Distribution of mast cells within the mouse heart and its dependency on Mitf

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ABSTRACT

Although mast cell distribution has been described in both human and canine hearts, cardiac mast cells in mice have yet to be categorically localized. We therefore sought to describe mast cell distribution within the mouse heart and characterize their dependence on the Microphthalmia-associated transcription factor (Mitf). Cardiac mast cells were visualized using Toluidine Blue and avidin staining, and their distribution within the heart described. Cardiac mast cells were most prevalent in the epicardium (50%) or myocardium (45%). Less frequently, mast cells were noted in the endocardium (5%). Within the myocardium, 31% of the mast cells had perivascular location. By studying two different Mitf mutant strains, Mitfmi-vga9 and MitfMi-wh, we demonstrated that these mutations led to near-complete deficiency of cardiac mast cells. Accordingly, expression of the mMCP-4 and mMCP-5 genes was lost and chymase enzyme activity was severely reduced. Additionally, hearts from mice heterozygous for these Mitf mutations contained significantly fewer mast cells compared to wild-type mice. Our results demonstrated that the distribution of cardiac mast cells in mice is different from humans and dogs. Cardiac mast cells are dependent on Mitf expression, with loss-of-function mutation in the Mitf gene leading to near-complete lack of cardiac mast cells. Loss of a single Mitf allele is sufficient for relative mast cell deficiency.

1. Introduction

Mast cells are primarily known for their role in allergic and anaphylactic reactions. However, studies have demonstrated that mast cells have various other physiological and pathological effects in peripheral tissues, including the heart (da Silva et al., 2014). Mast cells play an important role in heart pathology and have been linked to various cardiovascular diseases such as atherosclerosis, myocardial ischemia, heart failure, and cardiac hypertrophy (Alevizos et al., 2014; Bot et al., 2015; Hara et al., 2002; Reid et al., 2007). Importantly, the role of mast cells differs depending on their location. This stems from the fact that mast cell progenitors migrate to peripheral tissues, through organ-specific migration pathways and it is the microenvironnent of these organs which stimulates mast cell differentiation (Gurish and Austen, 2012). In accordance with this, cardiac mast cells have been shown to differ functionally from other organ-specific mast cells (Patella et al., 1995). Whereas the distribution of cardiac mast cells has been described in humans and dogs (Frangogiannis et al., 1999; Hellstrom and Holmgren, 1950; Sperr et al., 1994), their distribution in mice is not well characterized. This is unfortunate, as the mouse is the most widely used genetic model of cardiac physiology and pathology.

Here, we describe the distribution of mast cells within the mouse heart and compare it with mast cell distribution in other mammalian species. The Microphthalmia-associated transcription factor (MITF) is a basic helix-loop-helix leucine zipper master regulator that plays a critical role in the development of many cell types, including mast cells (Hemesath et al., 1994; Steingrimsson et al., 2004). We examined whether hearts from mice carrying two different Mitf mutations (Mitfmi-vga9 and MitfMi-wh) are mast cell deficient, and whether this is gene dosage dependent.

2. Methods

2.1. Animal handling

C57BL/6-J, C57BL/6-Mitfmi-vga9 and C57BL/6-MitfMi-wh mice were housed and bred in the animal facility at the University of Iceland. The use of laboratory animals was approved by the Icelandic Food and Veterinary Authority (permit ID: 2013-03-01). Maintenance and handling of animals was performed in accordance with Icelandic and European legislation on animal welfare.

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2.2. Histological staining and analysis

Mice were sacrificed and hearts fixed in formalin. Subsequently, the hearts were embedded in paraffin and 4 μm thick sagittal sections obtained, mounted, and stained with Toluidine Blue and avidin to visualize cardiac mast cells.

