Analysis of protein expression changes of rat plasma
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As the main difference in levels of plasma proteins is predominantly due to illness, circulating and specific proteins can be used for the diagnosis and prognosis of specific diseases. A comprehensive analysis of high-level proteins is the goal of proteomics. The aim of this study was to compare gels obtained from plasma (pool, strips with pH 4-7, polyacrylamide gels at 10% w/v) and to analyze changes in the expression of proteins of normal (G1), diabetic (G2) and diabetic treated with insulin (G3) rats (n=8/group) by two-dimensional electrophoresis. For the image analysis, it was found that the protein spots for both experimental groups were more concentrated in the range of 31-76 kDa and pI of 5-6; 251 spots were found in G1, 300 in G2 and 227 in G3; with a percentual matching of 77, 84 and 85% respectively (between eight replicates of gels of the same experimental groups). The estimated correlations between the protein spots of different experimental groups, considering normalized volume; were G1 and G2 (R>0.78), G1 and G3 (R>0.87), and the gels G2 and G3 (R>0.67). For changes in the protein expression, we considered relevant for this study a value of 95% (ANOVA). The differential analysis indicated 149, 175 and 143 coincident spots and difference in expression (p<0.05) of 13, 10 and 18 spots when groups G1xG2, G1xG3 and G2xG3 were compared, respectively. The next step to be taken with the plasma proteins is their characterization by mass spectrometry, which will permit the interpretation and discussion of all the results obtained.

Biography
Felipe Carlos Spereski Sperotto graduated from the Federal University of Mato Grosso, Brazil in 2011. Currently is a Master graduate in Agronomy (Energy in Agriculture) at the UNESP, Brazil.

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