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A kinematic analysis for shoulder and pelvis coordination in subjects with and without recurrent low back pain

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Aim: This presentation is to compare the shoulder and pelvis kinematics based on range of motion (ROM), angular velocity, and relative phase (RP) values during trunk axial rotation.

Materials & Methods: Nineteen subjects with recurrent low back pain (LBP) and 19 age-matched control subjects who are all right limb dominant participated in this study. All participants were asked to perform axial trunk rotation activities at a self-selected speed to the end of maximum range in standing position. The outcome measures included ROM, angular velocity, and RP on the shoulder and pelvis in the transverse plane and were analyzed based on the demographic characteristics between groups.

Results: The LBP group demonstrated decreased ROM ($p=0.02$) and angular velocity ($p=0.02$) for the pelvis; however, there was no group difference for the shoulder girdle. The ROM difference between the shoulder and pelvic transverse planes had a significant interaction with age ($F=14.75$, $p=0.001$). The LBP group demonstrated a higher negative correlation between the shoulder ($r=-0.74$, $p=0.001$) and pelvis ($r=-0.72$, $p=0.001$) as age increased while no significant correlations were found in the control group.

Conclusion: The results of this study indicated that there was a difference in pelvic rotation in the transverse plane between groups during axial trunk rotation. This pattern of trunk movement decreased due to possible pelvic stiffness with neuromuscular constraints. Since subjects with recurrent LBP demonstrated decreased pelvic rotation compared to the shoulder for postural control, increased pelvic flexibility could enhance coordinated movement patterns in order to integrate spinal motion in subjects with recurrent LBP.

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A network connecting miR-23a cluster and HOXA class factors regulate osteogenesis

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Studies of HOXA class genes have indicated their importance in skeletogenesis, but their regulation by specific miRNA in bone formation and homeostasis are incompletely defined. miRNA regulation contributes to every step of osteogenesis, including differentiation, skeletal patterning and homeostasis. We recently identified miRNA-23a cluster as a potential repressor of osteoblast maturation by targeting Runx2 and Satb2. In our study there is very strong evidence that miR-23a cluster is likely to regulate osteogenesis. Here we have established a mechanism where miR-23a cluster silenced Hoxa5, Hoxa10 and Hoxa11-mediated gene activation and also identified epigenetic changes associated with poor maturation and mineralization of osteoblasts. Among 11 HOXA class proteins, miR-23 a cluster directly targeted Hoxa5, Hoxa10 and Hoxa11 and decreased their expression. HOXA5, HOXA10 and HOXA11 are all interacted physically and functionally with RUNX2, to regulate tissue-specific promoter activity. Over-expression of miR-23 a cluster reduced while knock-down increased the recruitment of HOXA5, HOXA10 and HOXA11 to Runx2, Ocn, and Alp promoters and epigenetically control HOXA5 and HOXA11-facilitated chromatin remodeling. Targeted depletion of HoxA5 and HoxA11 by short hairpin RNA (shRNA) decreased expression of osteoblast-related genes while increased SIBLING protein osteopontin. Taken together, our results provide novel molecular evidence that miR-23a cluster and target HOXA5 and A11 functions in mi RNA-epigenetic regulatory network to control osteogenesis. Therefore, the analysis of this miR-23a cluster knockdown mouse model and supportive epigenetic changes by HOXA5, HOXA10 and HOXA11 will dramatically enrich our understanding of this newly recognized level of gene regulation in bone formation.

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