For avidin staining, the tissue sections were deparaffinized by xylene and then rehydrated with ethanol twice for 5 minutes each. Next, the slides were incubated in citrate buffer (p = 6.0) for 20 min at 95° for antigen retrieval. After cooling, slides were treated with 10% fetal bovine serum for 1 h at room temperature (RT). Subsequently, sections were rinsed with immunofluorescence (IF) buffer containing 0.15 M NaCl, 5 mM EDTA, 20 mM HEPES, and 0.1% Triton X-100 (pH = 7.5). Sections were then stained with Alexa Fluor 488 conjugated avidin at the dilution of 1:500 (Invitrogen, Austin, TX) and counterstained with 4’,6-diamidino-2-phenylindole (DAPI) 1:5000 (Sigma, St. Louis, MO) diluted in IF buffer for 1 h at RT. Lastly, sections were rinsed twice with IF buffer for 5 min, once with distilled water, and coverslip added following dehydration.

For mast cell quantification, Toluidine Blue positive cells and avidin positive cells were counted in two whole sections from each heart. Using the Fiji software, area measurements were performed, and mast cells quantified as cells per mm² within different regions of the heart.

2.3. Enzyme activity assays

Mice were sacrificed and hearts snap frozen in liquid nitrogen. Frozen hearts were put in 1 mL of TrisHCl buffer containing 0.5 M NaCl and 1 mM EDTA (pH = 8.0) buffer along with 20 μL of aprotinin and pulverized at 2600 rpm for 30 s. Sonication was thereafter performed for 5 min, followed by centrifugation at 14,000 rpm for 10 min. The supernatant was collected for analysis. Bradford assay was performed to estimate protein amount and heart samples diluted in TrisHCl buffer, containing 0.5 M NaCl and 1 mM EDTA (pH = 8.0), to 2200 μg/mL (Bradford, 1976).

For chymase activity assay, a solution containing 29.7 μL of 11 mM Suc-AAPF (Sigma-Aldrich, St. Louis, MO) and 240 μL of TrisHCl buffer containing 0.5 M NaCl and 1 mM EDTA (pH = 8.0) was prepared for each sample and allowed to incubate for 10 min. Thereafter, 60 μL of sample was added and allowed to incubate for 10 min, before adding 20 μL of 10 mM chymostatin (Sigma-Aldrich) to stop the reaction. Lastly, solutions were transferred to a 96 well plate (using 90 μL triplicates from each sample) and absorbance measured at 405 nm using EMax Plus Microplate Reader (Molecular Devices, Sunnyvale, CA).

Phosphatase activity assay was performed according to manufacturer’s suggestions with some modifications (Sigma-Aldrich). Briefly, for each sample, 10 μL of 0.67 mM pNPP solution were added to 0.58 mL of diethanolamine buffer containing 0.50 mM magnesium chloride (pH = 9.8), and allowed to incubate at 37° for 10 min. Thereafter, 10 μL of sample was added and allowed to incubate for 10 min before the reaction was stopped by adding 3 M NaOH. Lastly, solutions were transferred to a 96 well plate (using 150 μL triplicates for each sample) and absorbance measured at 405 nm using EMax Plus Microplate Reader (Molecular Devices, Sunnyvale, CA).

2.4. Quantitative real-time PCR

For quantitative real-time PCR, mice were sacrificed and hearts snap frozen in liquid nitrogen. Hearts were pulverized twice at 2600 rpm for 30 s and RNA isolated according to protocol (Chomczynski and Sacchi, 1987). Next, cDNA was generated using Superscript II (Invitrogen) and oligo(dT) primer mix. Real time PCR was performed using Power SYBR Green PCR Master Mix (ThermoFisher Scientific, Waltham, MA). The following primers were used for amplification: Actin sense, 5’-CAG TGT CGA GTC GCG TCC-3’; Actin antisense, 5’-TCA ATG GCC AAC TGG TG-3’; Mitf sense, 5’-AGG AGC ATT GGC TAA AGA-3’; Mitf antisense, 3’-GCA TGT CTG GAT CAT TTG ACT-5’; mmC5P-4 sense, 5’-GCC AAA GAG ACT CCC TCT GTG ATT-3’; mmC5P-4 antisense, 3’-GCA TCT CGG CTT AGA ACA-5’; mmC5P-5 sense, 5’-CAC TGT GGC GGA AGG TCT ATA ACA-3’; mmC5P-5 antisense, 3’-TT ACT TCC TGC AGT GTG TCG GAG-5’.

