### Detailed description of the applied statistical calculations for the analysis of amplitude curves

The k = 201 single time points of the time-normalized SEMG data had to be individually compared among the respective groups. Let x = (xk1, …, xk201) and y = (yk1, …, yk201) denote the two vectors (groups) to be compared and (µxk1, …, µxk201) and (µyk1, …, µyk201) be the respective means. The calculated p values for the rejection of the null hypotheses Hk1: µxk1 = µyk1, …, Hk201: µxk201 = µyk201 were ranked in ascending order where H1 denotes the smallest and H201 the largest p level. The p value for the rejection of each individual null hypothesis was then compared to its required α level (e.g., α1/k (0.05/201 = 0.000249) for H1; α2/(k-1) (0.05/200 = 0.00025) for H2 etc.). As long as a given p was smaller than its required α level, the respective null hypothesis was rejected and the algorithm continued until p exceeded the required α level. At this point, the differences among the different groups were no longer considered statistically significant.