothelium are capable to synthetize the peptide in relation to congestion or pro fibrotic stimuli.[47] In HFpEF patients the addition of ST2 to NPs provide additive prognostic information, therefore higher ST2 phenotype indicated a more compromised diastolic dysfunction. [48,49] Notably a mataanalysis demonstrated that ST2 is capable to predict outcome indepentently on EF values.[50]

Matrix Metalloproteinases (MMP) and tissue inhibitor of metalloproteinases (TIMP) are two endopeptidases inducing extracellular collagen deposition reasonable accounted as biomarkers of fibrosis in HFpEF. [51] Collagenases is an enzyme family with different characteristics and may be considered in the context between collagen synthesis and collagen degradation. Elevated levels of MMP2 and MMP9 are related to increased risk in HFpEF but are increased also in HFrEF after myocardial infraction. [52]In the PARAGON trial high level of TIMP, a markers of impaired collagen degradation, is associated with increased event rate. [53]

Additional collagen biomarkers such as Pro collagen type I (PIP) and procollagen type III N-terminal peptide (PIINP), demonstrated a predictive role in high risk patients for HFpEF development. Both biomarkers reflect collagen increases deposition and turnover. They appear to be associated with extent of collagen deposition in myocardial biopsies. [54] However in cross sectional analysis showed contrasting results: in Framingham sub-study PIIINP was not associated with echocardiographic abnormalities, whereas in Cardiovascular Health Study it was associated with increased risk of incident HF. [55,56]

Inflammation-Systemic inflammation is a typical features of HFpEF, it reflects the immune response to cardiac remodelling, systemic vascular injury and underling triggers often associated with diseases such as metabolic syndrome diabetes chronic lung disease and anemia. [57] Inflammation can occur differently in every HFpEF phenotype and it can be analyzed by several biomarkers showed a positive association with outcome. C-Reactive protein is the wider analyzed markers and it is associated with increased risk in ACS and HF. A comparison study differentiating CRP between HFrEF and HFpEF demonstrated that in the latter it has a better prognostication, adding new information respect to NP. [58] CRP and pentraxin are significantly higher in acute HFpEF patienst compared to stable and they correlated with diastolic dysfunction degree. [59]CRP has a direct role in inducing complement and cytokine stimulation causing myocyte loss and endothelial dysfunction by NO production decrease. CRP increase is also related to immune response mediated by lymphocyte T and monocyte cells. Current immune- inflammatory status may trigger microvascular dysfunction by inducing endothelial permeability and adhesion molecules, and the increase of reactive oxygen species bioavailability. [60]

Grow differentiation factor 15 (GDF-15) is a member of cytokines and it belongs to transforming grow factor beta family. It is highly expressed in inflammatory chronuic diseases, lung, kidney, and cardiovascular diseases. [61] Since it integrates information from cardiac and systemic diseases it reflects the interplay among different apparatus, but it is not specific of CV diseases or HF. [62] Recent metanalysis demonstrated in patients with high risk burden it is related to increased incidence of HF providing additional informations on LV remodeling and function. [63] In HFpEF it is similarly elevated than HFrEF but it has additional prognostic power compared to NTproBNP. Indeed, subjects with low NTpro BNP levels and high GDF-15 values, the risk of cardiovascular death is comparable to those with high NP. [62] This finding confirm the role of GDF15 as intermediate markers of inflammatory and multi organ injury.