2.5. Statistical analysis

All data are presented as mean ± SEM unless otherwise specified. The Wilcoxon test was used to compare differences between two groups. The Kruskal Wallis test was used to compare differences between multiple groups. The Conover test with Bonferroni correction was used as a post hoc test. All statistical tests were two-tailed and a P value less than 0.05 was considered significant.

3. Results

3.1. Distribution and localization of cardiac mast cells

To describe the location of mast cells within the heart, sagittal sections from wild-type (C57BL/6 J) mouse hearts were obtained and stained with Toluidine Blue in order to visualize mast cells. Mast cells were quantified in the epicardium, myocardium, and endocardium of the left and right ventricles and atria. Mast cells found within the heart valves, aorta, pulmonary vessels, and the fibrous and parietal pericardium were excluded from quantification since these were not consistently present in the samples. The majority of mast cells were located in the epicardium (Fig. 1a, e) or within the interstitium of the myocardium (Fig. 1b, f). They were less frequently observed within c) the endocardium or d) the myocardium. Mast cells were less frequently found within the adventitia of myocardial arteries or venules (Fig. 1d, h). Within the myocardium, 31% of the mast cells had perivascular location (Table 1).

When adjusted for area, mast cell density was more than twelvefold higher in the epicardium than in the myocardium or endocardium.

![Fig. 1. Distribution of mast cells within the mouse heart](image-url)
which had similar mast cell densities (8.29 ± 0.59 cells/mm² vs 0.52 ± 0.10 cells/mm²) as compared to the left ventricle (2.10 ± 0.25 cells/mm² vs 0.01 ± 0.001 mast cells/mm², p = 0.10). Interestingly, the number of mast cells found in Mifu-vga9 homozygous mice was reduced by half as compared to wild-type hearts (0.54 ± 0.07 mast cells/mm² vs 1.06 ± 0.06 mast cells/mm², p < 0.001) (Fig. 2a). Mifu-vga9 mutants had approximately two thirds of the number of mast cells found in wild type hearts (0.71 ± 0.07 mast cells/mm² vs 1.06 ± 0.06 mast cells/mm², p = 0.04). To confirm the reduction in mast cell numbers in Mifu mutants, we performed avidin staining on Mifu-vga9 hetero- and homozygotes. Consistently, avidin staining demonstrated near absence of cardiac mast cells in Mifu-vga9 homozygotes (0.01 ± 0.01 mast cells/mm²), and relative reduction in mast cell numbers in Mifu-vga9 heterozygotes compared to wild-type hearts (0.52 ± 0.08 mast cells/mm² vs 1.08 ± 0.35 mast cells/mm², p = 0.04) (Fig. 2b, d). Taken together, this demonstrates that Mifu is necessary for normal cardiac mast cell numbers and that a single mutant allele is sufficient for relative mast cell deficiency.

To estimate whether the reduced numbers of cardiac mast cells in heterozygotes affected the distribution of mast cells within the heart, we compared the mast cell distribution within different regions of the heart between wild-type, Mifu-vga9/+ , and Mifu-vga9/+ heterozygotes. The mast cell distribution was generally similar in the three genotypes. However, the percentage of mast cells found in the septum of Mifu-vga9/+ heterozygotes was significantly reduced compared to wild-type mice (p = 0.03) (Table 1).

