Summary

The **aim** of this work was the **proteomic analysis of the heart** to characterize the **influence of development, age, sex, genetic variance and senescence** (two mice strains with different life spans) on protein patterns of mice.

The age specific protein expression was studied throughout the whole life span of C57BL/6 mice, including embryonic, time of birth, postnatal and adult stages. A number of protein spots showed increased/decreased and present/absent profiles throughout these stages. Followingly, spot differences for each stage were characterized: 1. embryonic stage, 37 spots (1, 2 %) 2. time of birth, 104 spots (3, 4 %) 3. postnatal stage, 101 spots (3, 3 %) 3. adult stage, 86 spots (2, 8 %). At the time of birth for example 68 spots showed an increased profile and 60 spots in the postnatal stage showed a decreased profile. Proteins from the adult stage, 43 spots, and the time of birth, 49 spots, were identified by mass spectrometry. Nine proteins were present in both stages (birth: 16 spots; adult: 12 spots). The other proteins differed between adult stage (31 spots) and the time of birth (33 spots). Concluding that the proteins of these stages differed in protein expression, identity and function through various influences (time of birth: Accomodation intrauterine/extrauterine; adult stage: environmental influence, increase level of reactive oxgen species).

Moreover, six spots were identified as peroxiredoxin 2. With help of literature these spots were associated to be oxidatively modified. Three of these spots were only present throughout the embryonic stage until birth. Therefore, a correlation to an important redox regulation against reactive oxygen species (maternal transfer) of peroxiredoxin 2 was associated with the embryonic stagees including the time of birth.

The investigations with regards to sex specific protein spots were carried out for protein patterns of C57BL/6 and DBA/2 mice. The following spot differences were observed: C57BL/6, 29 spots; DBA/2, 20 spots. In the protein patterns of male mice four conspicious proteins classified as apolipoproteins. In some cases were detected as a series of spots. ApoJ (3 spots), ApoA2 (2 spots) and ApoE were exclusively observed within male protein patterns. ApoA4 (3 spots) showed an increased appearance in the male mice.

Furthermore, three protein spots of α1- Antitrypsin (1-1,1-3,1-5) showed a sex and age specific performance in C57BL/6 mice (14 and 100 weeks). The age and sex specific performance of α1- Antitrypsin was associated with the multifarious functions.

In another experiment we examined the influence of genetic variance on protein profiles. We elaborated 160 protein polymorphisms between the two suitable strains *Mus musculus* and *Mus spretus* (14 weeks). Moreover these elaborated protein polymorphisms were compared with the sex and age specific protein spots. Four sex specific spots (DBA/2) showed an appearance as protein polymorphisms. The sex specific proteins of the C57BL/6 mice were not polymorphic. In the case of the age specific proteins 16 spots were polymorphic.

In the last experiment we investigated the influence of differently life spans on protein patterns. The two mouse strains DBA/2 (100 weeks) and DBA/1J (approximately 60 weeks) were examined. A number of 31 spot changes were observed in this comparative study. A concspicuous intensity and volume of a single spot stuck out in the DBA/1J mice. This increased spot was identified by mass spectrometry as a mix of NADH dehydrogenase and NADH oxidoreductase. Both were a source for reactive oxygen species. Drawing a conclusion, these facts emphasized a relationship between reactive oxygen species and ageing in these mouse strains with different life spans.

In general proteome analysis allows separating thousand of proteins. Moreover, it provides the opportunity to find these proteins, which play a critical role in processes like ageing and gender differentation. These results may be regarded as a foundation for further investigations on the appearance of age and sex specific diseases and pathological mechanisms.