Intereleukin-6 (IL6) and interleukin 1ß (ILß) are the most famous members of citokyne family. They are produced by activated macrophages and they are involved in several inflammatory

and immunitary processes. [64] They contributes by direct myocites damage and indirect inflammatory burden elevation, to the cardiac damage and remodelling. Therefore cytokine mediated systemic inflammation impairs skeletal muscle metabolism and circulation. [65] Notably, the IL-1 inhibitor Anakinra, is capable to reduce hospitalization improving exercise tolerance in HFpEF. therefore the drug improves treadmill parameters and quality of life. [66]

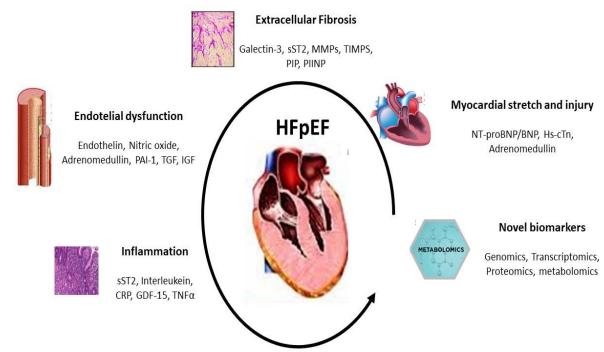
Tumor necrosis factor $\alpha(TNF)$ is another interleukin highly expressed in HFpEF, it correlates with adverse otcome in a cross sectional analysis.[67] However several confounding factors related to systemic immune system, may influence its levels. In stable HFpEF patients it correlates with atrial dimension and diastolic dysfunction degree, moreover it is additive compared with NP.In Health ABC study it correlates with HFpEF but it did not provide additional prognostic informations., finally anticitokyne treatment with specific antibody etanercept did not improve quality of life neither outcome. [68,69]

Endothelial dysfunction- microcirculation and endothelial cells are two important features for HFpEF occurrence, and microvascular dysfunction is one of the most therapeutic target. Dysfunctiona endothelium increases the expersion of adhesion molecules such as vascular cel adhesion molecules (VCAM) induced cell adhesion molecules (ICAM) and E selectin that activates von villerbrand and other pro thrombotic factors. Therefore Tissue grow factor (TGF) and Insulin grow factors (IGF) are other two items of vascular alteration and increased proliferation . [70] The pro thrombotic cascade is also emphasized by several coagulation alteration involving Factor V and VII, Tissue plasminogen activator (TPA), inducing endothelial damage and loss of vascular integrity. Current vascular, coagulative, and thrombotic alterations may lead to a progressive microvascular obstruction capillary obliteration and loss of capillary integrity. [71] These processes induce increased resistance and enhanced cardiac workload at systemic and pulmonary districts. Therefore vascular damage is characterized by intima media hyperplasia, disarray of smooth muscle cells, intimal fibrosis leading to progressive capillary reduction and narrowing. Current alterations reduces nitric oxide (NO) production and its mediator guanosine monophosphate cyclase (GMPc) causing vasoconstriction, reduction of viscoelastic properties, altered oxygen consumption and utilization with increased oxidative stress.[72,73] Unfortunately no reliable blood biomarker exist to measure these processes, and only in vitro studies can document these endothelial alterations. Nevertheless, a direct GMPc activator Vericiguat is capable to improve vascular tone and to reduce cardiac stiffness. A reliable marker of vascocntrictction and vascular tone is endothelin 1 (ET1) directly secreted by the endothelial cells in response to renin angiotensin system activation, hyperglicemia, hypertension and systemic inflammation. It is the most powerful vasoconstrictors

and is highly exporessed in pulmonary hypertension, severe hypertensive status and HF irrespective of EF.[74] Et-1 levels were predictive of all cause mortality and it was associated with increased hospitalization rate in a longitudinal study of HFpEF. [75] Therefore in a RELAX analysis ET1 correlates with reduced exercise oxygen consumption and significantly associate with hifghre NTproBNP and Galectin 3 levels. [76]

Plasminogen activator inhibitor (PAI-1) is the main inhibitor of tissue plasmimogen activator and intrinsic fibrinolytic system. It is increased in patients with HFpEF in association with D-dimer levels suggesting an association with pro thrombotic and procoagulant state in this setting. [77]In the LURIC study it is a prognostic index of mortality and CV events although a longitudinal study confirmed only an association with markers of renal damage and NP.[78]