### 3.3. Chymase activity and expression is absent from Mifu mutant hearts

Chymase is a mast cell-specific serine protease that is commonly used as a mast cell marker (Craig and Schwartz, 1989). Humans have a single chymase gene, whereas mice have five. Real-time PCR was performed to determine the expression of mMCP-4 and mMCP-5, the two mouse chymases that are functionally and structurally closest to the human chymase, respectively (Pejler et al., 2010). Our results demonstrated severely reduced expression of both mMCP-4 and mMCP-5 in homozygous Mifu-vga9 hearts compared to wild-type hearts (p < 0.001 for both genes) (Fig. 3a,b). Additionally, mMCP-5 expression in heterozygous Mifu-vga9 hearts was significantly lower than in wild-type hearts (p = 0.015). Similarly, mMCP-4 trended towards lower expression in heterozygotes compared to wild-type hearts (p = 0.11). Consistent with the effects of the Mifu-vga9 mutation, expression of Mifu in the heart was absent from homozygotes and reduced to approximately 40% in heterozygotes as compared to wild type mice (Fig. 3c).

Chymase enzymatic activity was determined to evaluate whether reduced chymase expression led to reduced functional activity of the enzyme. Our results demonstrated that chymase activity was severely reduced in Mifu-vga9/Mifu-vga9 hearts (Fig. 3d). Although chymase activity was also reduced in heterozygotes, the difference was not statistically significant. Alkaline phosphatase activity was used as a control measurement and no differences were observed between the three groups (Fig. 3e). We conclude that there is a near-complete loss of mature mast cells and mast-cell specific chymase in Mifu-vga9 mutant mice.

### 4. Discussion

Mast cells have been linked to various cardiovascular diseases (Reid et al., 2007). Here we demonstrate that mast cell distribution is

**Table 1** Mast Cell Distribution in Wild-Type and Heterozygous Mifu Mutant Hearts.

| Location       | Proportion of total mast cells (%)a |
|----------------|-----------------------------------|
|                | WT (n = 21) | Mifu-vga9/+ (n = 5) | Mifu-vga9/+- (n = 17) |
| Epicardium     | 50 ± 2     | 55 ± 5              | 56 ± 4               |
| Myocardium     | 45 ± 2     | 43 ± 5              | 40 ± 4               |
| Intersitial     | 69 ± 4     | 80 ± 7              | 75 ± 4               |
| Perivascular    | 31 ± 4     | 20 ± 7              | 25 ± 4               |
| Endocardium    | 5 ± 1      | 3 ± 2               | 4 ± 1                |
| Atria          | 8 ± 2      | 11 ± 5              | 8 ± 3                |
| Left ventricle  | 54 ± 3     | 59 ± 4              | 54 ± 4               |
| Right ventricle | 24 ± 2     | 31 ± 4              | 29 ± 2               |
| Septum         | 14 ± 2     | 13 ± 2              | 9 ± 3                |

Asterisks denote statistical significance at P < 0.05 (*) compared to wild-type mice.

a The mast cell proportion is calculated as the number of mast cells in a measurement and no differences were observed between the three groups (Table 1).

**Table 2** Mast Cell Density in Wild-Type Hearts.

| Location       | Density (n = 21) |
|----------------|-----------------|
| Epicardium     | 8.29 ± 0.59     |
| Myocardium     | 0.56 ± 0.05     |
| Endocardium    | 0.64 ± 0.09     |
| Atria          | 2.40 ± 0.46     |
| Left ventricle | 1.09 ± 0.09     |
| Right ventricle| 2.10 ± 0.25     |
| Septum         | 0.52 ± 0.10     |

Mast cell density is given as mast cells per mm².

which had similar mast cell densities (8.29 ± 0.59 cells/mm² vs 0.56 ± 0.05 cells/mm² and 0.64 ± 0.09 cells/mm² respectively) (Table 2). When looking at the different chambers of the heart, mast cell density was significantly higher in the atria as compared to the ventricles (2.40 ± 0.46 cells/mm² vs 1.03 ± 0.06 cells/mm², p = 0.03). Furthermore, mast cell density was lowest in the septum (0.52 ± 0.10 cells/mm²), and significantly higher in the right ventricle as compared to the left ventricle (2.10 ± 0.25 cells/mm² vs 1.09 ± 0.09 cells/mm², p < 0.001) (Table 2).

