Abstract

We can find a whole range of morphological differences between the spermatozoa of

different animal species, whether at the level of shape, size or intracellular arrangement. It

has been proven that these differences are likely to be driven by selective pressure caused

by sperm competition. This can cause morphological adaptations that give sperm a selective

advantage and increase the individual's success in fertilization. The main goal of my diploma

thesis was to determine whether individual morphological variability of spermatozoa is

detectable at the proteome level and possibly to determine what changes at the proteome

level occur in spermatozoa with changing morphology.

Three species of rodents, Mus musculus, Apodemus flavicollis and Microtus arvalis,

were selected for this study, and a thorough morphometric measurement of their sperm was

performed. Because the greatest variation was detected in the dimensions of the apical hook,

only acrosomal proteins were analyzed by mass spectrometry, and then the proteins that

distinguished the most sperm with long and short apical hooks were determined by

discriminant analysis and machine learning methods.

A significant trend among sperm-separating proteins with short and long apical

hooks, regardless of species, has been identified for proteins involved predominantly in

sugar metabolism and energy production. These include the FBP1, PGAM2, SORD and

PPP1CC proteins. No significant differences in the function of the most discriminating

proteins were found between species. Main differences was found between sperm with long

and short apical hooks, and the trend between these proteins is the same for all species we

have studied. It can be concluded that sperm with a longer apical hook have more metabolic

proteins generated during spermatogenesis.

Key words: sperm, sperm morphology, sperm competition, acrosome