Insulin grow factor binding (IGFBP) is associated with inflammation, cell adhesion and senescence. It is increased according to left atrial dysfunction and dilatation reflecting diastolic dysfunction in HFpEF. [79]In a machine learning study subjects with high inflammatory phenotype elevated comorbidity burden and renal dysfunction it is elevated and associated with increased hospitalization risk. [80]In I-PRESERVE trial IGFBP was associated with increased risk of CV events and HF severity.[81] Finally in asymptomatic patients with LV hypertrophy IGFBP identifies subjets with altered diastolic function suggesting a role in early identification and screening of HFpEF.[82] FIGURE 2 (graphical abstract)



Soluble ST2 (sST2), Matrix metalloproteinases (MMPs), Tissue inhibitors of metalloproteinases (TIMPs), Plasminogen activator inhibitor 1 (PAI-1), C-reactive protein (CRP), N-terminal pro-B-type natriuretic peptide (NT-proBNP), high-sensitivity cardiac troponin (hs-cTn), Pro collagen type I (PIP), procollagen type III N-terminal peptide (PIINP), Grow differentiation factor 15 (GDF-15), Tumor necrosis factor α (TNFα), Tissue grow factor (TGF), Insulin grow factors (IGF)

METABOLOMIC SIGNATURE

HFpEF is associated with indices of increased inflammation and oxidative stress, impaired lipid metabolism, increased collagen synthesis, and downregulated nitric oxide signaling. [83]. The most studied metabolites involved in the metabolic profile of HFpEF are serine, Lysophosphatidilcolyne (LPC), kynurenine and cystine, hydroxyproline, lactate, cGMP, symmetric dimethylarginine (SDMA), arginine, cAMP and acylcarnitine. [83]

In HFpEF mouse models, serine deficiency has been associated with inflammatory response and oxidative stress [84] Serine is a non-essential amino acid and has different physiological functions, including the immunoregulatory actions. Through one-carbon metabolism in macrophages, serine is critical for the generation of phospholipid, biosynthesis of purine and thymidine, and production of methyl donor of S-adenosyl-methionine (SAM) and cellular glutathione. Serine is essential for production of proinflammatory cytokines in M1 macrophages [85]. In the inflammatory process the activation of serine proteases induces a serine deficiency. Cathepsin G is another serine protease of PMN azurophile granules that hydrolyses several types of proteins. Cathepsin G exerting strong pro-inflammatory effects with vascular and systemic impact. [86] Elastase is the most involved serine protease contained in the azurophile granules of polymorphonuclear cells (PMN, or neutrophils). When discharged upon PMN activation elastase, it has a direct effects on the degradation of collagen, elastin and fibronectin. These processes could represent the potential basis of HFpEF development and strictly related to the reduced myocardial compliance with diastolic dysfunction and consequent LA dilatation. Similarly, few studies found a significant increase of hydroxyproline. It is produced by hydroxylation of proline by prolyl hydroxylase and have the role of stability of collagen and this dysregulation contribute to the myocardial fibrosis in HFpEF. [87,88]

In endothelial cells, NO is generated by endothelial nitric oxide synthase (eNOS) through the conversion of its substrate, L-arginine to L-citrulline. Arginine is known to act as a substrate for NO production by endothelial cells [89]. The lower levels of NO substrate arginine reflects higher concentrations of SDMA associated with worsening renal function and microvascular dysfunction reduced vasodilatory properties [90,91].

Activation of cGMP precursors via natriuretic peptide increase the cGMP levels and a subsequent protein-kinase G (PKG), [83]. Furthermore the cGMP/PKG signaling cascade phosphorylates many sarcomeric and cytosolic proteins. Downregulation of myocardial cGMP-PKG signalling in HFpEF is related to reduced myocardial brain-type NP (BNP) expression and

increased microvascular inflammation and oxidative stress, which impair both the NP-cGMP and NO-cGMP axes. Decreased levels of cGMP in HFpEF, and subsequently of PKG, were associated with increased resting tension and myocyte stiffness. This activation leads to Titin phosphorilation reduction that modulates passive stiffness of cardiac muscle that negatively affects passive diastolic distention. [92,1]