To confirm our findings, histological staining was performed using avidin, a marker that has been demonstrated to bind mast cell granules specifically (Tharp et al., 1985). Consistently, quantification of avidin positive cells demonstrated similar mast cell distribution as described above (Suppl. Table 1).

**3.2. Mifu mutation leads to cardiac mast cell deficiency**

Microphthalmia-associated Transcription Factor (MITF) is a basic helix-loop-helix leucine zipper master regulator that plays a critical role in mast cell differentiation (Qi et al., 2013). To assess the effects of Mifu mutation on mast cell numbers in the heart we studied cardiac mast cells in two different Mifu mutant alleles, Mifu-vga9 and Mifu-vga9. Sagittal sections from hearts of wild-type (C57BL/6J) mice as well as hetero- and homozygous B6-Mifu-vga9 and B6-Mifu-vga9 mutant mice were examined. The Mifu-vga9 mutant allele contains a transgene insertion resulting in severely reduced expression of the Mifu mRNA (Hodgkinson et al., 1993; Kataoka et al., 2002). The Mifu-vga9 mutant allele contains a point mutation that affects DNA binding but had little effect on Mifu expression (Kataoka et al., 2002; Steingrimsson et al., 1994). Homozygotes carrying the Mifu-vga9 mutation are characterized by the absence of mast cells in the peritoneum, mesentery, and stomach. Additionally, mast cell numbers in the skin are reduced to one third of the number observed in the skin of wild type mice (Kataoka et al., 2002; Morii et al., 2004a). Cardiac mast cells were near absent from Mifu-vga9 and Mifu-vga9 homozygous mice and significantly fewer than in both heterozygotes for each mutation and wild-type (Fig. 2a,c). Mice homozygous for the Mifu-vga9 mutation trended towards higher mast cell numbers than Mifu-vga9 homozygous mice (0.09 ± 0.03 mast cells/mm² vs 0.001 ± 0.001 mast cells/mm², p = 0.10). Interestingly, the number of mast cells found in Mifu-vga9/+ heterozygous hearts was reduced by half as compared to wild-type hearts (0.54 ± 0.07 mast cells/mm² vs 1.06 ± 0.06 mast cells/mm², p < 0.001) (Fig. 2a). Mifu-vga9/+ heterozygotes had approximately two thirds of the number of mast cells found in wild type hearts (0.71 ± 0.07 mast cells/mm² vs 1.06 ± 0.06 mast cells/mm², p = 0.04). To confirm the reduction in mast cell numbers in Mifu mutants, we performed avidin staining on Mifu-vga9 hetero- and homozygotes. Consistently, avidin staining demonstrated near absence of cardiac mast cells in Mifu-vga9 homozygotes (0.01 ± 0.01 mast cells/mm²), and relative reduction in mast cell numbers in Mifu-vga9 heterozygotes compared to wild-type hearts (0.52 ± 0.08 mast cells/mm² vs 1.08 ± 0.35 mast cells/mm², p = 0.04) (Fig. 2b, d). Taken together, this demonstrates that Mifu is necessary for normal cardiac mast cell numbers and that a single mutant allele is sufficient for relative mast cell deficiency.

To estimate whether the reduced numbers of cardiac mast cells in heterozygotes affected the distribution of mast cells within the heart, we compared the mast cell distribution within different regions of the heart between wild-type, Mifu-vga9/+ , and Mifu-vga9/+ heterozygotes. The mast cell distribution was generally similar in the three genotypes. However, the percentage of mast cells found in the septum of Mifu-vga9/+ heterozygotes was significantly reduced compared to wild-type mice (p = 0.03) (Table 1).
different in mouse hearts, compared to humans. This is important as the mouse remains the most widely used genetic model of human physiology and pathology. Although the distribution of cardiac mast cells has been described in humans and dogs (Frangogiannis et al., 1999; Hellstrom and Holmgren, 1950; Sperr et al., 1994), this is to our best knowledge the first time that mast cell distribution has been categorically described in mouse hearts. Cardiac mast cells in mice are most prominent within the epicardium (50%) and the myocardium (45%). They are less frequently found within the endocardium (5%). When adjusted for area, mast cell density is highest in the epicardium, whereas it is lower but similar in the myocardium and the endocardium. The high density of epicardial mast cells is interesting since it has not been described in other mammalian species. Although epicardial mast cell numbers in rats trend towards higher numbers compared to the endocardium (Facoetti et al., 2006), the difference in mice is twofold. Epicardial mast cells have also been described in humans but there have not been quantified (Sperr et al., 1994). The mouse myocardium and endocardium have approximately equal mast cell densities, similar to human and canine hearts (Frangogiannis et al., 1999; Sperr et al., 1994). Mast cell density in mice was found to be significantly higher in atrial appendages compared to ventricles. This is similar to humans but differs from dogs which have equal atrial and ventricular densities (Frangogiannis et al., 1999; Sperr et al., 1994). Taken together, this suggests that mast cell distribution is different between mammalian species.

When looking at the different chambers of the heart, mast cell density was greatest in the atria, followed by the right ventricle, left ventricle, and interventricular septum in descending order. Since the bulk of cardiac mast cells are located epicardially, this order is likely due to higher proportion of epicardium within these regions of the heart. Mast cell distribution is important as mast cells play a role in regulating cardiac function, such as the release of mediators that can affect cardiac contractility and remodeling (Sperr et al., 1994).
heart. Supporting this, the septum, which has no overlying epicardium, has similar mast cell density as both the myocardium and endocardium. In the current study, perivascular mast cells were defined as those found within the adventitia of myocardial arteries or venules. We found that 31% of mouse mast cells residing in the myocardium have periarteriolar or perivenular location. For comparison, while 49% of canine cardiac mast cells have been described as perivascular, 27% had periarteriolar or perivenular location, which is consistent with our results.

In order to establish the role of cardiac mast cells in heart pathology it is important to establish diverse models of cardiac mast cell deficiency. Currently, only Kit-mutant and Cre/loxP-based mouse models are available (Feyerabend et al., 2011; Kitamura et al., 1978). Although Mitf mutant mice have been shown to have reduced numbers of mast cells in both the peritoneum and the skin (Jippo et al., 2003; Kataoka et al., 2002), the effect of Mitf in cardiac mast cells has not been documented previously. Here we report that cardiac mast cells are Mitf dependent and suggest that Mitf mutant mice may be a suitable model for investigating mast cell function in the heart. In the current study, mast cell deficiency in Mitf mutant hearts was demonstrated by Toluidine Blue and avidin staining, and by loss of mast cell-specific chymase activity.

This demonstrates that Mitf+/− and Mitf+ mice have normal mast cell numbers as opposed to Mitf−/− mice which have reduced numbers (Kataoka et al., 2002). In addition to guiding mast cell differentiation, MITF regulates the expression of many mast cell-specific genes, including chymes. Chymase is an angiotensin II-forming serine protease that is secreted from mast cells following acute or chronic stimuli. In the Mitf−/− mouse heart both chymase expression and enzymatic activity is lost, as expected. Additionally, hearts from Mitf+/− heterozygotes have both reduced numbers of cardiac mast cells and reduced chymase expression compared to wild-type hearts. This suggests that both alleles of Mitf are required for normal cardiac mast cell numbers. Since Mitf plays a key role in mast cell development, the loss of cardiac mast cells in Mitf mutants is likely due to failure of mast cell differentiation. Alternatively, it may be explained by defective migration. As mast cell precursor cells migrate from the bone marrow and differentiate in their target environment, it is possible that the local environment secretes cardiac mast cell localization. Supporting this, Mitf is not only expressed in mast cells in the heart, but also cardiomyocytes and valvular melanocytes (Tshori et al., 2007; Yajima and Larue, 2008). A study examining the role of Mitf in mast cell development demonstrated that bone marrow transplantation from a wild-type host to an Mitf−/− homozygote recipient led to reduced mast cell density in skin, peritoneum, mesentery, stomach, and spleen. Interestingly, transplantation of Mitf−/− homozygous bone marrow cells to W/Wv mice, a strain with mast cell deficiency but normal tissue environment, also led to reduced mast cell density (Mori et al., 2004b). Consistently, the cardiac mast cell deficiency observed in our study may be due to combination of both defective intracellular pathways in mast cell precursor cells and changes in the local environment.