Another finding is high levels of cystine that is an indirect index of inflammation [93]. Cystine enters the cell and then is reduced to cysteine, which is involved in the synthesis of glutathione (GSH). Glutathione peroxidase 4 uses GSH as a substrate to scavenge lipid peroxidation and reduce oxidative stress. The important role of cysteine in maintaining and transducing redox signals in the mitochondria. [94] Redox-dependent cysteine modification has been studied most extensively in cardiac tissue following ischemia/reperfusion injury, which deprives cardiac tissue of oxygen in the ischemic state and generates a ROS burst. [95]

Kynurenine (Kyn) is a regulator of immune response, metabolized from tryptophan (Trp) during inflammatory conditions. [96]. The Kyn pathway of Trp is the most active process of Trp metabolism and produces metabolites including kynurenic acid and nicotinamide adenine dinucleotide (NAD+). Notable is the involvement of NAD+ in oxidative phosphorylation. The Kyn pathway is initiated by the enzymes tryptophan 2,3-dioxygenase (TDO) and indoleamine 2,3-dioxygenase (IDO and IDO2). Kyn is incressed in HFpEF and have a role in the regulation of inflammation response mediated through the function as a ligand of the aryl hydrocarbon receptor (AhR) and as a transcription factor that controls local and systemic immune responses.

cAMP is produced via β -AR signalling and inhibited via AMP-hydrolysing enzyme phosphodiesterases , at least 5 families expressed in the heart (PDE1, PDE2, PDE3, PDE4 and PDE8) Low cAMP levels in HFpEF suggesting impaired cell signaling. Disruptions in β -Adrenergic R microdomains in HFpEF, in the Obese individuals with type 2 diabetes heart exhibiting altered β -AR expression levels, blunted β -AR responsiveness and evidence of altered β 2-AR-coupled PDE activity [97] . Current signal cell dysregulation may alter both intracellular calcium (Ca) membrane signal, and myocyte energetic process linked to glycogenolysis and lipolysis.

Additionally, HFpEF patients displayed an elevated concentrations of medium and long-chain acylcarnitines [98]. The acyl derivatives play a key role in fatty acid uptake and mitochondrial metabolism, an increase in acylcarnitines may imply inefficient β -oxidation in HFpEF patients[99] Several reports have demonstrated the detrimental effects of long-chain

acylcarnitines, in this HF model because of pro-inflammatory and pro-arrhythmogenic activity [99, 100].

Low levels of lysophosphatidylcholine suggests a dysregulated phospholipid metabolism.[83] Lysophosphatidylcholine (LPC), also called lysolecithins, is a class of lipid biomolecule derived by the cleaving of phosphatidylcholine (PC) via the action of phospholipase A2 (PLA2). Phosphatidylcholine is required for assembly of VLDLs and chylomicrons. Moreover, small alterations in phospholipid levels appear to have large implications related to the metabolic syndrome and fatty acid oxidation signaling. [101]. Dysregulated lipid metabolism could drive to adipose accumulation around pericardium and muscle compartment. Also, circulating fatty acids impair insulin sensitivity through binding to the plasma membrane receptor Toll-like receptor 4 in tissues of obese animals. This process results in the activation of signaling proteins, such as inhibitor of nuclear factor- κ B kinase, c-Jun N-terminal kinase, and mitogen-activated protein kinase, that negatively dysregulate the metabolic axis of macrophage and favoring chronic inflammation. [102] TABLE 2

	Biomarkers	Altered Cell Mechanism
Increased inflammation	↓ Serine	immunoregulatory actions: essential for production of proinflammatory cytokines in M1 macrophages
	↑ Cathepsin G	stimulating the production of cytokines and chemokines.
	↑ Cystine	key player in conditions of oxidative stress
	↑ Kynurenine	controls local and systemic immune responses
Increased collagen syntesis and reduced myocardial compliance	↑ Hydroxyproline	role of stability of collagen and this dysregulation contribute to the myocardial fibrosis
	↑ Elastase	degradation of extracellular matrix components, including collagen, elastin and fibronectin
	↓ cGMP/PKG signaling	phosphorilation reduction associated to passive stiffness of cardiac muscle

Endothelial dysfunction	↓ Arginine	substrate for NO production by endothelial cells with reduced vasodilatory effects
	↑ SDMA	alternative methylation product of L- arginine associated with worsening renal function and microvascular dysfunction
Energetic impairment	↓cAMP	is produced via β-AR signalling
	↑ Acylcarnitine	imply inefficient β-oxidation
	↑ Tryptophan	produces metabolites including kynurenic acid and nicotinamide adenine dinucleotide
Metabolic lipides impairment	↓ Lysophosphatidylcholine	is required for assembly of VLDLs and chylomicrons
	↓ cAMP	involved in lipolysis

CIRCULATING MicroRNA EVIDENCES

The non coding genome which indicates small and long non coding RNA is involved in gene regulation. Multi-microRNA are 21-22 nucleotide single stranded RNAs that bind complementary messenger leading the degradation. They have been implicated in phathophisiologic processes that conduct to HFpEf. miRNA correlated with NT-proBNP are highly discriminatory and improved specificity and accuracy in identifying nonacute HF. [103] The subtype stratification, mir-24-3p has been reported to regulate apoptosis and vascularity in ischemic heart disease; mir-503-5p has been implicated in driving cardiomyocytes specification; miR-30a-5p has been shown to regulate autophagy during myocardial injury induced by Angiotensin II; and miR-106a-5p promotes hypertrophy through targeting mitofusin 2, a mitochondrial protein in regulating cardiac function. [104]. There are also pro-hypertrophic miRNAs, such as miR-208, miR-22, miR-21, miR-25, miR-34, miR-199a, miR-212/132, and miR-23. [105] miR-3135b and miR-3908 were significantly upregulated in HFpEF and are involved in metabolic regulators for serum lipids and blood glucose[106]. Certain circulating miRNA may serve as markers of response of therapy: Sucharov et al. identified a set of miRNAs (miRNA 208a-3p and miRNA-591) differentially expressed in HF patients who respond to beta-blockers therapy.[107] Despite increasing literature in this setting, there is no current consensus on the choice of a specific circulating miRNA serve as HFpEF biomarker. This is due to the lack of standardized methods, different population analyzed

and deficienty in multi center trials combining laboratory data in systematic methods with homogeneous analysis.

CONCLUSIONS

Since HFpEF is an heterogeneous syndrome characterized by multiple risk factors and several associated conditions, by the simple phenotypical classification is hard to distinguish the main pathophysiological driver. In this framework a detailed laboratory screening may better elucidate underlying mechanisms responsible for HFpEF appearance and evolution. Behind new and traditional biomarkers of inflammation, cardiovascular dysfunction and fibrosis, some emerging metabolites responsible for altered cell signals, energetic substrate, and excessive immune response revealed additional diagnostic properties. The challenge of future researches may systematically address the real value of clinical laboratory and metabolomic combination, to effectively initiate a precision medicine methodology.

FIGURES AND TABLES LEGEND

FIGURE 1: distinct HFpEF clinical phenotypes based on clinical presentation associated metabolic disorders and comorbidities

FIGURE 2: potential pathophysiological mechanisms occurring in HFpEF: each disorders can be recognized by specific biomarker increase and overexpression. The partnership between clinical and laboratory information may better target HFpEF profile

TABLE 1: Circulating biomarkers responsible for cardiac remodeling reflecting myocardial injury, collagen overexpression, inflammation, and vascular damage

TABLE 2: most common metabolomic pathways analyzed in HFpEF: different mechanisms suggest metabolic and energetic substrate alterations involving several cells including myocytes, macrophages, fibroblasts, and endothelium.

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