The loss of cardiac mast cells and chymase activity has major implications for heart pathology. Chymase, angiotensin I converting enzyme (ACE), and cathepsin G all degrade Angiotensin I (Ang I) to...
Angiotensin II (Ang II). In the blood, circulating serine protease inhibitors restrict chymase and cathepsin G activity (Tojo and Urata, 2013). Ang II formation is therefore mostly contributed by ACE activity in the blood, while chymase seems to be the principal Ang II forming enzyme in the heart (Urata et al., 1993). Mast cell-derived chymase has been linked to a role in various cardiovascular diseases, such as atherosclerosis, arrhythmias, heart failure, and hypertrophy (Reid et al., 2007). As well as being the key Ang II-forming enzyme in the heart, chymase directly induces activation of TGF-β (Lindstedt et al., 2001). TGF-β has been shown to be a downstream mediator of Ang II-induced cardiac hypertrophy (Schultz et al., 2002). Furthermore, chymase induces extracellular matrix degradation, cardiomyocyte apoptosis, and fibroblast proliferation (Hara et al., 1999; Janicki et al., 2006). These are all key characteristics in hypertrophy of failing hearts. Cardiac hypertrophy occurs in response to increased cardiac load. Interestingly, Mitf is required for cardiac hypertrophy in response to β-adrenergic or Ang II stimulation in mice, and Mitf mutant hearts fail to appropriately respond to these hypertrophic stimuli (Liu et al., 2014; Tshori et al., 2006). There is added complexity due to the fact that in the heart Mitf is not only expressed in mast cells but in cardiomyocytes as well. In fact, Mitf has been shown to induce cardiac hypertrophy through negatively regulating miR-541 expression in cardiomyocytes (Liu et al., 2014). This hypertrophic response was induced by Ang II treatment, which, as stated above, is primarily generated by chymase (Urata et al., 1993). Based on the complete loss of chymase activity in the MitfM115fsXp11 mutant heart we suggest that the role of Mitf in inducing cardiac hypertrophy is, at least in part, mast cell and cardiac dependent.

Our results must be interpreted in the context of several limitations. First, as mast cell differentiation in their target environment, we cannot exclude the possibility that cardiac mast cell progenitor cells, that do not contain granules or express the major mast cell proteases, may be present in Mitf mutant mice. If so, they are unlikely to be functional as mast cells. Second, all quantification and distribution measurements were acquired using sagittal sections. It is possible that mast cell localization differs in lateral sections. Whole mount staining may be performed for better visualization of mast cells within the whole heart. Lastly, our distribution analysis was gathered by studying C57BL/6J mice, the most commonly used inbred mouse strain. Further analysis of different mouse strains is needed to determine whether the distribution observed is specific to the C57BL/6J strain.

5. Conclusions

Our results demonstrate that the distribution of cardiac mast cells in mice is different from humans and dogs. This is particularly important since mice remain the most widely used animal model for cardiac pathologies and physiology. The different cellular composition of mammalian hearts must be considered when basic research from animal models is translated to clinical settings. In addition, we demonstrate that cardiac mast cells are Mitf dependent, with loss-of-function mutation in the Mitf gene leading to near-complete lack of mature cardiac mast cells.

Disclosures

The authors report no conflicts of interest.

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Appendix A. Supplementary data

Supplementary material related to this article can be found, in the online version, at doi:https://doi.org/10.1016/j.molimm.2018.11.009.

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